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AF421380 Homo sapi

AF279145 Homo sapi

BC012074 Homo sapi

AF001463 Homo sapi

AK005429 Homo sapi

AK001463 Homo sapi

AK001207 Homo sapi

AK002160 Homo sapi

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AC10518 Homo sapi

AC105612 Rattus no

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HOmor Saprens anthrax toxin receptor mRNA, complete cds.
AF421380
AF421380.1 GI:16566412
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2 (bases 1 to 1414)
Bradley,K.A., Mogridge,J., Mourez,M., Collier,R.J. and Young,J.A.T.
Direct Submission
Submitted (19-SEP-2001) Department of Oncology, University of
Wisconsin-Madison, 1400 University Ave., Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1414)
Bradley,K.A., Mogridge,J., Mourez,M., Collier,R.J. and Young,J.A.T.. Identification of the cellular receptor for anthrax toxin Mature 414 (6860), 225-229 (2001)
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Post-processing:

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1 (bases 1 to 5540)
25. Crolix, B., Rago, C., Velculescu, V., Traverso, G., Romans, K. E., Montgomery, E., Lal, A., Riggins, G.J., Lengauer, C., Vogelstein, B. ar Kinzler, K.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       St. Croix, B., Vogelstein, B. and Kinzler, K.W.

St. Croix, B., Vogelstein, B. and Kinzler, K.W.

Direct Submission

Lybring (16-JUN-2000) Johns Hopkins Oncology Center, Johns Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, USA Bases 1 to 5540)

S. St. Croix, B., Vogelstein, B. and Kinzler, K.W.

Direct Submission

Lybring (09-MAY-2001) Johns Hopkins Oncology Center, Johns Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, USA Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, USA Sequence update by submitter

On May 9, 2001 this sequence version replaced gi:9857405.
                                                                                                                                                                                                                    precursor (TEM8) mRNA,
                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes expressed in human tumor endothellum Science 289 (5482), 1197-1202 (2000)
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Homo sapiens tumor endothelial marker 8 l
complete cds.
AF279145.2 GI:14017380
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/db_xref="taxon:9606"
/chromosome="4"
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RQGLEELQKVLPGGDTYMHEGFERASBQIYYENROGYRTASVIIALTDGELHBDLFFY
SERBANKSRDGAIYYCOWRONFOTOLARIADSKDHVFYNNDGFQALQGIIHSILKK
SCIEILAAEPSTIGAGESFQVWVRGNGFRHARNVDRVLCSFKINDSVTLNBKPFSVED
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/db_xref="GI:16566413"
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SCIELLAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNERFFSVED
TYLLCPPALILKEVGMRAALGYSNNGGLFFISSSVITTTHTGSGSILAALLILLLL
ALALLWWFWPLCCTYLIKEVGRARANARVKMPEQEXEFDEPRNLNNNMRRPSSPRKWTSPI
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Pred. No. 0;
0; Mismatches
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/gene="TEM8"
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/gene="TEM8"
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Best Local Similarity 99.8%;
Matches 1092; Conservative
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PRI 06-AUG-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2112)
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Submitted (02-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                   840
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                                                                                                       923
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BC012074
BC012074.1 GI:15082332
                                                                                                                                            atcgaaattctagcagctgaaccatccaccatatgtgcaggagagtcatttcaagttgtc
                   gtgagaggaascggcttccgacatgcccgcaacgtggacagggtcctctgcagcttcaag
                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

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Carson Walter, E. B., Watkins, D. N., Nanda, A., Vogelstein, B., Kinzler, K. W. and St. Croix. B. Croi
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Carson-Walter, E.B., Vogelstein, B., Kinzler, K.W. and St. Croix, B. Direct Submission
Submitted (10-May-2001) Oncology, Johns Hopkins University, 1650
Orleans Street, Baltimore, MD 21231, USA
Location/Qualifiers
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GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCCACTCAATTTTGAAGAAGTCCTGC 772
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274. .1962
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                 Series: IRAL Plate: 29 Row: g Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7022737.
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Pred. No. 2.4e-276;
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illarity 99.9%;
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AK001463
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/organism="Homo sapiens"
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T. Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.

Direct Submission

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AL Direct Submission

AL Submitted (29-AKG-2000) Sumio Sugano, Institute of Medical Science, Submitted (29-AKG-2000) Sumio Sugano, Institute of Medical Science, Submission

AL Sana (29-AKG-2000) Sumio Sugano, Institute of Medical Science, Japan (F-mai): cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,

Fax:81-3-5449-5416)

NEDO human ChNA sequencing project supported by Ministry of International Trade and Industry of Japan; CNNA full insert Sequencing: Research Association for Blotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, Dana Construction, 5'-& 100 Submit Science and Technology, Dana Construction, Strates of Science Construction, Strates of Science and Technology, Dana Construction, Strates of Science and Technology, Dana Construction, Strates of Science Science of Science of 
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                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db.xref="taxon:9606"
/db.ref="taxon:9606"
/coln="theP00171"
/cell_type="hep62"
/clone_lib="hep7"
/note="cloning vector pME]
323. 1147
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/protein_id="BAB15128.1"
/db_xref="G1:10437939"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens cDNA: FLJ21776 fis, clone HEP00171.
AK025429
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S
                     ed. No. 4e-227;
Mismatches
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
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Homo sapiens cDNA FLJ32754 fis, clone TESTI2001671.
AK057316
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Homo sapiens testis cDNA to mRNA, clone_lib:TESTI2
clone:TESTI2001671.
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Pred. No. 6.1e-66;
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/clone="TEST12001671"
/tissue_type="test1s"
/clone_lib="TEST1s"
/note="cloning vector: pl
a 614 c 517 g 45
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56.6%;
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PRI 20-AUG-2001
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;

Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 1297)

Strausberg, R.

Direct Submission

Submitted (15-AUG-2001) National Institutes of Health, Mammalian
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199
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                        cccgaggaacaaccttaatgaaactgacagaagacagagaacaaatccgtcaaggcctag
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                                                                              aacagttggctcacaaattcatcagcccacagttgagaatgtcctttattgttttctcca
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VLSGRGFMLGSRNGSYLCTYTVNETYTTSVRPVSYQLNSMLCPAPILNKAGEWGLTYT
QAGVKWHDLTHCTFGLSGSGDPPTSAS"
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Isogal, T. Otsukir, and Sugiyama, T.
Isogal, T. Otsukir, T. and Sugiyama, T.
Submitted (24-0CT-2001) Takao Isogai, Helix Research Institute,
Submitted (24-0CT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Genail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
REDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; CDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
Research Association for Entitute (HRI) (supported by Japan
RRY, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: RAB and
                                                                                                                                                  Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
Ninomiya, K., Wagatsuma, M., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,
Sato, K., Tanikawa, M., Tanikawa, T., Ishi, S.,
Yamamoto, J., Isono, Y., Rawai-Hoo, Y., Saito, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.,
Nagohama, CDNA, sequencing project
  oligo capping; fis (full insert sequence).
Homo saplens synoviccytes from rtheumatioid arthritis (HS-RA) cDNA to mRNA, clone_lib:HSYRA2 clone:HSYRA2001476.
                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone/lib="HSYRA2"
/note="cloning vector: pME18SFL3-primary culture,
synoviocytes from rtheumatioid arthritis"
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59.9%; Pred. No. 8.7e-59;
Live 0; Mismatches 268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/protein_id="BAB70976.1"
/db_xref="GI:16550415"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HSYRA2001476"
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Best Local Similarity 59.9
Matches 409; Conservative
                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 28 Row: k Column: 23
This clone was salected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 10437938.

Location/Qualifiers

1. 1297

/ Organism="Homo sapiens"
/ Clone="IRAGE: 475862"
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/ tissue_type="Breast, mammary adenocarcinoma."
/ Clone="IRAGE: 475862"
/ tissue_type="Breast, mammary adenocarcinoma."
/ Clone=Libb="NIH_MGC_87"
/ Lab host="Bloom"
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                                                                                                                                                                                                                      Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
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Homo sapiens cDNA FLJ31074 fis, clone HSYRA2001476
AK055636
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                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
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Pred. No. 5.5e-60;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV-SPORT6"
                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <1. .295
/codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.4%;
98.0%;
                                                                                                   Contact: MGC help desk
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/protein_id="AAK77222.1"
/db_xref="di=1A4K77222.1"
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KEAKISRSIGARSVYCVGVLDFEQAQLERIADSKEQVFPVKGGFQALKGIINSSNGIAA
IIVILVLLLGIGLWWWFWPLCCKVVIKDPPPPPPAPKREEEEEFLFTKKWPTVDAS
YNGGRQGIKRMEVWRQDKGSTEGARLEKAKNAVKIPEETEEPIRPRPPRPTH
297 c 377 g 326 t
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Oligo capping; fis (full insert sequence).
Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE1
clone:PLACE1009794.
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one PLACE1009794
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Pred. No. 2e-
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59.0%;
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(Dases 1 to 1343)

Bell,S.E., Mavila,A., Salazar,R., Bayless,K.J., Kanagala,S., Maxwell,S.A. and Davis,G.E.
Maxwell,S.A. and Davis,G.E.
collagen matrices: regulated expression of genes involved in basement membrane matrix assembly, cell cycle progression, cellular differentiation and G-protein signaling

J. Cell. Sci. 114 (Pt 15), 2755-2773 (2001)
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AY040326.1 GI:15418998
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Submitted (14-JUN-2001) Pathology, Texas A&M University System
Health Science Center, 208 Reynolds Medical Building, College
Station, TX 77843-1114, USA
Location/Qualifiers
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ggatttgaaagggccagtgagcagatttattatgaaaacagacaagggtacaggacagcc
                             GGACTAAAGCTAGCGAATGAACAAAT - - - - - TCAGAAAGCAGGAGGCTTGAAAACCTCC
                                                                agogicatcatigotitigacigatggagaactccatgaagatcictititctaticagag
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/db_xref="taxon:9606"
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/organism="Homo
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141. .1301
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Davis, G.E. and Bell, S.E.
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www.shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3484366"
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RS Isogai,T. and Otsuki,T.
Direct Submission Claubi, Caboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, NEDO human CDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert International Trade and Industry of Japan; CDNA full insert Helix Research Institute (supported by Japan Key Technology; Conternations for and Department of Virology, Institute of Medical Science, Institute of machanal Science, Institute of Medical Science,
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Submitted (28-FEB-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         839 igigiccagogoctatottaaaagaagitggoaigaaagoigoactocaggicagoaiga 898
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partial cds.
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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307 t
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Mus musculus, clone IMAGE:3484366, mRNA,
BC003908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="cloning vector: }
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Best Local S:
Matches 113;
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AC025010 81017 bp DNA linear HTG 13-JUL-2000
Homo sapiens chromosome 4 clone RP11-85D17 map 4, LOW-PASS SEQUENCE
SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATECTNGIAAIVAILVLLLLGGAALMWWFWPLCCKVVIKDPPPPPSRPMEEEEEDPL
PNKKWPTVDASYYGGRGVGGIKRMEVRWGDKGSTEEGARLEKAKNAVVWVPEEEIPIP
SRPPRPRPTHQAPQTKWYTPIKGRLDALWALIMKQYDRVSLMRPQEGDEGRCINFSRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 7 Row: e Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Unknown (protein for IMAGE:3484366)"
/protein_id="AAH03908.1"
/db_xref="G1:13278124"
/translation="EKPVSIQPSSILCPAPVLNKDGETLEVSISYNDGKSAVSRSLTI
                                                                                                                                                                                                                                                                                   /tissue_type="Manumary tumor. WAP-TGF alpha model. 7 months
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Pred. No. 1.8e-16;
0; Mismatches 122;
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                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                      old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH108"
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19643 19742; gap of 100 bp 10.

19643 19742; gap of 100 bp 100 bp 19743 20493; contig of 775 bp in 1.

20494 20593; gap of 100 bp 20593; gap of 100 bp 21337; contig of 744 bp in len 21338 21202; contig of 765 bp in leng 22303 22302; contig of 765 bp in leng 22303 22302; contig of 765 bp in lengt 3073 21312; contig of 769 bp in lengt 3073 21312; contig of 769 bp in lengt 3073 21329; contig of 769 bp in length 302 22667; contig of 769 bp in length 302 22667; contig of 769 bp in length 302 22657; contig of 769 bp in length 56 26515; gap of 100 bp 22657; contig of 769 bp in length 58 2567; gap of 100 bp 22657; contig of 769 bp in length 58 2567; gap of 100 bp 22655; contig of 760 bp in length 22338; gap of 100 bp 22425; contig of 760 bp in length 22338; gap of 100 bp 22424; contig of 766 bp 760 bp 76
                                                                                                                                                                                                                                                                                                                                                                      58 12857; gap of 100 bp 103719; gap of 100 bp 100 b
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                                                                                                                                                                                 8 10287: gap of 100 bp 8 11042: gap of 100 bp 3 11142: gap of 100 bp 1 112010: contig of 788 bp ir 12010: gap of 100 bp 1 12010: gap of 100 bp 1 1 12757: contig of 747 bp ir
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                                                           8567: gap of 100 bp
9320: contig of 753 bp
9420: gap of 100 bp
10187: contig of 767 bp
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29969: contig of 765 bp
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contig of 764 bp
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contig of 768 bp
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31710: cont
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8467: con
8567: gap of
9320: con
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                                                                                                                                                                                                                                                                   Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boukhagalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galadan, J., Gardyna, S., Glnde, S., Goyette, M., Graham, L., Karatas, A., Klein, J., LaRocque, K., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Medrim, J., Menneus, L., Mihova, T., Mirada, C., Minova, T., Mirada, C., Minova, T., Mirada, C., Minova, T., Mirada, C., Peterson, K., Peterson, K., Peterson, K., Paand, C., Pollara, V., Raymond, C., Righ, Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Tralamas, J., Vasiliev, H., Vilel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J., Zhmer, A., Milson, B., Wu, X., Wyman, D., Ye, W., J., Lead, J., Zhmer, J., Lander, J., Zhmer, J., Zhmer, J., Lander, J., J., Lander, J., L
                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini; Hominidae, Homo.
1 (bases 1 to 81017)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This record contains 94 individual
* sequencing reads that have not been assembled into
confligs. Runs of N are used to separate the reads
confligs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 bp
of 766 bp in length
100 bp
of 760 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 bp
f 766 bp in length
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f 777 bp in length
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f 763 bp in length
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810 1567: contig of 758 bp in length
                                                                                                                                                    Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 4, clone RP11-85D17
Unpublished
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1568 1667: gap of
1668 2433: con
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4176: con
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5036: con
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                                                                                                                                                                                                                                                   (bases 1 to 81017)
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                             Homo sapiens
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                             ORGANISM
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SOURCE
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Birren, B. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Birren, B., Linton, L., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Bowkhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Campoplano, A., Castle, F., Dewar, K., Daz, J.S., Collymore, A., Cooke, P., Dertellano, K., Dewar, K., Diaz, J.S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grahm, L., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Lilev, I., Johnson, R., Jones, C., Kanh, L., Karatas, A., Helin, J., Lakocque, K., Limazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Morheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
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Homo sapiens chromosome 4 clone RP11-85D17 map 4, LOW-PASS SEQUENCE
SAMPLING.
                                                                                                               Martinstied, GERMANY
Clone from S. Wiemmann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemmann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s. wiemmann@dkfz-heidelberg.de;
Research Center (DKFZ); Email s. wiemmann@dkfz-heidelberg.de;
consortium of the German Genome Project.
This clone (DKFZ)586F1324) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@tzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.blochem.mgg.de/proj/CDNA/.
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1 (bases 1 to 81017)

Birran, Ba. Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chomosome 4, clone RP11-85D17
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKF2586F1324"
/clone="DKF2586 (synonym: hutel). Vector pSportl; host
/clone_sites Noti + Sall/MluI"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1026 ctggccctctgctgcactgtgattatcaaggaggtcctccacccctgccgaggagag 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wiemann,S.
Direct Submission
Submitted (15-AUG-1999) MIPS, Am Klopferspitz 18a, D-82152
     Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 9; Length 1877; Pred. No. 0.0064;
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1840. .1845
1858
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AC025010.1 GI:7145054
HTG; HTGS_PHASE0.
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Matches 57; Conservative
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polyA_site
BASE COUNT 52
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AC025010/c
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KEYWORDS
SOURCE
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AL110155
AL110155.1 GI:5817057
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                128: gap of 100 bp 49883: contig of 755 bp in length 183: gap of 100 bp 50748: contig of 765 bp in length
                                                                              40545: gap of 100 bp
41316: contig of 771 bp in length
41416: gap of 100 bp
42181: contig of 765 bp in length
                           39663: gap of 100 bp 40445: contig of 782 bp in length
        in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.5%; Score 72.2; DB 2;
96.1%; Pred. No. 7.6e-10;
tive 0; Mismatches 3;
             contig of
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58593 59364; cont
59365 59464; gap of
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Matches 74; Conserv
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HSM800800
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3 22302: gap of 100 bp in length 2302: gap of 700 bp in length 2302: contig of 700 bp in length 2302: contig of 769 bp in length 100 bp 240: gap of 100 bp 240: gap of 100 bp 2560: contig of 768 bp in length 100 24899: gap of 100 bp 25615: contig of 748 bp in length 100 24899: contig of 748 bp in length 100 24899: gap of 100 bp 26515: contig of 760 bp in length 100 24899: gap of 100 bp 2000: contig of 760 bp in length 100 24899: gap of 100 bp 2000: contig of 760 bp in length 100 24899: gap of 100 bp 2000: gap of 1000: gap of
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16 37915: gap of 100 bp

16 38676: contig of 761 bp in length

17 38776: gap of 100 bp

18 39663: gap of 100 bp

18 40445: contig of 782 bp in length
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45631: contig of 761 bp in length
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14 20593: gap of 100 bp
21377: contig of 744 bp 1r
18 21437: gap of 100 bp
18 22202: contig of 765 bp 1r
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16 17900: contig of 74 18000: gap of 18000: jap of 1867: cc
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                                             Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Ollvar, T.M., Ollvar, J., Peterson, K., Pierre, N., Pisani, C., Pollvar, T.M., Ollver, J., Peterson, K., Pierre, N., Pisani, C., Pollvar, T.M., Ollver, J., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N. Stolanovic, N., Severy, P., Spencer, B., Stange-Thomann, N., Stolanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Tavers, M., Trigillo, J., Vassillev, H., Viell, R., Voh., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vangillev, H., Viell, R., Voh., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vangillev, H., Viell, R., Voh., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vangillev, H., Viell, R., Voh., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vangillev, R., Volley, M., Viell, Viell,
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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Web Site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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15448: gap of 100 bp
16206: contig of 758 bp in length
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49272 49028: contig of 757 bp in length 49029 49128: gap of 100 bp 49984 4998: gap of 100 bp 50749 50749: contig of 755 bp in length 49984 50748: contig of 755 bp in length 50749 50848: gap of 100 bp 51750 5179: gap of 5179: gap of 527719: gap of 527719: gap of 52774 52573: gap of 52774 52573: gap of 52774 52573: gap of 52774 52573: gap of 100 bp 53328 5327: contig of 774 bp in length 53429 53528 54198: contig of 774 bp in length 53428 55221: contig of 775 bp in length 55625 5514: gap of 100 bp 55625 5524: gap of 5670 bp in length 55622 55738: gap of 5670 bp in length 55622 55738: gap of 5750 bp in length 55638: gap of 5750 bp in length 55638: gap of 5750 bp in length 55638: gap of 5750 bp in length 55739 55821: contig of 750 bp in length 55739 57838: gap of 100 bp 57739 58493: contig of 757 bp in length 55739 55922: gap of 100 bp 57739 58493: gap of 100 bp 5773 bp in length 55739 59364: contig of 772 bp in length 58833 58592: gap of 100 bp 58833
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; 0 0; Gaps Query Match

4.3%; Score 48; DB 2; Length 81017;
Best Local Similarity 79.2%; Pred. No. 0.017;
Matches 57; Conservative 0; Mismatches 15; Indels

1086 tgaggaaaataa 1097 δy

Search completed: August 9, 2002, 00:24:29 Job time: 12526 sec

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| SIDSI/gcgdata/hold-geneseq/geneseqp-embL/AA1990.DAT:
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343.114 Million cell updates/sec
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1 MATAERRALGIGFQWLSLAT......VIIKEVPPPPAEESEENKIK 368
                                                                                                                                                                                                             August 9, 2002, 10:30:01; Search time 119.13 Seconds
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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		Description	Human gene 4 encod	Human gene 4 encod	Human TANGO 197.	Human polypeptide	Human protein sequ	A human TANGO 216	Amino acid sequenc	A human TANGO 216	A human TANGO 216	Human novel extrac	A murine TANGO 216
		ID	AAE01439	AAE01469	AAB01422	AAM38976	AAB92985	AAB18456	AAB18447	AAB18455	AAB18457	AAU19662	AAB18458
		DB	22	22	21	22	22	21	21	21	21	22	21
		Length	403	403	333	297	218	488	488	488	488	587	487
ø	Query	e Match Length DB ID	98.7	97.7	86.2	72.7	50.5	50.1	50.0	49.9	49.9	49.0	49.0
		Score	1889	1870	1649	1392	996	958.5	957.5	955.5	954.5	938.5	937.5
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WO200134626-A1

17-MAY-2001

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## ALIGNMENTS

AAE01439 standard; Protein; 403 AA

AAE01439

RESULT

(first entry)

17-JUL-2001

AAE01439;

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Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoletic disorder; infimume system disorder; AlDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer; adisease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; agstrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; chromosome 19.
                                                                                             Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:94.
                                                                                                                                                                                                                                                                                                                                                                               1.27
|Jabel= Signal_peptide
28.403
|/note= "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                              Location/Qualiflers
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241 vrgngfrharnvdrvlcsfkindsvtlnekpfsvedtyllcpapilkevgmkaalqvsmn 300
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/label= Signal_peptide
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/note= "Encoded i
Misc-difference 368
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/note= "Encoded
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30-JUN-2000; 2000US-0215133.
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                                                                                                                                                                                                                                                                                                                                  AAD05300-AAD05379 represent CDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the protein genes, and AAE0144 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, the genes and their secreted proteins are useful for preventing, the genes and their secreted proteins e.g., by protein or gene treating or ameliorating madical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the presence of amount of the new protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of a genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of the abordary and include developing products for the diagnosis or treatment of abordary and include developing products (e.g., rheumatoid arthritis), inflammation, AIDS, autoimmuned diseases (e.g., rheumatoid arthritis), inflammation, asthma, allergies, neurological disorders, ce.g., alzehimer's diseases, comparence, sand infections. The proteins can also be used to aid wound disorders, and infections. The proteins can also be used to aid wound closure of primary tissues, to regenerate tissues, to identify their contact ligands or binding partners, and in chemotrasis, and on abordaries and one and and partners, and infections associated with the disorders and independent apporting of alleriating symptoms associated with the disorders mentioned above, and in diagnostic immunosasays e.g., radioimmunosasay or enzyme linked in diagnostic immunosasays e.g., radioimmunosasay or enzyme linked in diagnostic immunosasays e.g., radioimmunosasay or enzyme linked protein of the invention.
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                                                                                                                                                                                                                                 New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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100.0%; Pred. No. 4.2
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                               Claim 11; Page 485-486; 562pp; English.
                                                                                                                                                   Ruben SM, Komatsoulis GA, Moore PA,
                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                              99US-0163581.
2000US-0215133.
                            01-NOV-2000; 2000WO-US30045.
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Best Local Similarity
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                                                                05-NOV-1999;
30-JUN-2000;
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Best Loca Matches

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New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; AIDseimer; disease; sparkinson; disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; shin disorder; anglogenic disorder; kidney disorder; agastrointestinal disorder; pregnancy-related disorder; endocrine disorder; pregnancy-related disorder; endocrine disorder; food additive; gene therapy; binding partner identification; chromosome 19.
DGLSFISSSVIITTTHCSDGSILAIALLILELLIALANEWPPCCTVIIKEVPPPPAE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:125.
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(first entry)

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      NAMES OF COLOR OF STREET STREE
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                                           AAD05300-AAD05379 represent CDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode. AAE01514-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 28 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, and infeases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders, disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, schizophrenia, asthma, skin disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, for prevent skin aging due to sunburn, to maintein organs before transplantation, for supporting culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding pattners, and in chemotaxis, and can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunososays e.g., radioimmunosasay or enzyme linked immunosozbent assay (ELISA). The present sequence represents a human secreted protein of the invention.
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; Mismatches 3;
Claim 11; Page 505-506; 562pp; English.
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Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chiseases e.g. myasthemia gravis, autoimmune diabetes and autoimmune diseases e.g. myasthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
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TANGO, 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases, rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; crohn's disease; chronic myelogenous leukemia; cancer; liver disease; chronic myelogenous leukemia; cancer; liver disease; dolfacase; osteoarthritis; Lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus erythematosus; transgenic animal; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 1.5e-167;
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100.0%; Pred. No. _
'... 0; Mismatches
                                                                                                                                                                                                                                                               prognosis; prophylatic; therapeutic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cellular disorders can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Fig 4; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0223546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US31025
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Matches 318; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                             WO200039284-A1.
                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Holtzman DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-2000.
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                     AAB92985;
                                                 Sequence
                                                                               Query Match
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                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral scleroslis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                         300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
            VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN
                                                    Ren F, W
Zhang J;
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Yang Y,
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Xu C, Xue AJ,
{, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen R,
                                                                                                                                                            AA.
                                                                                                                                                                                                                         Human polypeptide SEQ ID NO 2121.
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Yang Z, Wehrman T, X
Zhou P, Goodrich R,
                                                                                                                                                            AAM38976 standard; Protein; 297
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2000US-0653450.
2000US-0662191.
2000US-0693036.
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2000US-0552317.
2000US-0598042.
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                                                                                                301 dglsfisssviitthcs 318
                                                                                     301 DGLSFISSSVIITTHCS 318
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N-PSDB; AAI58132.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang Z,
                                                                                                                                                                                                                                                                                                                                          WO200153312-A1.
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19-JUL-2000;
03-AUG-2000;
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19-OCT-2000;
29-NOV-2000;
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25-APR-2000;
                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                      22-OCT-2001
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Zhao QA,
                                                                                                                                                                                                                                                                                                   leukaemia.
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                                                                                                                                                                                  AAM38976;
     181
                         181
                                                                                                                                          RESULT
AAM38976
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                          Note: The sequence data for this patent did not form part of the printed specification.
assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                  KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
                                                                                                                                                                                                                                                                                                                                                                                 HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                       1 MATABRRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
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                                                                                                                                                 Length 297;
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                                                                                                                                                                                    Indels
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Otsuki
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                                                                                                                                                    Score 1392; DB 22;
Pred. No. 4e-140;
2; Mismatches 0;
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence SEQ ID NO:11706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 VRGNGFRHARNVDRVLCSFKINDSVTLNE 269
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Sugiyama T, Wakamatsu
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27-AuG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                    72.7%;
nilarity 99.3%;
Conservative 2
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Matches 267; Conserv
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01-MAR-2000; 2000WO-US05226.

99US-0122458

01-MAR-1999;

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The present invention describes primer sets for synthesising 5602 full-length cDMAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligouncleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence of the comprises a 1'-end sequence of 3'-end sequence of 3'-end sequence of 3'-end sequence of an oligonucleotide which comprises a 1'-end sequence of an oligonucleotide which comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers and also useful for the full-length cDNAs are primers allow obtaining of the full-length cDNAs are primers allow obtaining of the full-length cDNAs and 19418633 to AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13632 to AAH13632 to AAH13633 to 
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80 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 139 Length 218; Indels Score 966; DB 22; Pred. No. 9.5e-95; 2; Mismatches 0; 50.5%; 98.9%; Best Local Similarity 98.9 Matches 188; Conservative 218 AA; Seguence Query Match ò

RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 199 61 121 140 200 a g g ò ò

260 KINDSVTLNE 269 ò g

AAB18456 standard; Protein; 488 AA. 15-JAN-2001 (first entry) AAB18456; AAB18456 RESULT

A human TANGO 216 polypeptide clone.

TANGO 266; TANGO 216;; TANGO 261; TANGO 267;

cellular proliferation; cellular differentiation; cellular adhesion;

von Willebrand factor-associated disorder; cell trafficking; cancer;

hematopoietic associated disease; atelectasis; pulmonary congestion;

oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;

intestinal disorder; spleen associated disease; renal disorder;

cardiovascular disorder; ischemic heart disease; hydrocephalus;

brain herniation; iatrogenic disease; inflammation, meningitis;

Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;

multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder. 

WO200052022-A1

Homo sapiens.

08-SEP-2000.

AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO cecilular be used to used to modulate cellular specification, modulate cellular adhesion. The polypeptides can be used to creat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, ulmenary congestion or cedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases modulate the proliferation differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral cartilage associated with the ovaries, and cerebral cartilage associated disease, multiple sclerosis, brain corers, hydrocephalus and encephalitis, and treat hepatic disease, inflammations, hydrocephalus and encephalitis, and treat hepatic disorders.

Occartilage associated does not appear in the specification; it was an experient and core and an encephalitis, and treat hepatic disorders. Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -50.1%; Score 958.5; DB 21; Length 488; 51.6%; Pred. No. 2.1e-93; Pred. No. 2.1e-93; 3; Mismatches 107; Indels ပ္ပဲ Fraser Sharp JD, Disclosure; Page -; 175pp; English. created using information provided. 63; (MILL-) MILLENNIUM PHARM INC 189; Conservative Barnes TM, Holtzman DA, WPI; 2000-579269/54. Query Match Best Local Similarity 488 AA; N-PSDB; AAA75158 Seguence Matches 

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183 FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 242 241 grgfmlgsrngsvlctytvnetyttsvkpvsvglnsmlcpapilnkagetldvsvsfngg 300 123 GFERASEQIYYENRQGYRTASVIIALIDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD 182 63 YYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHE 122 Gaps 4 AERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEI 62 3 aersparspgswlfpglwllvlsgpggllraqdqpscrrafdlyfvldksgsvannwle1 62 GNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDG 243 g g ò ద δ g ò a ò

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The present sequence represents a human TANGO 216 polypeptide. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 265, TANGO 267. THE TANGO POLYpeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand
                                                                                                                                                                                  cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectrasis; pulmonary congestion; hematopoietic associated disease; atelectrasis; pulmonary congestion; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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44..213
/note= "yon Willebrand factor A domain"
                                                                                                                                                                            266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
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35..488
/wote= "mature protein"
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                                                                                          AAB18447 standard; Protein; 488 AA.
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98..317
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N-PSDB; AAA75149.
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                  359 AEESEE 364
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                                                                                                                                                                                                                                                                                                                              Key
Peptide
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factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative cellular interactions, modulate the proliferation, disorders, such as cancer, modulate the proliferation, differentiation, disorders, such as cancer, modulate the proliferation, differentiation, cells that appear in the bone marrow, and leukocytes, creat bone marrow, blood and hematopoletic associated diseases and chronic bronchits, bronchial asthma and bronchiectasis, intestinal chronic bronchits, bronchial asthma and bronchiectasis, intestinal cardiovascular disorders such as ischemic heart disease, modulate the cardiovascular disorders astoriated diseases or cells and to treat bone and/or function of bone and cartilage proliferation, differentiation, and/or function of bone and cartilage covaries, cerebral ocema, hydrocephalus, brain herniations, iatrogenic covaries, cerebral codema, hydrocephalus, brain meningitis, Alzheimer's bisease, inflammations, bacterial and viral meningitis, and treat hepatic consistences, hydrocephalus and encephalitis, and treat hepatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 YYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHE 122
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50.0%; Score 957.5; DB 21;
Best Local Similarity 51.6%; Pred. No. 2.7e-93;
Matches 189; Conservative 63; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A human TANGO 216 polypeptide clone.
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361 keeeee 366
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AAB18455
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AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 262 calcular differentiation and/or modulate cellular adhesion, modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferation, and/or function of cells modulate the proliferation, differentiation. and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchitals and bronchiectasis, intestinal disorders, spleen associated disease, modulate the proliferation, differentiation, as ischemic heart disease, modulate the proliferation, differentiation, as ischemic heart disease, modulate the proliferation, differentiation, as ischemic heart disease, with the ovaries, and cerebral oedema, cartilage cells and cerebral oedema, chronic bronch and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral concephalus, brain herniations, iatrogenic disease, inflammations, brain cancers, hydrocephalus and encephalitis, and treat hepatic disease, cerebral toxelers associated with the ovaries, and cerebral concepts the present sequence does not appear in the specification; it was created using information provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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N-PSDB; AAA75157.
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                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                           Barnes TM,
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                                                                                                       74 ISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYY 133
                                                                                                                    SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                              WLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEOLAHKF 73
                             Gaps
                                                                   7;
                          Indels
            ; Pred. No. 4.4e-93;
63; Mismatches 99;
49.9%; Score 955.5; 52.4%; Pred. No. 4.4
Query Match
Best Local Similarity 52.45
Matches 186; Conservative
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AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 262, and TANGO 267. The TANGO 260 cescribes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO cellular be used to used to modulate cellular proliferation, modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder. regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, that appear in the bone marrow, and leukocytes, treat bone marrow, and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial astochamic heart diseases, modulate renal disorders, pred cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations,
                                                                                                                                                                                                                                                                                                                                                                                                TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; cellular proliferation; cellular differentiation; cellular adhesion; concer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiatis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflammation; meningitis; Alzhelmer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
254 RVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIIT 313
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                          314 TTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPP----PAEESEE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser CC;
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                                                                                                                                                                                                                                   AAB18457 standard; Protein; 488 AA
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 bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders: note: the present sequence does not appear in the specification; it was created using information provided.
                                                                                                                                                                                                   123 GFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD 182
                                                                                                                                                                                                             FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 242
                                                                                                                                                                                                                                                                             GNGFRHARNYDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDG 302
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                                                                                                                         4 AERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEI 62
                                                                                                                                                                                                                                                   YYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHE
                                                                                                        7;
                                                                                      DB 21; Length 488;
                                                                                    Query Match
Best Local Similarity 51.4%; Pred. No. 5.6e-93;
Matches 188; Conservative 64; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human novel extracellular matrix protein, Seq ID No 312.
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2000US-0180628.
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20000S-0232399.
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2000US-0229287
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29-SEP-2000;
02-OCT-2000;
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25-SEP-2000;
25-SEP-2000;
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12-SEP-2000; 2
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18-AUG-2000;
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21-SEP-2000;
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07-JUL-2000;
07-JUL-2000;
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14-AUG-2000;
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06-SEP-2000;
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07-JUN-2000;
28-JUN-2000;
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17-MAR-2000;
18-APR-2000;
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Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
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                                                                                             2000US-0244617.
2000US-0246476.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246478.
2000US-0246524.
2000US-0246526.
2000US-0246527.
2000US-0246528.
2000US-0246528.
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2000US-0246528.
2000US-0246528.
2000US-0249208.
2000US-0249218.
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2000US-0241808.
2000US-0241809.
2000US-0241826.
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2000US-0250160.
2000US-0250391.
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2000US-0251988.
2000US-0256719.
2000US-0251479.
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N-PSDB; AAS31233.
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17-NOV-2000;
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05-DEC-2000;
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08-DEC-2000;
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17-NOV-2000;
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The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (5Ps). The novel human secreted extracellular matrix proteins (5Ps). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing them may be administered to dreat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPs may also be used to dreat the anti-(SP) antibodies and antagonists may also be used to down regulate expression and activity of antagonists may also be used to down regulate expression and activity of SP and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/discases (e.g. HIV) (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis, cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and caucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 RVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIIT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 WLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKF 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 TTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPP----PAEESEE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 49.0%; Score 938.5; DB 22; Length Best Local Similarity 52.1%; Pred. No. 3.8e-91; Matches 185; Conservative 59; Mismatches 104; Indels
Claim 11; SEQ ID No 312; 577pp; English.
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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 260 cellular proliferation, modulate polypeptides can be used to modulate cellular adhesion. The cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Wilebrand factor-associated disorder, requilate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferation, modulate cellular interaction, differentiation, and/or function of cells and hematopoietic associated diseases and disorders, atelectasis, that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, spleen associated diseases, modulate renal disorders, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as interaction of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human and murine secreted proteins designated TANGO 216, 261, 266, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC.
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Best Local Similarity
Matches 186; Conserv
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TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; ocllular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; ocdema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; isohemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; hazhelmer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                      NDGLSFISSSVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPA 359
                                                                    240 VVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSM 299
                         238 vltgravtsishdgsvlctftanstytksekpvsiqpssilcpapvlnkdgetlevsisy 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                                                                                                                                                                                                                                                        Amino acid sequence of a murine TANGO 216 polypeptide.
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/note= "transnmembrane domain"
342..487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "signal peptide"
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j..317
not.e= "cytoplasmic d
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                                                                                                                                                                                                            AAB18448 standard; Protein; 487 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC.
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N-PSDB; AAA75150.
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cell trafficking; cancer;

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specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267, TANGO 261, TANGO 261, TANGO 262, and TANGO 267, TANGO 261, TANGO 262, and TANGO 267. The TANGO 261, TANGO 261, TANGO 262, and TANGO 262, and TANGO 261, TANGO 261, TANGO 262, and TANGO 
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                                    The present sequence represents a murine TANGO 216 polypeptide. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 VKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQV
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ches 115; Indels
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300 NDGLSFISSSVIITTTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPA 359 TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; 240 VVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSM A murine TANGO 216 polypeptide clone. AAB18460 standard; Protein; 487 AA. 15-JAN-2001 (first entry) 358 apmeeeeedpl 368 360 --- EESEENKI 367 AAB18460; g g ô ç ò

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120 MHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVG 179

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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO Collular differentiation and/or modulate cellular adhesion. modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Wilebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate the proliferation, differentiation, and/or function of cells matrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, and hematopoietic associated diseases and disorders, spleen associated diseases. Modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate trenal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral codema, hydrocephalus, brain hermiations, iatrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, inflammations, bydrocephalus and encephalits, and treat hepatic disorders, the present sequence does not appear in the specification; it was considered the proliferation of the constants.
                   hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchietestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; lschemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflammation; meningitis; altrogenic caracteristic parkinson's disease; authorized parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
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63; Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; ocdema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflammation; meningitis; Alzhelmer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 260 polypeptides can be used to modulate cellular proliferation, modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferation disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells
                                                                                                                                                                                                  NDGLSFISSSVIITTTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPA 359
                                                                                                                                                                                                               240 VVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSM 299
                                                                                                                                              Novel human and murine secreted proteins designated TANGO 216, 261, 266, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
VKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A murine TANGO 216 polypeptide clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        AA.
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                                                                                                                                                                                                                                                                          ---EESEENKI 367
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that appear in the bone marrow, and leukocytes, treat bone marrow, blood and homatopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as isohemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

Created using information provided.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 MHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 933.5; DB 21;
; Pred. No. 9.9e-91;
64; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB01428 standard; Protein; 381 AA.
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Best Local Similarity 49.9
Matches 185; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             487 AA;
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WO200039284-A1

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                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachexia and autoimmune diseases, osteoarthritis, Lyme's disease, cachexia and systematic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial Carnosic biology, for diagnostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a clistorder associated with aberrant TANGO expression. A wide range of cellular disorders can be treated.
                                                                                                                                                                                                                                                                  Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 QLARIADSKDHVFPVNDGFQALQCIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 909; DB 21; Length 381;
Pred. No. 2.8e-88;
2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                      Claim 8; Fig 27; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.58;
                                                                                                                                         (MILL-) MILLENNIUM PHARM INC
                                                                                                  98US-0223546.
                                                                    99WO-US31025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.3
Matches 175; Conservative
                                                                                                                                                                                                               WPI; 2000-465743/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381 AA;
                                                                                                                                                                                                                                  N-PSDB; AAA47479
                                                                                                      30-DEC-1998;
                                                                  23-DEC-1999;
                                                                                                                                                                           Holtzman DA;
                                06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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307 SSSVIITTHCSDGSILAIALLILFLLLALAMWFWPLCCTVIIKEVPPPAEESEE 364 ò

247 RHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFI 306 

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Search completed: August 9, 2002, 10:32:10 Job time: 129 sec

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Compugen Ltd.
  GenCore version
Copyright (c) 1993 - 2000
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OM protein - protein search, using sw model

August 9, 2002, 10:33:17; Search time 31.3 Seconds (without alignments) 455.233 Million cell updates/sec uo o

US-09-970-076-2

1914 1 MATAERRALGIGEQWLSLAT......VIIKEVPPPAEESEENKIK 368 Perfect score: Sequence:

**BLOSUM62** Scoring table:

105224 seqs, 38719550 residues Gapop 10.0 , Gapext 0.5 Searched: 105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O9h6x2 homo sapien	mus m	рошо	уошоц	homo	homo	gallu	mus mus	Snu	mus m		gallu			notop	gallu	homo	homo	homo	mus m	Bus	Snw	089029 mus musculu	mus mus	gallu	homo	homo		drosc		plasn	homo	рошо
SUMMARIES	ID		ATR_MOUSE	CMG2_HUMAN	ITAD_HUMAN	ITAM_HUMAN	ITAX_HUMAN	CA1C_CHICK	ITAM_MOUSE	CA1C_MOUSE	CO2_MOUSE	CA1C_HUMAN	CA1E_CHICK	YNX3_CAEEL	CAMA_HUMAN	CA1C_NOTVI	MIN3_CHICK	CFAB_HUMAN	MTN2_HUMAN	CA17_HUMAN	CFAB_MOUSE	CA26_MOUSE	CAMA_MOUSE	MIN4_MOUSE	MTN2_MOUSE	CAMA_CHICK	ITAH_HUMAN	MTN4_HUMAN	MTN3_HUMAN	ROP_DROME	- 1	TRAP_PLAFA	CA26_HUMAN	CA36_HUMAN
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æ	Query Match I	99	93.7	4	8.3	7.6	7.5	7.5	7.4	7.3	6.8	8.9	6.8	6.7	6.3	6.2	6.1	5.9	5.9	2.8	5.8	5.7	5.7	5.7	5.7	9.6	5.6	5.4					5.2	
	Score	1894	1793	651	59	145.5	₽	143	141	139	131	131	130	128	120.5	118	117.5	113.5	113.5	111.5	110.5	109.5	108.5	108.5	108.5	107.5	107	103	_	99.5	66	66	66	98
	Result No.	-	7	m	4	5	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33

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09k0n4 neisseria m 090615 gallus gall P56199 homo saplen P1598 gallus gall Q28902 oryctolagus P38570 homo saplen P18614 rattus norv 060677 mus musculu P58079 caulobacter 043405 homo saplen 091vq9 neisseria m 075578 homo saplen
DNAK_NEIMB ITA1_CHICK ITA1_HUMAN CA5_CHICK CA1C_RABIT ITAE_HUMAN ITA1_RAT ITAE_MOUSE HUTT_CAUCK COCH_HUMAN DNAK_NEIMAN ITAG_HUMAN
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97.5 97.9 97.9 96.5 95.5 92.5 92.5
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## ALIGNMENTS

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-:- SUBCELLUIAR LOCATION: Type I membrane protein (Probable).
-:- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4; seem to be produced by alternative splicing.
-:- TISSUE SPECIFICITY: Highly expressed in tumor endothelial cells but not in normal endothelial cells.
-:- DOMAIN: Binding to PA seems to be effected through the VWA domain.
-:- SIMILARITY: BELONGS TO THE ATR FAMILY.
-:- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Okamoto S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 184-564 FROM N.A. (ISOFORM 1), AND SEQUENCE FROM N.A. (ISOFORM 3).

(ISOFORM 3).

Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto & Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;

"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bradley K.A., Mogridge J., Mourez M., Collier R.J., Young J.A.T.; "Identification of the cellular receptor for anthrax toxin."; Nature 414:225-229(2001).
                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhlni, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                      , 'B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: Cellular role is not yet known.
                                 ATR_HUMAN STANDARD; PRT; 564 AA. Q9H6X2; Q9H0X3; Q0H6X2; Q9H0X3; Q0H6X2; Q9H0X3; Q1-MAR-2002 (Rel. 41, Last sequence update) Q1-MAR-2002 (Rel. 41, Last annotation update) Q1-MAR-2002 (Rel. 41, Last annotation update) Antrax toxin receptor precursor (Tumor endothelial marker 8). ATR OR TEM8.
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-20407466; PubMed=10947988;
St Croix B., Rago C., Velculescu V., Traverso G., Romans K.E.
Montgomery E., Lal A., Riggins G.J., Lengauer C., Vogelstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Strausberg R.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                     "Genes expressed in human tumor endothelium."; Science 289:1197-1202(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=11700562;
                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anthracis.
                                                                                                                                                                                                                                                                                                                                       Kinzler K.W.
RESULT 1
ATR_HUMAN
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/
                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. ..) (POTENTIAL).
BDDD -> NRIK (IN ISOPORM 2).
MISSING (IN ISOPORM 2).
NEKPPSVEDTYLLCPAPILKEVGMKAALQV -> SKSLQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 VRGNGFRHARNYDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WVSSTSGFKEGNSHPCLPARPHT (IN ÏSOFORM 3).
MISSING (IN ISOFORM 3).
DGSILAIALLILFLL -> LHKIASGPTTAACME (IN
                                                                                                   InterPro; IPR002035; vWFA.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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0
                                                                                                                                                                                                                                                                                                                                                                                                  Length 564;
                                                                                                                                                                                                                  ASP/GLU-RICH (HIGHLY ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                          ANTRAX TOXIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                      MISSING (ÎN ISOFORM 4).
B118A00AD5DF2233 CRC64;
                                                                                                                                                                              POTENTIAL.
CYTOPLASMIC (POTENTIAL).
VWFA.
                                                                                                                                                                                                                                                                                                                                                                                                  Score 1894; DB 1; I
Pred. No. 3.1e-147;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    562 AA.
                                                                                                                                                                                                                                                                                                                                              ISOFORM 4)
                         or send an email to license@isb-sib.ch)
                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                PRO-RICH.
                                                     EMBL; AK025429; BAB15128 1; ALT_INIT.
EMBL; AK001463; BAA91707 1; ALT_FRAME.
EMBL; BC012074; AAH12074 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.0%; Sco
Best Local Similarity 100.0%; P:
Matches 364; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATR_MOUSE STANDARD; I
Q9CZ52;
01-MAR-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                    MM:
                                              EMBL; AF279145; AAK52094.1; -.
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368
368
166
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297
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ESEE 364
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ID ATR_MC
AC Q9CZ55
DT 01-MAE
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                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21085660; PubMed=11217861;
A Rawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rakawal J., Shinagawa A., Shibata K., Yonon H., Adachi J., Fukuda S., Anamanaka I., Anisawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Golobori T., Bono H., Rasukawa T., Saito R., Radto K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radto K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radto K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radto K., Matsuda H., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T., Radenin M., Anno H., Baldarelli R., Barsh G., Schrim I.D., Bojunga N., Carninci P., de Bonaldo M.F., Radto Sakai K., Okido T., Furucher C., Fujita M., Gariboldi M., Ratincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Rotincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H., RA Brownstein M.J., Bult C., Seya T., Shibata Y., Storch K.-F., Rawani H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;

Nature 409:685-690(2001).

I. Subcillura role is not yet known.

I. FUNCTION: Cellular role is not yet known.

I. Subcillura Role of a full-length mouse cDNA collection.";

I. Subcillura Binding to Pa seems to be effected through the VWA domain C. Beroduced by alternative splicing.

C. -- Subcillurity. Binding to Pa seems to be effected through the VWA domain C. SIMILARITY: CONTAINS I VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Signal; Alternative splicing.
                                                                              Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                            Kinzler K.W., St Croix B.; "Cell surface tumor endothelial markers are conserved in mice and
              Last annotation update) precursor (Tumor endothelial marker 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASP/GLU-RICH (HIGHLY ACIDIC).
PRO-RICH.
                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=21443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTRAX TOXIN RECEPTOR. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat.
Antrax toxin receptor precursor (Tumor endo
                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 88-562 FROM N.A. (ISOFORM 2).
STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                Cancer Res. 61:6649-6655(2001).
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ITAD_HUMAN
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
GRCINFTRYNNSQPAKYPLNYTYPPSSPPAPIYTPPPPAP
HCPPPAPSAPTPPIPSPFSTLPPPPQAPPRNRAPPPSRPPP
RPSV -> RFROMLUTICLGSKHVHPGRHDKGPETPLLKQA
MMFSSFLERAFQ (IN ISOFORM 2).
6AC92049B4BB4F7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21539596; PubMed-11683410; Bell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S., Bell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S., Maxwell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S., Maxwell S.A., Davis G.E.;

"Differential gene expression during capillary morphogenesis in 3D collagen matrices: regulated expression of genes involved in basement membrane matrix assembly, cell cycle progression, cellular differentiation and G-protein signaling.";

"I SIBUNIT: Seems to bind to collagen type IV and laminin." SUBCELGULAR LOCATION: Type I membrane protein (Probable).

"I SIMILARITY: BELONGS TO THE ATR FAMILY."
                                                                                                                                                                                                                                   LAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERAS 128
                                                                                                                                                                                                                                                                      EQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQL 188
                                                                                                                                                                                                                                                                                                                                                                      ARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISS 308
                                                                                                                                                 Gaps
                                                                                                                                                                                              99
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                        LGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQ
                                                                                                                                                                                                                                                                                                                      ARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRH
                                                                                                                                                                                                                                                                                                                                                                                                                    SVIITTTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPAEESEE 364
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 562;
                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Capillary morphogenesis protein-2 precursor (CMG-2).
                                                                                                                        Score 1793; DB 1;
Pred. No. 5.6e-139;
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01-MAR-2002 (Rel. 41, Last annotation update)
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MM
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96.18;
                                                                                                                                                 Conservative
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                                                                                                                                    Similarity
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SEQUENCE FROM N.A.
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P58335;
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CARBOHYD
CARBOHYD
CARBOHYD
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Matches 342
                                                                                     SEQUENCE
                                      VARSPLIC
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GFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 YYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 GNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDG 302
                                                                                                                                                                                                                                                                                                     Gaps
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novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T., Staunton D.E., Gallatin W.M.;
                                                                                                                                                                                                                                                                                                                                                                 4 AERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEI
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                 (POTENTIAL).
                                                                              CAPILLARY MORPHOGENESIS PROTEIN-2
                                                                                                                                                                                                                                                                                                     69; Indels 110;
                                                                                                                                                                                                                                                             Length 386;
                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                               N-LINKED (GLCNAC. . .) (P
0F9B2D6688EAB17A CRC64;
                                                                                                                                         CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DB 1; I
7.3e-46;
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16-0CT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                     45; Mismatches
                                                                                                                                                                                                                                                               34.0%; Score 651;
                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                        POTENTIAL
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MEDLINE-20187620; PubMed-10722744;
Noti J.D., Johnson A.K., Dillon J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE~Spleen;
MEDLINE~96111956; Pubmed-8777714;
EMBL; AY040326; AAK77222.1; -. PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                      Ψ.
                               Transmembrane; Glycoprotein; SIGNAL 1 33
                                                                                                                                                                                                                                                                                    38.88;
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                                                                                                                                                                                                                                                                                                     Conservative
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215
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44
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386 AA;
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Best Local Similarity
Matches 142; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLULAR LOCATION: Type I membrane protein.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: EXPRESSED MODERATELY ON MYELOMONOCYTIC CELL.

-!- INES AND SUBSETS OF PERIPHERRAL BLOOD LEUKOCYTES AND STRONGLY ON TISSUE-SPECIALIZED CELLS, INCLUDING MACROPHAGES FOAM CELLS WITHIN TISSUE-SPECIALIZED CELLS, INCLUDING NACROPHAGES FOAM CELLS WITHIN THEROSCLEROTIC PLAQUES, AND ON SPLENIC RED PULP MACROPHAGES.

-!- DOMAIN: THE INTEGRIN I DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I DOMAINS TO NOT UNDERGO PROTEASE CLEAVAGE.

-!- SIMILARITY: CONTAINS I VWFA DOMAIN.

-!- SIMILARITY: CONTAINS I VWFA DOMAIN.
                                                                                                                                                                                      MEDLINE-99059812; PubMed-9841932; Graphinsky S.A., Michael Gallatin W., Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W., Hoffman P.A., Staunton D.E., Bochner B.S.; "alphadbeta2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule 1 (VCAM-1).";
                                                                                         Wong D.A., Davis E.M., LeBeau M., Springer T.A.; "Cloning and chromosomal localization of a novel gene-encoding a human beta 2-integrin alpha subunit."; Gene 171:291-294(1996).
"Structural and functional characterization of the leukocyte integrin gene CD11d. Essential role of Sp1 and Sp3."; J. Biol. Chem. 275:8959-8969(2000).
                                                                                                                                                                                                                                                                                                                                     MEDINE-997002: Pubbed-10438935;
MEDINE-997002: Pubbed-10438935;
MEDINE-9970002: Pubbed-10438935;
Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
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J. Immunol. 163:1984-1990(1999).
VCAMI. MAY PLAY A ROLE IN THE ATHEROSCILEROTIC PROCESS SUCH AS VCAMI. MAY PLAY A ROLE IN THE ATHEROSCILEROTIC PROCESS SUCH AS CLEARING LIPOPROTEINS FROM PLAQUES AND IN PHAGGOSTOSIS OF BLOODEROWN THE BYTHOGENS, PARTICULATE MATTER, AND SENESCENT ERYTHROCYTES FROM THE BY THE BY THOUGHTES AND SENESCENT ERYTHROCYTES
                                                               SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A.
MEDLINE-96257236; PubMed-8666289;
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Pfam; PF00357; integrin_A; 1.
Pfam; PF00357; integrin_A; 1.
PRINTS; PR00185; INTEGRINA.
PRINTS; PR00453; VWRDDOMAIN.
SMART; SM00191; INT_AIDHA; 4.
SMART; SW00327; VWR, 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
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EMBL; U40274; AAB60634.1; --
EMBL; U40275; AAB60635.1; --
EMBL; U40277; AAB60637.1; --
EMBL; U40277; AAB60637.1; --
EMBL; U40279; AAB60638.1; --
EMBL; U40278; AAB60638.1; JOINED.
EMBL; AF1878
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184 NETQLAR-----IADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGES 236
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PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
Signal; Repeat; Calcium;
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    SEQUENCE FROM N.A.
MEDLINE-88190151; PubMed=2833753;
Arnaout M.A., Remold-0'Donnell E., Pierce M.W., Harris P., Tenen D.G.;
Annout M.A., Remold of Lonnell E., Pierce M.W., Harris P., Tenen D.G.;
"Molecular cloning of the alpha subunit of human and guinea pig
leukocyte adhesion glycoprotein Mol: chromosomal localization and
homology to the alpha subunits of integrins.";
Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
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MEDLINE=93123748; PubMed=8419480;
Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;
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Annino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mol (complement receptor type 3).";
J. Cell Biol. 106:2153-2158(1988).
01-JUL-1989 (Rel. 11, Created)
01-C77-1996 (Rel. 34, Last sequence update)
01-C77-1996 (Rel. 14, Last sequence update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha
subbunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1)
ITGAM OR CR3A OR CD11B.
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                                                                                             Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-89098893; Pubmed-2563162;
Hickstein D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L.,
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MEDLINE-87076671; PubMed=3539202;
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-!- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
-!- SIMILARITY: CONTAINS I VWFA DOMAIN.
-!- SIMILARITY: CONTAINS I FG-GAP REPEATS.
-!- DATABASE: NAME-PROW; NOTE-CD guide CD11b entry;
--- WWW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd11b.htm".
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                                                                                           Lee J.O., Rieu P., Arnaout M.A., Liddington R.; "Crystal structure of the A domain from the alpha subunit of integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.; "Two conformations of the integrin A-domain (I-domain): a pathway for
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MEDLINE-98362595; PubMed-9687375;
Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
Fairbanks M.B., Finzel B.C., Midar R.R., Heinrikson R.L.,
Horton N.C., Kelley L.L., Midner A.M., Moon J.B., Mott J.E.,
Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;
"Catton binding to the integrin CD11b I domain and activation model
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X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331
MEDLINE=95171458; PubMed=7867070;
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MEDLINE=98226734; PubMed=9560195;
Oxvig C., Springer T.A.;
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AAB24821.1;
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AAB24821.1;
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                                                                                                                                                                                                       (CD11b/CD18).";
80:631-638(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M18044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         $52227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J04145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S52161;
S52164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S52159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activation?'
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                NCBI_TaxID=9606;
                          ITAX_HUMAN P20702:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
EMBL;
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RESULT 6
ITAX_HUMAN
                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 DIAFLIDGSGSIIPHDFRRMKEFVST-----VMEQLKKSKTLFS-----LMQYSEEFRIH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 FTFKEFQNNPNPRSLVKPIIQLL--GRTHTATGIRKVVRELFNITNGARKNAFKILVVIT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKDFNETQLAR-----IADS--KDHVFP 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 DLYFILDKSGSVL-HHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTED---- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00342; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; WPA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 145.5; DB 1; Length 1152; Pred. No. 0.0006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTEGRIN ALPHA-M.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL). FG-GAP 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; Magnesium; Calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.2%; Pred. No. 0.00 iive 45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM. 120980;
Interpro: IRR00013; Integrin_alpha.
Interpro: IRR002035; vWFA.
Pfam; PF01839; FG-GAP; 5.
Pfam; PF00357; integrin_A; 1.
Pfam; PF00092; vwa; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00185; VMFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; Integrin N PRINTS;
                                    552174, ARBAR2111, JOINED.
552180, ARBAR2111, JOINED.
552181, ARBAR2111, JOINED.
552181, ARBAR2111, JOINED.
552189, ARBAR2111, JOINED.
552191, ARBAR2111, JOINED.
552192, ARBAR2111, JOINED.
552203, ARBAR2111, JOINED.
552203, ARBAR2111, JOINED.
552213, ARBAR2111, JOINED.
552216, ARBAR2111, JOINED.
552216, ARBAR2111, JOINED.
552216, ARBAR2111, JOINED.
552221, ARBAR2111, JOINED.
                                                                                                                                                                                                                                                                                          M76724; AAA58410.1; -. M84477; AAA51960.1; -. A31108; RWHUIB. A26091; A26091.
                                      $52174; AAB24821.1; US52180; AAB24821.1; US52181.1; AAB24821.1; US52189; AAB24821.1; US52199; AAB24821.1; US52192; AAB24821.1; US52212; AAB24821.1; US52212; AAB24821.1; US52212; AAB24821.1; US52212; AAB24821.1; US52213; US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 26.2 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                CarbBank; CCSD:33581; -. CarbBank; CCSD:33582; -. CarbBank; CCSD:33584; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1104
1128
1152
84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal; 3D-structure; SIGNAL
                                                                                                                                                                                                                                                                                                                                                        188%; 17-JUN-98.
1BHO; 18-NOV-98.
1BHO; 18-NOV-98.
1IDN; 25-NOV-98.
1IDO; 01-AUG-96.
1JUM; 11-JAN-97.
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TRANSMEM
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                                                                                                                                        EMBL;
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PIR;
PDB;
PDB;
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PDB;
 EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE-- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFFYSEREANRSRDLGAIVYCVGV------KDFNETQLARIAD--SKDHVFPVNDG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                 PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00191; Int.alpha; 4.
SMART; SM00242; VWA; 1.
PROSITE; PS50234; VWFA; 1.
PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.5%; Score 143.5; DB 1; Length 1163; 24.8%; Pred. No. 0.00089;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> A (IN REF. 2).
-> D (IN REF. 2).
6C4E19CC3F62A473 CRC64;
                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.

BY SIMILARITY.

CECNAC.

CHARED (GLCNAC.)

CHARED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL) FG-GAP 1.
                                                                                                                                                                                                                                                                                                  INTEGRIN ALPHA-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                       FG-GAP 2.
                                                                                             InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                       Signal; Magnesium; Calcium; Repeat.
EMBL; M29486; AAA51620.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127885 MW;
                                                                                                                          Pfam, PF01839; FG-GAP; 5.
Pfam, PF00357; integrin_A; 1.
Pfam; PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                      Carbbank; CCSD:33581; -. Carbbank; CCSD:33582; -. Carbbank; CCSD:33584; -.
                                                                                                                                                                                                                                                                                                             1107
1128
1163
                                                                                                                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1050 109
490 49
756 75
1163 AA;
             PIR; A36584; RWHUIC.
HSSP; P11215; 1A8X.
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1108
1129
34
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Best Local Similar
                                                                               MIM; 151510;
                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
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DISULFID
DISULFID
CARBOHYD
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                                                                                                                                                                                                                                                                                 SIĞNAL
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REPEAT
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINAL TISSUE FORM OF COLLAGEN XII MAY CONTAIN HOMOTRINERS OF EITHER THE LONGER OR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTEOGLYCAN. THE LARGE ISOFORM HAS MORE RESTRICTED EXPRESSION IN EMBRYONIC TISSUE THAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-WHITE LEGHORN:
MEDLINE-92011862; PubMed-1918137;
Yamagata M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka H.,
Nishida Y., Obara M., Kimata K.;
"The complete primary structure of type XII collagen shows a chimeric
molecule with reiterated fibronectin type III motifs, yon Willebrand
factor A motifs, a domain homologous to a noncollagenous region of
type IX collagen, and short collagenous domains with an Arg-Gly-Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95370352; Pubmed-7642694;

Roch M., Bohrmann B., Mathison M., Hagios C., Trueb B., Chiquet M.;

"Large and small splice variants of collagen XII: differential
expression and ligand binding.";

J. Cell Biol. 130:1005-1014(1995).

-!- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
CONTAINING FIBRILS, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE
SURFACE OF THE FIBRILS, AND THE COLL AND NC3 DOMAINS MAY BE
LOCALIZED IN THE PERFIEBRILLAR MATRIX.

-!- SUBDUNT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 KDa OF
NONTRIPLE-HELICAL SEQUENCES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gordon M.K., Gerecke D.R., Dublet B., van der Rest M., Olsen B.R.; Type XII collagen. A large multidomain molecule with partial homology to type IX collagen. In the collagen. Biol. Chem. 264:19772-19778(1989).
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MEDLINE-87317590; Pubmed-3476925;
Grodon M.K., Gerecke D.R., Olsen B.R.;
Type XII collagen: distinct extracellular matrix component discovered by cDNA cloning.";
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                                                                                                                                                                                                                                                                                                                            P13944; 004509; 01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 35, Last sequence update) 01-NNY-2002 (Rel. 41, Last annotation update) collagen alpha I(XII) chain precursor (Fibrochimerin).
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FOALOGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGF 246
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MEDLINE=93042014; PubMed=1420368;
Trueb J., Trueb B.;
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                                                                                                                                                           this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
C. -1- TISSUE SPECIFICITY: TYPE XII COLLAGEN IS PRESENT IN TENDONS,
LIGAMENTS, PERICHONDRIUM, AND PERIOSTEUM, ALL DENSE CONNECTIVE
TISSUES CONTAINING TYPE I COLLAGEN.
C. -1- DOMAIN: THIS SEQUENCE DEFINES FLYE DISTINCT DOMAINS, TWO TRIPLE-
HELICAL DOMAINS (COLLAND COL2) AND THREE NONTRIPLE-HELICAL
DOMAINS (NIL, NC2, AND NC3).
C. -2 PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT
EACH END.
C. -1- PTM: TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT
C. -2 PTM: THE TRIPLE-HELICAL TAIL IS SOME OR ALL OF THE CHAINS.
C. -1- PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
C. -1- PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
C. -1- STMILARITY: DELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
INTERRUPTED HELICES (FACITY) FAMIL.
C. -1- SIMILARITY: CONTAINS 4 WERA DOMAINS.
C. -1- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
C. -1- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
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EMBL; X61024; CAA43358.1; --
EMBL; X61024; CAA43358.1; --
EMBL; J05137; AAA4818.1; --
EMBL; X67327; CAA47744.1; --
PIR; A28037; A28037, PIR; A34485; A34485.
InterPro; IPR000087; Collagen.
InterPro; IPR000087; FN_III.
InterPro; IPR003961; FN_III.
InterPro; IPR003961; FN_III.
InterPro; IPR003129; TSPN.
InterPro; IPR003129; TSPN.
Pfam; PF00201; TSPN.
Pfam; PF00201; TSPN.
Pfam; PF00201; TSPN.
Pfam; PF00201; TSPN.
Pfam; PF00091; TSPN.
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PRINTS; PR00014; FNTYPEIII.
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01-NOV-1998 (Rel. 17, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
11-MAR-2002 (Rel. 41, Last annotation update)
11-MAR-2003 (Rel. 41, Last annotation update)
11-MAR-2003 (Rel. 41, Last annotation update)
11-MAR-2003 (Rel. 41, Last annotation update)
12-MAR-2003 (Rel. 41, Last annotation update)
13-MAR-2003 (Rel. 41, Last annotation update)
13-MAR-2003 (Rel. 41, Last annotation update)
14-MAR-2003 (Rel. 41, Last annotation update)
15-MAR-2003 (Rel. 41, Last annotation update)
16-MAR-2003 (Rel. 41, Last annotation update)
17-MAR-2003 (Rel. 41, Last annotation update)
18-MAR-2003 (Rel. 41, Last annotation update)
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1; Mismatches 97; Indels 36; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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TRIPLE-HELICAL REGION (NC1).

MITH 2 IMPERECTIONS.

NORHELICAL REGION (NC1).

ASP/GLU-RICH (ACIDIC).

ASP/GLU-RICH (BASIC).

TO CHONDROITIN SULFATE (POTENTIAL).

TO CHONDROITIN SULFATE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

MISSING (IN SHORT ISOFORM).

I -> S (IN REF. 4).
NONHELICAL REGION (NC3).
TRIPLE-HELICAL REGION (COL2)
WITH 1 IMPERFECTION.
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7 -> E (IN REF. 4).
P -> A (IN REF. 2).
L -> F (IN REF. 2).
20 -> AG (IN REF. 3).
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26.1%; Pred. No. v...
51; Mismatches
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                                                                                                                                                                                                                                                                                                              ADHESIVE INTERACTIONS OF MONCYTES, MACROPHAGES AND GRANULOCYTES
ADHESIVE INTERACTIONS OF MONCYTES, MACROPHAGES AND GRANULOCYTES
AS WELLA SI N MEDITATING THE UPTAKE OF COMPLEMENT-COATED PARTICLES.
IT IS IDENTICAL WITH GR-3, THE RECEPTOR FOR THE IC3B FRAGMENT OF
THE THIRD COMPLEMENT COMPONENT. IT PROBABLY RECOGNIZES THE R-G-D
PEPTIDE IN C3B. INTEGRIN ALPHA M/BETA-2 IS ALSO A RECEPTOR FOR
FIBRINGEN, FACTOR X AND ICAMI. IT RECOGNIZES PI AND P2 PEPTIDES
OF FIBRINGEN GAMMA CHAIN. ALPHA M/BETA-2 PLAY A CRITICAL ROLE IN
MAST CELL DEVELOPMENT AND IN IMMUNE COMPLEX-MEDIATED
GLOMBRULONEPRRITIS. MICE BRARESSING A NULL MUTATION OF THE ALPHA-M
SUBBUIT GENE DEMONSTRATE INCREASE IN NEUTROPHIL ACCUMULATION, IN
RESPONSE TO A IMMAIRED DEGRANULATION AND PHAGOCYTOSIS, EVENTS THAT
APPARENTLY ACCELERATE APOPTOSIS IN NEUTROPHILS. THESE MICE DEVELOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mac-1 alpha chain reveals homology ditional domain related to von
                                                                                                                 SEQUENCE OF 11-45 FROM N.A.
STRAIN=BALB/C; TISSUB-Spleen;
MEDLINE-86287312; PubMed-2942940;
Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,
Larson R.S., Roberts T.M., Springer T.A.;
A partial genomic DNA clone for the alpha subunit of the mouse complement receptor type 3 and cellular adhesion molecule Mac-1.";
Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
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-! SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. ALPHA-M ASSOCIATES WITH BETA-2.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-! TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND GRANULOCYTES.
                                                                                                                                                                                                                                                                Springer T.A., Teplow D.B., Dreyer W.J.; "Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion glycoproteins and unexpected relation to leukocyte interferon."; Nature 314:540-542(1985).
                                                                with the integrin family and an additional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:96607; Itgam.
Interpro; IPR000413; Integrin_alpha.
Interpro; IPR002035; WFA.
Pfam; PF01839; FG-GAP; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
                                                    "Amino acid sequence of the murine
                                                                                                                                                                                                                         [3]
SEQUENCE OF 17-28.
MEDLINE-85188276; PubMed-3887182;
[1]
SEQUENCE FROM N.A.
MEDLINE-88312584; PubMed-3044779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS: PR01185; INTEGRINA.
PRINTS: PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
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                                                                              Willebrand factor.";
EMBO J. 7:1371-1378(1988).
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----REQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYE-NRQGYRTASVIIALT 149
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Cell adhesion; Receptor; Glycoprotein; Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.4%; Score 141; DB 1; Length 1153; Best Local Similarity 24.2%; Pred. No. 0.0014; Matches 71; Conservative 50; Mismatches 96; Indels 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178DB988AECB0343 CRC64;
                                 INTEGRIN ALPHA-M.
EXTRACELLULAR (POTENTIAL)
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FG-GAP 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT EACH END (BY SIMILARITY).

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
                                                                                                                                                                           SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
STRAIN=SWISS WEBSTER, AND C57BL/6J; TISSUE=Skin;
BEDIINE=961070611. PubMed=8601036; TISSUE=Skin;
Boehme K., ii Y., Oh P.S., Olsen B.R.;
"Primary structure of the long and short splice variants of mouse collagen XII and their tissue-specific expression during embryonic development.";
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- PTM: GLYCÓSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) PAMILY.
-i- SIMILARITY: CONTAINS 4 WUFA DOMAINS.
-i- SIMILARITY: CONTAINS 10 FIBRONECTIN TYPE III-LIKE DOMAINS.
     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
05-MAR-2002 (Rel. 41) chain precursor.
COL12A1.
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INTERPRO: IPRO00087; CO11agn.
InterPro: IPRO03067; FN_III.
InterPro: IPRO03052; FN_III.
InterPro: IPRO03129; TSPN.
InterPro: IPRO03129; TSPN.
InterPro: IPRO02035; VWFA.
Pfam; PF001391; CO11agen; 4.
Pfam; PF001391; CO11agen; 4.
Pfam; PF00041; fn3; 18.
Pfam; PF00092; VWa; 4.
PRINTS; PR00041; FNTYPEIII.
PRINTS; PR00046; FNTYPEIII.
PRINTS; PR00060; FNTYPEIII.
SWART; SM00100; TSPN; 16.
SWART; SM00210; TSPN; 1.
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                                                                                              Mus musculus (Mouse)
                                                                                                                                            NCBI_TaxID=10090;
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12;
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PROSITE; PS50234; VWFA; 4.

Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                               WITH 2 IMPERFECTIONS.
NONHELICAL REGION (NC1).
TO CHOUDROITIN SULFATE (POTENTIAL).
TO CHOUDROITIN SULFATE (POTENTIAL).
TO CHOUDROITIN SULFATE (POTENTIAL).
CELL ATTACHMENF SITE (POTENTIAL).
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TRIPLE-HELICAL REGION (COL1)
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                                            COLLAGEN ALPHA 1(XII) CHAIN.
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FIBRONECTIN TYPE-III 13.
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FIBRONECTIN TYPE-III 16.
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FIBRONECTIN TYPE-III 4
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FIBRONECTIN TYPE-III 7
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MISSING (IN SHORT ISC
                                                                     VWFA 1.
FIBRONECTIN TYPE-III
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M60571;
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M57891;
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   MEDLINE-91035430; PubMed-2229060;
MEDLINE-91035430; PubMed-2229060;
MEDLINE-91035430; PubMed-2229060;
Murine complement C2 and factor B genomic and cDNA cloning reveals
The Complement C2 and factor B genomic and cDNA cloning reveals
The COMPLEMENT C2 WHICH IS PART OF THE CLASSICAL PATHWAY OF
THE COMPLEMENT SYSTEM IS CLEAVED BY ACTIVATED FACTOR C1 INTO TWO
FRAGMENTS: C2B AND C2A. C2A. A SERINE PROTEASE, THEN COMBINES WITH
COMPLEMENT FACTOR 4B TO GENERAȚE THE C3 OR C5 CONVERTASE.

COMPLEMENT FACTOR 4B TO GENERAȚE THE C3 OR C5 CONVERTASE.

C1- CATALYTIC ACTIVITY: CLEAVES C3 IN THE ALPHA-CHAIN TO YIELD C3A AND C5B. BOTH
CLEAVES C5 IN THE ALPHA-CHAIN TO YIELD C5A AND C5B. BOTH
CLEAVES C5 IN THE ALPHA-CHAIN TO YIELD C5A AND C5B. BOTH
CLEAVES C5 IN THE ALPHA-CHAIN TO YIELD C5A AND C5B. BOTH
CLEAVES C5 IN THE ALPHA-CHENINAL OF AN ARGININE RESIDUE.

C1- MISCELLANEOUS: C2 IS A MAJOR HISTOCOMPATIBILITY COMPLEX CLASS-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                             SSDAF---RDPAIKLRNSDVEIFAVGVKDAVRSELEAIASPPAETHVFTVED-FDAFQRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN.
-!- SIMILARITY: WITH COMPLEMENT FACTOR B.
-!- SIMILARITY: CONTAINS 3 SUSHI (SCR) DOMAINS.
-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
HEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD -- SKDHVFPVNDGFQALQGI
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                            01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Complement C2 precursor (EC 3.4.21.43) (C3/C5 convertase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOINED.
                                                                                                  613 SFVLTQSICLRIEQELAA 630
                                                                            212 IHSILKKSCIEI---LAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M60579; AAA37380.1;
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AAA37380.1;
AAA37380.1;
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AAA37380.1;
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AAA37380.1;
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EMBL; M60566; AAA37380.1;
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                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                      musculus (Mouse)
                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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M60578;
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M60568;
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M60571;
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M60573;
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P21180;
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16;
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Signal; Repeat; Sushi; Alternative splicing.
SIGNAL 18
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SIMILARITY).
SIMILARITY).
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BY SIMILARITY.

N-LINKED (GLCNAC. ...) (POTEWITAL).

N-LINKED (GLCNAC. ...) (POTEWITAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.8%; Score 131; DB 1; Length 760;
23.2%; Pred. No. 0.0054;
iive 56; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IN SHORT ISOFORM)
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RELAY SYSTEM (BY
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SUSHI 2.
SUSHI 3.
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                                                                                                                                                                                                                                                                                               InterPro; IPR001314; Chymotrypsin.
InterPro; IPR00143; Sushi_SCR_CCP.
InterPro; IPR001254; Trypsin.
InterPro; IPR002035; WWFA.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50240; TRYPSIN_DOM; 1. PS05ITE; PS00134; TRYPSIN_HIS; 1. PROSITE; PS00135; TRYPSIN_SER; 1. PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00084; sushi; 2.
Pfam; PF00089; trypsin; 2.
Pfam; PF00092; vwa; 11.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00032; CCP; 2.
SMART; SM0020; Tryp_SPC; 1.
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                AAA37381.1;
AAA37381.1;
AAA37381.1;
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AAA37381.1;
AAA37381.1;
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AAA37381.1;
AAA63294.1;
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                                                                                              AAA37381.1;
AAA37381.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.8
Best Local Similarity 23.2
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250
250
760
150
150
211
760
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689
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89
1136
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474
474
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606
760 AA;
                                                                                                                                                                                                                                                  HSSP; P00757; ISGF.
MEROPS; S01.194; -.
MGD; MGI:88226; C2.
                                                                                                                                                                                                                                     PIR; A38876; C2MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                               HSSP;
PEDGINEE FROM N.A., AND PARTIAL SEQUENCE (LONG AND SHORT FORM).

REDLINE=97288521; Pubmed=9143499;
REDLINE=97288521; Pubmed=9143499;
REDLINE=97288521; Pubmed=9143499;
Recke D.R., Olson P.F., Koch M., Knoll J.H.M., Taylor R.,
Rudson D.L., Champliaud M.-F., Olsen B.R., Burgeson R.E.,
"Complete primary structure of two splice variants of collegen XII,
and assignment of alpha 1(XII) collagen (COL12A1), alpha 1(XI)
collagen (COL9A1), and alpha 1(XIX) collagen (COL12A1) to human

TO collagen (COL9A1), and alpha 1(XIX) collagen (COL19A1) to human

TO collagen (COL9A1), and alpha 1(XIX) collagen (COL19A1) to human

TO collagen (COL9A1), and alpha 1(XIX) collagen (COL19A1) to human

TO collagen (COL9A1), and alpha 1(XIX) collagen (COL19A1) to human

TO collagen (COL9A1), and alpha 1(XIX) collagen (COL19A1) to human

TO collagen (COL9A1), and alpha 1(XIX) collagen (COL19A1) to human

TO collagen (COL19A1), and alpha 1(XIX) collagen (COL19A1) to human

TO complete primary STREATH COLLAGEN INTERACTS WITH TYPE I COLLAGEN

CONTAINING FIBRILS, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE COLL AND LG3 DOMAINS MAY BE

LOCALIZED IN THE PERIFFERENTIARE MATRIX (BY SIMILARITY).

COLLAGEN COLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NONTRIPLE-HELICAL SEQUENCES.
ANDITATION AND ALLERNATIVE SPLICALS.
SEQUENCES.
ALCHERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A ALTERNATIVE SPLICING. THE FINAL TISSUE SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINAL TISSUE FORM OF COLLAGEN XII MAY COMBINATION OF LONG AND SHORT ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTEOGLYCAN.
IISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTEOGLYCAN.
SHORT AND LONG ISOFORMS APPEAR IN ADMINON, CHORION, SKELETAL MUSCLE, SMALL INTESTINE, AND IN CELL CULTURE OF DERMAL.
FIBROBLASTES, KERATINOCTIES, AND ENDOTHELIAL CELLS. ONLY THE SHORT ESOFORM IS FOUND IN LUNG, PLACENTA, KIDNEY, AND A SQUAMOUS CELL CARCINOMA CELL LINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT EACH END (BY SIMILARITY).
                                                                                                                           371
                                                                                                                                                            144 -----VIIALTDGELHEDLFFYSEREANRSRDLGAI------VYCVGV------KD 182
                                                                                                                                                                                                                                                                   472
                                                                                                                                                                                                                                                                                                                           EACH END (BY SIMILARITY).

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY SIMILARITY).
                                                                                                                :| | : :| :| :| :| :| ERSQ-----DVTEVITSLDSASYKDHENATGANTYEVLIRVYSMMQTQMDRLGMETSAW
                                                                                                                                                                                                                                                                                                     GNGFRHARNVDRV--LCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMK--AALQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                    GGFDLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLR--MSFIVFSTRGTTLMKLTE
                                                                                                                                                                                183 FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR
                                                                                                                                                                                                                                                                430 LNE--LGSKKDGERHAFILODA-KALOQIFEHMLDVSKL-----TDTICG-----V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: GLYCOŚYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (Rel. 36, Last Sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) collagen alpha 1(XII) chain precursor. COL12A1.
                                                                                               DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAIC_HUMAN STANDARD; F 099715; 099716; 15-7UL-1998 (Rel. 36, Last sequol 15-7UL-1998 (Rel. 36, Last sequol 1-MAR-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                            299 MND-----GLSFISSSVII 312
                                                                                                                                                                                                                                                                                                                                                                                                   : | | : | | | 531 VGDPTSQHGKEFLVEDVII 549
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                               41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART: SHOULT: WIFD: 4.
PROSITE: PS50224. WIFD: 4.
Extracellular matrix: Connective tissue; Repeat; Hydroxylation;
Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WITH 2 IMPERFECTIONS.
NONHELICAL REGION (NCI).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
INTERRUPTED HELICES (FACIT) FAMILY.
SIMILARITY: CONTAINS 4 VWFA DOMAINS.
SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYDROXYLATION (BY SIMILARITY)
HYDROXYLATION (BY SIMILARITY)
HYDROXYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WITH 1 IMPERECTION.
NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION (COL1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRIPLE-HELICAL REGION (COL2)
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PIBRONECTIN TYPE-III 10.
FIBRONECTIN TYPE-III 11.
FIBRONECTIN TYPE-III 12.
FIBRONECTIN TYPE-III 12.
FIBRONECTIN TYPE-III 14.
FIBRONECTIN TYPE-III 14.
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-III 16.
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FIBRONECTIN TYPE-III 4
FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 7
FIBRONECTIN TYPE-III 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIBRONECTIN TYPE-III VWFA 2.
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                                                                                                                                                                                                                                                                                                    InterPro; IPR000087; Collagen.
InterPro; IPR003961; FN III.
InterPro; IPR003962; FILI_Irepeat.
InterPro; IPR003129; TSPN.
                                                                                                                                                                                                                                                                                                                                                                                                    pfam; PF0131; Collagen; 4. pfam; PF00041; fn3; 18. pfam; PF02010; TSN; 1. pfam; PF00092; vwa; 4. prints; PR00014; FNTYPEIII. PRINTS; PR000453; VWFADOMAIN.
                                                                                                                                                                                                                                  EMBL; U73778; AAC51244.1; -. EMBL; U73779; AAD40483.1; -.
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SMART; SM00327; VWA; 4.
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1932
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BINDING
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Trueb J., Trueb B.;
"Type XIV collagen is a variant of
Eur. J. Biochem. 207:549-557(1992)
                                                                                                                                                                                                                                                                                                                                                                                        RECEPTORS.
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       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 PWTAGSRQHALSVG------PQTTTLSVRDLSADTEY------QISVSAMKGWTS 412
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII 212
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MEDLINE-93185668; PubMed-8444186;
Waelchli C., Trueb J., Kessler B., Winterhalter K.H., Trueb B.;
"Complete primary Structure of Chicken collagen XIV.";
Eur. J. Biochem. 212:483-490(1993).
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Last annotation update)
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SEQUENCE OF 402-1549 FROM N.A.
MEDLINE-92339443; PubMed-1339349;
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(Rel. 41, Last anno
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Best Local Similarity 22.19
Matches 74; Conservative
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--- TISSUE SPECTIFICITY:
--- TISSUE SPECTIFICITY:
--- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
C--- PTM: LYSINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
C--- PTM: LYSINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
C--- PTM: LYSINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
C--- PTM: MAY CONTAIN CYSTEINE RESIDUES INVOLVED IN INTER- AND
INTRAMOLECULAR DISULFIDE BONDING:
C--- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
INTERRUPTED HELICES (FACIT) FAMILY:
--- SIMILARITY: CONTAINS 2 VWFA DOMAINS:
C--- SIMILARITY: CONTAINS 6 FIBRORECTIN TYPE III-LIKE DOMAINS.
                                                                                             STRUCTURE BY NMR OF 1852-1885.

MEDLINE-99280705; PubMed=10350466;

Montserret R., Aubert-Foucher E., McLeish M.J., Hill J.M., Ficheux D., Jaquinod M., van der Rest M., Deleage G., Penin F.;

"Structural analysis of the heparin-binding site of the NCI domain of collagen XIV by CD and NMR.";

Biochemistry 38:6479-6488(1999).

FIORNILS VIA COLI. THE COLE BY INTEGRATING COLLAGEN BUNDLES. IT IS PROBABLY ASSOCIATED WITH THE SURFACE OF INTERSTITIAL COLLAGEN FIRELS VIA COLI. THE COLE DOMAIN MAY THEN SERVE AS A RIGID ARM WHICH STICKS OUT FROM THE FIBRIL AND PROTRUDES THE LARGE N-TERNINAL GLOBULAR DOMAIN INTO THE EXTRACELLULAR SPACE, WHERE IT MITERACT WITH OTHER MATRIX MOLECULES OR CELL SURFACE
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Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Cell adhesion; Collagen; Glycoprotein; Signal; 3D-structure. SIGNAL
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FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
of undulin.";
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InterPro; IPR000961; FNLIII.
InterPro; IPR003961; FNLIII.
InterPro; IPR003129; FNIII.
InterPro; IPR003129; TSPN.
InterPro; IPR002139; VWFA.
Ffam; PF00131; Collagen; 4.
Ffam; PF00210; TSPN; 1.
Ffam; PF00210; TSPN; 1.
FRINTS; PR00014; FNNYPEIII.
FRINTS; PR00519; VWFADOMAIN.
SWART; SW00210; TSPN; 1.
SWART; SW00210; TSPN; 1.
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EMBL; X70792; CAA50063.1; -.
EMBL; X66138; CAA46928.1; -.
PIR; S22916; S22916.
PDB; 1B9P; 25-FEB-99.
PDB; 1B9Q; 25-FEB-99.
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SEA 1.
EGF-LIKE 40.
SRA 1.
EGF-LIKE 41.
EGF-LIKE 42.
EGF-LIKE 44.
EGF-LIKE 44, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 45.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                    PROSITE; PS00010; ASX_HYDROXYL; 28.
PROSITE; PS00021: EGF_1; 1.
PROSITE; PS01186: EGF_2; 5.
PROSITE; PS01187: EGF_CA; 1.
PROSITE; PS0124: SEA; 2.
PROSITE; PS5024; SEA; 2.
Hypothetical protein; EGF-like domain; Repeat; Transmembrane.
                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
EGF-LIKE 1 (PARTIAL).
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
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EGF-LIKE 6.
EGF-LIKE 7.
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        Interpro; IPR000082; SEA.
Interpro; IPR002035; vWFA.
Pfam; PF001390; EGF, 2.
Pfam; PF01390; SEA; 2.
Pfam; PF00092; vwa; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00200; EGF_11ke; 38.
SMART; SM00200; SEA; 2.
EGF_Ca
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                                                                                                                                                                                                       1042 DLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGPDGTQVAIIQFSDDPRTEFKLNAYK 1101
                                                                                                                                                                                                                                 DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII 212
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                                                                                                                                                                                           98 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                    26; Gaps
                                                                                                                                                     44 DLYFILDKSGSV-LHHWNELYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E 97
            NOWHELICAL REGION (NC4).
TRIPLE-HELICAL REGION 1.
TRIPLE-HELICAL REGION 2.
POLY-THR.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                 6.8%; Score 130; DB 1; Length 1888; 25.0%; Pred. No. 0.021; Live 44; Mismatches 116; Indels 28
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16-17-FEB-1994 (Rel. 28, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein T20G5.3 in chromosome III (Fragment).
T20G5.3.
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MormPep; T2055.3; CE00478.
InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR000561; EGF-like.
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                                                                                          202666
                                                                                                                                        Conservative
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57 72 BY 104 120 BY 112 129 BY 113 143 BY 157 172 BY 157 173 BY 157 173 BY 158 224 BY 251 265 BY 251 265 BY 251 265 BY 317 330 BY 317 330 BY 3182 330 BY 365 380 BY	4108 4158 421 458 458 466 483 472 468 709 717 736 749 754 768 768 768 768 768	809 822 BY 816 813 BY 816 813 845 BY 851 867 BY 876 BY 876 BY 896 909 BY 920 939 BY 920 953 968 BY 996 1010 BY 996 1010	10004 1019 10021 1038 1047 1060 1072 1070 1095 1113 1105 1124 1150 1164 1157 1173 1175 1194 1201 1224 1228 1223	1251 1264 BY 1275 1275 1275 1273 BY 1302 1315 BY 1305 1345 BY 1366 1345 BY 1367 1367 1367 1367 1401 1415 BY 1426 1424 BY 1456 1443 BY 1456 1464 BY 1456 1466 BY
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                       PRINTS; PRO0453; "WFADOMAIN.
SMART; SM00181; EGF; 1.
SMART; SM00327; VWA; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50234; VWFA; 2.
PROSITE; PS50234; VWFA; 2.
EGF-like domain; Signal; Glycoprotein; Cartilage; Repeat; Coiled coil.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 ENRQGYRTAS--VIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 FIV---ESTRGTILMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY----Y 133
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To JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 41, Last annotation update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DC 01hagen alpha l(XII) chain (Fragment).

COLhagen alpha l(XII) chain (Fragment).

COLhagen Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 TVSSGARPGAQKVGIVFTDGRSQD----YINDAAKKAKDLGFKMFAVGVGNAVEDELREI
                                                                                                                                                                                                                                                                                                                                   . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 120.5; DB 1; Length 496;
Pred. No. 0.023;
7; Mismatches 95; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
2D880A8114C7940F CRC64;
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Pfam; PF00092; vwa; 2.
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RED [1, Yang E.V., Klatt K.P., Tassava R.A.;

MEDINE-9524625; PubMed=7729585;

MEDINE-9524625; PubMed=7729585;

MED [2, Yang E.V., Klatt K.P., Tassava R.A.;

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PIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 8.
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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--- SIMILARITY BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY.
--- SIMILARITY: CONTAINS 2 VWFA DOMAINS.
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
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FIBRONECTIN TYPE-III 2.
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Extracellular matrix; Cc
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SMART; SM00327; VWA; 1.
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Pfam; PF00092; vwa; 1.
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AK001463 Homo sapi
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AK055429 Homo sapi
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AK05536 Homo sapi
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AF421380.1 GI:16566412
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2 (bases 1 to 1414)
Bradley.K.A., Mogridge,J., Mourez,M., Collier,R.J. and Young,J.A.T.
Direct Submission
Submitted (19-SEP-2001) Department of Oncology, University of
Wisconsin-Madison, 1400 University Ave., Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1414)
Bradley K.A., Mogridge, J., Mourez, M., Collier, R.J. and Young, J.A.T., Jennification of the cellular receptor for anthrax toxin Nature 414 (6860), 225-229 (2001)
                                                                                                                                                                                                                     AX34694 Sequence
AC010712 Homo sap1
AC102488 Mus muscu
AX346581 Sequence
AX346804 Sequence
AX346804 Sequence
AX346433 Sequence
AX346433 Sequence
AX351565 Sequence
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Compugen Ltd.
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                 GenCore version
Copyright (c) 1993 - 2000
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100.0%; Pred. No. 0;
tive 0; Mismatches
                         /organism="Homo sapiens"
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/cell_line="HeLa"
1. 103
104. .1210
/note="ATR"
Location/Qualifiers
1. .1414
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5540)
24. Croix, B., Rago, C., Velculescu, V., Traverso, G., Romans, K.E.,
Montgomery, E., Lalla, Riggins, G.J., Lengauer, C., Vogelstein, B. a.
Kinzler, K.W.
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Genes expressed in human tumor endothelium Science 289 (5482), 1197-1202 (2000)
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AF279145.2 GI:14017380
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SRREANRSRDLGALVYCVGVKDFREFARANDSKDHYFPNNDGFALALDEGELFY
SCIEILAAEPSTICAGESFQVVKRGNFFHARNVDRVLCSFKINDSVILNEKPSVED
TYLLCPAPTLKEVGMKAACQVSMNDGLSFISSSVIITTTHCSGGSILAIALLIELLL
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KGKLDALWYLRKGYDRYSWRPQPGDTGRCINFTRWNNORAYPLSNBPP
KGKLDALWYLRKGYDRYSWRPQPGDTGRCINFTRWNNORAYPLSNBPP
APIYTPPPRAPHCPPPPRAPTPPIPSPPTLLPPPPQAPPPRAPPSV"
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St. Croix, B., Vogelstein, B. and Kinzler, K.W.

Direct Submission
L Submission
L Submission
Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, USA
S St. Croix, B., Vogelstein, B. and Kinzler, K.W.
Direct Submission
L Submitted (09-MAY-2001) Johns Hopkins Oncology Center, Johns Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, USA
Sequence update by submitter
On May 9, 2001 this sequence version replaced g1:9857405.
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Pred. No. 2.9e-306;
0; Mismatches 2;
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/db_xref="taxon:9606"
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1104 1172
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144. .1838
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/gene="TEM8"
225. .1835
/gene="TEM8"
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99.8%;
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Matches 1195; Conservative
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                                                               AUTHORS
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      AUTHORS
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Homo sapiens, Similar to tumor endothelial marker 8, clone MGC:19967 IMAGE:4563020, mRNA, complete cds.

BC012074
BC012074.1 GI:15082332
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2112)
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                            tgaaccatccaccatatgtgcaggagagtcatttcaagttgtcgtgagaggaaacggctt
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22-FEB-2000
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Homo sapiens cDNA FLJ10601 fis, clone NT2RP2005000
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Oligo capping; fis (full insert sequence).
Homo sapiens teratocarcinoma cell_line:NT2
clone_lib:NT2RP2 clone:NT2RP2005000.
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Mammalia; Eutheria; Primates;
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
infoebcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Heiso, Martin Krzwyninski, Reta Kutsche, Oliver Lee, Soo
Letticia Heiso, Martin Krzwyninski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lilsa Prabhu, Parvaneh Saeedi, Jacqueline
Res, Daune Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Mcchael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
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             Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/lab_host="DH10B-R"
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                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
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Pred. No. 8.7e-269;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:19967 IMAGE:4563020"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pOTB7"
113. .1114
                                                                               Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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ilarity 99.9%;
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(Tem8) mRNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 5220)
Carson-Walter, E.B., Vogelstein, B., Kinzler, K.W. and St. Croix, B.
Direct Submission
Submitted (JO-MAY-2001) Oncology, Johns Hopkins University, 1650
Orleans Street, Baltimore, MD 21231, USA
Location/Qualifiers
 ggctctgcaaggcatcatccactcaattttgaagaagtcctgcatcgaaattctagcagc
                                                                                                                                                                                                                                                                                                                        /product-"tumor endothelial marker 8 precursor"
/protein_id="AAL11999.1"
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/db_xref="taxon:10090"
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Mus musculus tumor endothelial r
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274. 1962
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/gene="Tem8"
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                       "Isogai,T. and Otsuki,T.
Direct Submitsion

Submitted (16-FBB-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@fhi.co.jp, Tel:81-438-52-3951, Pas.81-438-52-3952)
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="Baa91707.1"
/db_xref="G1:7022738"
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VVRGNGFRHARNVDRVLCSFKINDSVTLSKSLQSPWVSSTSGFKEGNSHPCLPARPHT
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Pred. No. 1.2e-225;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                            /note="unnamed protein product"
                                                                                                                                                                                                                                                                              /cell_line="NT2"
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/db_xref="taxon:9606"
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/db_xref="G1:15987505"
/translation="MDRAGRICAGGIRGLCVAALVUVCAGHGGRREDGGPACYGGFDLY
FILDKGGSVLHHWNETYFYEQLAHRFISPQLRMEFINFSTRGTTLAKLTEDREQIRG
GLEELGKVLPGGDTYRHEGFERASEQIYYENGGGFRASVITALTOGELHEDLFFYSE
REANBSRDLGAALVYCWGVKDFNETQLARIANSVEHTPFPVNDGFQALGGIHSTLKKSC
IEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPPAVEDTY
LLCPAPTLIKEVGWARALQVSMNGLSFISSSVITTTHTGSDGSILAALLLVLFLLLAL
ALLWWFWPLCCTVIIKEVPPPPVESSEEEDDDGLEKKKWPTWDSYYGGSGVGGGIRRM
EVRGEKGSTEEGAKLEKAKNARVKMPEQEFEFPRALNNWRRPSSPRKWYSPIKG
KLDALWWLLRKGYPRSVMRROPGGFGGRGINFTRVKNORDAXYPLNNTYHPSSPPAPP
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Pred. No. 1e-215;
); Mismatches 136; Indels 0;
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1329 c 1235 g 1250
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1228. .1293
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/gene="Tem8"
355. .1959
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87.3%;
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/gene="Tem8"
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/qene="Tem8"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens cDNA: FLJ21776 fis, clone HEP00171.
AK025429
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/clone_lib="HEP"
/note="Cloning vector pl
323. 1147
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Submitted (124-007-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full Insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- 6 3'-end one pass sequencing: RNA, HRI, and Blotechnology Center, National Institute of Technology and Evaluation; clone selection for full Insert sequencing: RAB and
Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y.,
Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y.,
Sekine, M., Kikuchi, H., Kanda, K., Waqatsuma, M., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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Pred. No. 7.7e-57;
0; Mismatches 377;
                                                                                                                           Isogai, T., Otsuki, T. and Sugiyama, T. Direct Submission
                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="testis"
/clone_lib="TEST12"
/note="cloning vector: |
614 c 517 g 4
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56.6%;
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                             /translation-"MKAALQVSMNDGLSFISSSVIITTHCSDGSILAIALLIFELL
ALALLWWFWDFLCTVIIKEVPPPAEESEEEDDDGLEKKWWFPUDASYYGGRGVGGIK
RMEVRWGEKGSTEEGAKLEKRNAMRVKMPEQEYEFPEPRILNINNMRRPSSPRKWYSPI
KGKLDALWYLLAKGYDRYSVMRQPGDTGRCINFTRYKKNNOPAKYPLNNAYHTSSPPP
APIXTPPPPAPHCPPPPPSAPTPPIFSPPSTLPPPPPQAPPRNRAPPFSRPPRSV"
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Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,
Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiquchi,S.,
Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
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Catarrhini; Hominidae;
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Pred. No. 4.2e-133;
0; Mismatches 2;
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/protein_id="BAB15128.1"
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Mammalia; Eutheria; Primates;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center Center Center Center Code: BCM-HGSC Center Code: BCM-HGSC Center Cede: BCM-HGSC. Center Center Center Center Center: villalon@bcm.tmc.edu.
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B. Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRI 20-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (15-AUG-2001) National Institutes of Health, Mammalian
Submitted (15-AUG-2001) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                   aagaagttggcatgaaagctgcactccaggtcagcatgaacgatggcctcttttatct 1022
                                                                                                                                                                                                                                                                                                                             843 gacatgcccgcaacgtggacagggtcctctgcagcttcaagatcaatgactcggtcacac 902
                                                                                                                                                                      Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
723 ctctgcaaggcatcatccactcaattttgaagaagtcctgcatcgaaattctagcagctg
                                783 aaccatccaccatatgtgcaggaggtcatttcaagttgtcgtgaggaggaacggcttcc
                                                                                                        740 AGGCTTCCTCTGAGTGTGGAGAACCCTACCATGTGGGTTATTCATGGAAATGGCTTTC
                                                                                                                                                                                                                             Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutele
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Abass 1 to 1297)
Strausberg, R.
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Homo sapiens, clone IMAGE:4705862, mRNA, partial cds.
EC012475
EC012475.1 GI:15214683
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/clone_lib="NIH_MGC_87"
/lab_host="DH108"
/note="Vector: pcMV-SPORT6"
<1. 295
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Unpublished

2 (bases 1 to 2026)

2 (bases 1 to 2026)

2 (bases 1 to 2026)

3 (sisgal_T., Otsuki,T. and Sugiyama,T.

Direct Submission

Submitted (24-0cT-2001) Takao Isogai, Helix Research Institute,

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hii.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Blocchonology (RAB); cDNA library

Construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: RAB and
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Ninomiya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kodaira, H., Furuya, T., Takahashi, M., Tanikwa, M., Yamazaki, M.,
Kamihara, K., Katsuta, N., Sato, K., Tanikwa, M., Yamazaki, M.,
Yangiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishi, S.,
Yamamoto, J., Isono, Y., Rawai-Hio, Y., Saito, K., Nishikwa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kimura, K., Yamashita, H., Watsuo, K., Yamahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakani, B., Suzuki, Y., Sugano, S.,
Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.,
Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.,
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/translation="FQVVRNDGISFISSSVIITTTQGSLHKIASGPTTAACME"
333 c
333 c
276 g
323 t
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oligo capping; fis (full insert sequence).
Homo sapiens synoviocytes from rtheumatioid arthritis (HS-RA) cDNP-
Homo sapiens synoviocytes from rtheumatioid arthritis (HS-RA) cDNP-
Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens cDNA FLJ31074 fis, clone HSYRA2001476.
AK055636
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Pred. No. 1.2e-51;
0; Mismatches 5;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 134)

1 (bases I to 134)

1 (bases I to 134)

Bell, S. B., Mavila, A., Salazar, R., Bayless, K.J., Kanagala, S., Maxwell, S.A. and Davis, G.E.

Differential gene expression during capillary morphogenesis in 3D collagen matrices: regulated expression of genes involved in basement membrane matrix assembly, cell cycle progression, cellular differentiation and G-protein signaling

J. Cell. Sci. 114 (Pt 15), 2755-2773 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens capillary morphogenesis protein-2 mRNA, complete cds. AY040326 GI:15418998
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/note="CMG-2; contains a von Willebrand factor A domain;
regulated during endothelial cell morphogenesis; targets
to the endoplasmic reticulum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission State Submission Submitted (14-JUN-2001) Pathology, Texas A&M University System Submitted (14-JUN-2001) Pathology, Texas A&M University System Health Science Center, 208 Reynolds Medical Building, College Station, TX 77843-114, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 ATGGTGGCGGAGCGGTCCCCGGCCCCGGGAGCTGGCTGCTGTTCCCCGGGCTGTGG 200
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Pred. No. 3.9e-44;
0; Mismatches 257;
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/chromosome="4"
                           677
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Davis, G.E. and Bell, S.E.
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GCACCTATCCTGAATAAAGCTGG
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59.0%;
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Best Local Similarity 59.0'
Matches 378; Conservative
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                                                                                                                                                                                                                                                                                                                                       /protein_id="BBB70976.1"
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                                                                                                                                                                              /note="cloning vector: pWE18SFL3~primary culture, synoviceytes from rtheumatioid arthritis" 46. ~783
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                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC025010 81017 bp DNA linear HTG 13-JUL-2000
Homo sapiens chromosome 4 clone RP11-85D17 map 4, LOW-PASS SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           644 aaagatttcaatgagacacagctggcccggattgcggacagtaaggatcatgtgtttccc 703
                                                                                                                                                                                                                                                                                                                          acagecagegtcatcattgetttgactgatgagaactccatgaagatctcttttctat 583
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                                                                                                                                                                                                                                                               344 tootttattgtttttotocacccgaggaacaaccttaatgaaactgacagaagaaa
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Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                     9309 9320; cont.19 1100 bp 9421 10187; contig of 767 bp in length 10188 10287; gap of 100 bp 10288 11042; contig of 755 bp in length 11043 11142; gap of 100 bp 100 bp 11143 11910; contig of 788 bp in length 11911 12757; contig of 747 bp in length 12758 12857; gap of 100 bp 12858 13619; contig of 762 bp in length 12858 13619; contig of 762 bp in length 13620 13719; gap of 100 bp 13620 13719; gap of 100 bp 13720 14493; contig of 762 bp in length 13620 13719; gap of 100 bp 100 bp 13720 14493; contig of 774 bp in length
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18001 18767: contig of 767 bp in length
18768 18867: gap of 100 bp
18868 19642: contig of 775 bp in length
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2433: contig of 766 bp in length
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3310: con+:..
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of 748 bp in length
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467: contig of 755 bp in length
agap of 100 bp
320: contig of 753 bp in length
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contig of 766 bp in length
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763 bp in <sup>]</sup>
                                                                                                                        Web site: http://www-seq.wi.mit.edu
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                                                        Genome Center
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5899: con'
5999: gap of
6764: con'
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                                 23072: contig of 770 bp 11

172: gap of 100 bp

123941: contig of 769 bp 14

1041: gap of 100 bp

124799: contig of 758 bp 14

1899: gap of 100 bp

25667: contig of 768 bp 14
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53427: gap of
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Signatory

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HOMO Sapiens chromosome 4 clone RP11-85D17 map 4, LOW-PASS SEQUENCE
SAMPLING.
AC025010
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1 (bases 1 to 81017)

Birran, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 4, clone RP11-85D17
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pred. No. 5.7e-40;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                    25 56021; gap of 100 bp 10 length 25 5681; contig of 760 bp in length 32 5681; contig of 760 bp in length 100 bp 1
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771 bp 1
100 bp
756 bp 1
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55054: contig of
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HTG; HTGS_PHASE0.
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99.58;
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TITLE
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AUTHORS
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48171: contig of 731 bp in

8271: gap of 100 bp

49028: contig of 757 bp in

9128: gap of 100 bp

49883: contig of 755 bp in
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29104: contig of 766 bp
04: gap of 100 bp
29969: contig of 765 bp
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28238: contig of 763 bp
28338: gap of 100 bp
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34337: contig of
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                                                        for Genome
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                                                                                                                                                                                                                                                                                                                                                                                            * sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
                               100 bp
of 755 bp in length
100 bp
of 753 bp in length
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11910: contig of 768 bp in length
12010: gap of 100 bp
12857: contig of 747 bp in length
12857: gap of 100 bp
13619: contig of 762 bp in length
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18867: gap of 100 bp
19642: contig of 775 bp in length
19742: gap of 100 bp
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            Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This record contains 94 individual
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of 765 bp i.
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.34 3310: contig of 77
1 3410: gap of
4176: contig of 777
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5 6864: gap of 100
7612: contig of 7
3 7712: gap of 100
8467: contig of 7
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10187: contig of
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9320: contig
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13619;
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11042: cont
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11143 11910: cont
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5036; c
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5899: c
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6764: c
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.C. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
/db_MGE:3484366"
/tissue_type="Hammary tumor. WAP-TGF alpha model. 7 months old, gross tissue."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROD 12-JUL-2001
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/XLNL at: http://lmage.llnl.gov series: IRAK Plate: 7 Row: e Column: 5 Series: RAK Plate: 7 Row: e Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (28-FEB-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECUUJSUU 2557 bp mRNA linear RK
Mus musculus, clone IMAGE:3484366, mRNA, partial cds.
ECUUJSUU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1189;
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                                                                                                                                                                                                                                                                                                                                                                                         vector: pME18SFL3"
50 q 307 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.0%; Score 113; DB 9; 1
.00.0%; Pred. No. 6.3e-19;
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Matches 113; Conservative 0; Mismatches
                                                                                                                                                                            1.1169
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1009794"
/clone_lib="PLACE1"
                                                                                                                                                                                                                                                                                                                                                     /tissue_type="placenta"
/note="cloning vector: F
304 c 250 g 30
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                                                                                                                   University of Tokyo.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg, R.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens placenta conA to mRNA, clone_lib:PLACE1
clone:PLACE1009794.
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Homo sapiens cDNA FLJ11298 fis, clone PLACE1009794.
   11719: gap of 100 bp 52473: contig of 754 bp in length 52573: gap of 100 bp 53327: contig of 754 bp in length 53427: gap of 100 bp 100 bp 55921: contig of 771 bp in length 55054: contig of 775 bp in length 55921: contig of 765 bp in length 55921: contig of 767 bp in length 56021: gap of 100 bp 55921: contig of 760 bp in length 5681: gap of 100 bp 55921: contig of 760 bp in length 5881: gap of 100 bp 55781: contig of 760 bp in length 5881: gap of 100 bp 55781: contig of 760 bp in length 5681: gap of 100 bp 10
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58492: contig of 754 bp in length
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59364: contig of 772 bp in length
100 bp
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Pred. No. 5.7e-
0; Mismatches
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55921: contig
56021: gap of
          51719: gap of
52473: contig
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59365 59464: gap of
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99.5%;
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Matches 195; Conservative
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Genome
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                     /translation="EKPVSIQPSSILCPAPVLNKDGETLEVSISYNDGKSAVSRSLTI
TATECTNGIAAIVALIVLLLLGGAALMWWFWPLCCKVVIKDPPPPPPSAPMEEEEEDPL
PNKKWPTVDASYYGGRGVGGIKRMEVRWGDKGSTEEGARLEKAKNAVVWPEEEIPIP
SRPPRPRPTHQAPQIKWYTPIKGRLDALMALIMKQYDRVSLMRPQEGDEGRCINFSRV
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                                                                                                                                                                                                                                                                                                            AGATGGAGAAACTCTTGAAGTTTCAATCAGCTATAATGATGGGAAGTCTGCTGTCTCAAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 3 clone RP11-734E15, WORKING DRAFT SEQUENCE,
                                                                                                                                                                     Gaps
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                                                                                                                                                                                                    1 TGAGAAGCCAGTGAGCATTCAGCCAAGTTCCATCCTTTGTCCTGCACCTGTCCTGAACAA
                                                                                                                                                                                                                                                                      967 agttggcatgaaagctgcactccaggtcagcatgaacgatggcctctctttatctccag
                                                                                                                                                                     ;
0
                                         /product="Unknown (protein for IMAGE:3484366)"
/protein_id="AAH03908.1"
/db_xref="GI:13278124"
                                                                                                                                                    Length 2557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                               tgtgattatcaaggaggtccctccaccccctgccgaggaggaggga 1194
                                                                                                                                                                                                                                                                                                                                          241 AGTGGTTATCAAGGACCCTCCCCACCACCATTGTGCACGAATGGAGGA 288
                                                                                                                                                                     Indels
                                                                                                                                                    Score 92.8; DB 10;
Pred. No. 1.9e-13;
); Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-2000 (Rel. 63, Created)
13-JUL-2000 (Rel. 64, Last updated, Version 3)
                  /note="Vector: pCMV-SPORT6"
  /clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                            standard; DNA; HTG; 162448 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.H.;
"The sequence of Homo sapiens clone";
Unpublished.
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                                       /codon_start=2
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Sequencing Center, Washington University School of Medicine, 4444 park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 45 contigs. The true order of the pleces as is not known and their order in this sequence record is runs of N but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                       On Jul 12, 2000 this sequence version replaced gi:8810547
                                                                                                                                                          center coue: wouse.

Web site:http://genome.wustl.edu/gsc/index.shtml

Center project name: H_NBO734E15

Centering vector: plasmid; 0%

Consensus quality: 14001 bases at least Q40

Consensus quality: 14018 bases at least Q20

Consensus quality: 149318 bases at least Q20

Consensus quality: 149318 bases at least Q20

Consensus quality: 149318 bases at least Q20

Consensus quality: 140318 bases; agarose-fp

Quality coverage: 3.25 in Q20 bases; sum-of-contigs
                                                                                                                        Center: Washington University Genome Sequencing Center
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9: contig of 5281 bp in length

9: gap of unknown length

7: contig of 3588 bp in length

7: gap of unknown length

8: contig of 4583 bp in length

8: contig of 4583 bp in length

8: contig of 5348 bp in length

8: gap of unknown length

8: gap of unknown length

9: contig of 4792 bp in length

9: contig of 4997 bp in length

7: contig of 4997 bp in length

7: gap of unknown length

7: gap of unknown length

1: contig of 4514 bp in length

1: gap of unknown length

1: gap of unknown length

1: gap of unknown length
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1193 gaaaataaaataaaataacaagaagaagaaagaaagaaatcccacagaaacagataact 1252 1253 aacacagcccgtgcaacgtattttatacaatgctctgaaaatcatagtctcaatctagac 1312 Gaps ö Length 162448; /note="assembly\_name:Contig27 clone\_end:SP6 vector\_side:left" 1639. .17828 1339. .17828 1700te="assembly\_name:Contig28" 17929. .19840 Indels Ouery Match 4.4%; Score 62; DB 30; L. Best Local Similarity 55.0%; Pred. No. 0.00012; Matches 122; Conservative 0; Mismatches 100; /note="assembly\_name:Contig29"
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22018. :24146
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9, 2002, 10:35:58; Search time 98.32 Seconds (Without alignments) 388.682 Million cell updates/sec US-09-970-076-10 1131 1 MSFIVFSTRGTTLMKLTEDR.....stSGFKEGNSHPCLPARPHT 218 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model Gapop 10.0 , Gapext 0.5 BLOSUM62 August Title: Perfect score: Scoring table: Sequence: Run on:

528882 Total number of hits satisfying chosen parameters:

528882 segs, 175299045 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	å Query Match	% Query Match Length DB	рв	ID	Description
1	1131	100.0	218	2	US-09-629-469A-11706	Sequence 11706, A
7	996	85.4	328	φ	US-10-038-307-26	
m	996	85.4	333	ø	US-10-038-307-2	
4	996	85.4	342	φ	US-10-038-307-22	22,
5	996	85.4	345	ø	US-10-038-307-24	24,
9	996	85.4	551	ဖ	US-10-038-307-18	18,
7	996	85.4	564	П	PCT-US02-08253-187	Sequence 187, App
œ	996	85.4	564	٦	PCT-US02-08253-232	Sequence 232, App
6	996	85.4	564	9	US-10-038-307-20	Sequence 20, Appl
10	996	85.4	564	^	US-60-389-987-1823	Sequence 1823, Ap
11	096	84.9	562	7	PCT-US02-08253-194	
12	096	84.9	562	-	PCT-US02-08253-301	Sequence 301, App
13	945	83.6	534	φ	US-10-038-307-12	12, 7
14	945	83.6	543	ø	US-10-038-307-10	10,
15	945	83.6	543	9	US-10-038-307-14	14,
16	945	83.6	543	9	US-10-038-307-16	16,
17	704	62.2	538	9	US-10-047-542-99	66
18	206	44.7	488	ဖ	US-10-104-047-2639	2639
19	206	44.7	488	ø	US-10-038-307-6	Sequence 6, Appli
20	206	44.7	488	7	US-60-373-595-10	П
21	505	44.7	587	ø	US-10-125-540-312	312
22	495	43.8	487	9	US-10-038-307-8	Sequence 8, Appli
23	415	36.7	381	9	US-10-038-307-4	4
24	111	8.6	1152	'n	US-09-592-617A-43	Sequence 43, Appl
25	105.5	9.3	3063	П	PCT-US02-08253-257	257
56	105.5	9,3	3063	٦	PCT-US02-19669-61	Sequence 61, Appl

63, Appl	61, Appl	63, Appl	33525, A	22380, A	1, Appli	116, App	33, Appl	2170, Ap	27, Appl	27, Appl	5698, Ap	5699, Ap	5700, Ap	34, Appl	294, App	294, App	294, App	294, App
Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Sequence	Sequence	Sequence	Sequence	Seguence	Seguence
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9.3	6.3	9.3	8.8	8.8	8.7	8.7	8.7	8.5	8.4	8.4	8.2	8.2	8.2	8.1	8.1	8.1	8.1	8.1
105.5	105.5	105.5	99.5	99.5	96	86	96	96.5	95	95	92.5	92.5	92.5	92	92	92	92	92
27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

APPLICANT: 1204A, TETSUO
APPLICANT: HAYASH, KOJI
APPLICANT: HAYASH, KOJI
APPLICANT: HAYASH, KOJI
APPLICANT: SHITO, KAONGU
APPLICANT: SHITO, KAONGU
APPLICANT: SHITO, KAONGU
APPLICANT: SHITO, SHIZUKO
APPLICANT: SHITONO, JUNICHI
APPLICANT: SHIZUKO
APPLICANT: ORGITANA, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: NAGAMATSI, AI
APPLICANT: PRING DATE: 2000-07-28
PRIOR PRIOR PAPLICANTON NUMBER: JP 2000-118776
PRIOR PAPLICANTON NUMBER: JP 2000-118776
PRIOR APPLICANTON NUMBER: JP 2000-118776
PRIOR APPLICANTON NUMBER: JP 2000-05-09
PRIOR PRILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-18
PRIOR APPLICANTON NUMBER: 60/159,590
PRIOR APPLICANTON NUMBER: 60/159,590
PRIOR APPLICANTON NUMBER: 60/159,590
PRIOR PILING DATE: 2000-02-17
NUMBER OF SEQ 1D NOS: 19025
PRIOR FILING DATE: 2000-02-17
NUMBER OF SEQ 1D NOS: 19025 Length 218; Query Match 100.0%; Score 1131; DB 5; Best Local Similarity 100.0%; Pred. No. 5.6e-106; Matches 218; Conservative 0; Mismatches 0; Sequence 11706, Application US/09629469A GENERAL INFORMATION: APPLICANT: OTA, TOSHIO APPLICANT: ISOGAI, TAKAO ; ORGANISM: Homo sapiens US-09-629-469A-11706 RESULT 1 US-09-629-469A-11706

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; ORGANISM: Homo sapiens
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260 KINDSVTLNE 269
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Matches 188; Conserv
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; Sequence 2. Application US/10038307
; GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'REFF
APPLICANT: Engin OSKAYNAR
; APPLICANT: Engin OSKAYNAR
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; TILE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; FILE REFRENCE: 7853-253-999
; CURRENT FILING DATE: 2002-06-28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SED ID NOS: 26
; SOFTWARE: PASTSEQ for Windows Version 4.0
; SED ID NO 2
; LENGTH: 333
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60
                        RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
                                         Sequence 26, Application US/10038307
Sequence 26, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Engin OZKAYNAK
APPLICANT: Budith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REPERENCE: 7833-253-999
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 966; DB 6; Length 328;
Pred. No. 4.2e-89;
2; Mismatches 0; Indels
                                                                                                                                         Query Match 85.4%;
Best Local Similarity 98.9%;
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Homo sapiens
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KINDSVTLNE 269
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US-10-038-307-2
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LENGIH: 328
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                                                                                 Sequence 22, Application US/10038307

Sequence 22, Application US/10038307

GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Heresa L. O'KEFF
APPLICANT: Engin OZKANANA
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT FILIGH DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY
                                                               1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY
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 Length 333;
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Pred. No. 4.4e-89;
2; Mismatches 0; Indels
Score 966; DB 6;
Pred. No. 4.2e-89;
2; Mismatches 0
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98.9%;
     85.4%;
98.9%;
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                     Best_Local Similarity 98.9
Matches 188; Conservative
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US-10-038-307-22
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TYPE: PRT
ORGANISM: Homo sapiens
                         260 KINDSVTLNE 269
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      181 KINDSVTLSK 190
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PCT-US02-08253-232
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LENGTH: 564
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APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ 1D NOS: 26
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: James B. ROTTWAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
ITILE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
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                                                                                                                                                                                                                      85.4%; Score 966; DB 6; Length 345; 98.9%; Pred. No. 4.4e-89;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity
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                                                                                                                 SEQ ID NO 24
LENGTH: 345
TYPE: PRT
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LENGTH: 551
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Gibson, Bradford
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US-60-389-987-1823
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Best Local Similarity
Matches 187; Conserv
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260 KINDSVTLNE 269
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US-10-038-307-20
Sequence 2.0, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Engin OZKATNAK
APPLICANT: Engin OZKATNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-99
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 564
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Pred. No. 8.7e-89;
. . . . . . . . . . . . Indels
                                                   Length 564;
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                                                 Score 966; DB 1;
Pred. No. 8.7e-89;
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                                                                            2; Mismatches
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2.60-389-987-1823

Sequence 1823, Application US/60389987

GENERAL INFORMATION:

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Fahy, Eoin D.

APPLICANT: Zhang, Bing
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98.9%;
                                                      85.4%;
98.9%;
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Matches 188; Conservative
                                                                                 Conservative
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US-10-038-307-20
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260 KINDSVTLNE 269
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                                                                 Best_Local Similarity
Matches 188; Conserv
                  PCT-US02-08253-232
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                                                        Query Match
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APPLICANT: Taylor, Steven W. APPLICANT: Taylor, Steven W. APPLICANT: Glenh, Gary M. APPLICANT: Glenh, Dale E. TILLE OF INVENTION: TARGETS FOR THERAPEUTIC INVERVENTION TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME FILE REPERENCE: 660088.465P2 CURRENT APPLICATION NUMBER: US/60/389,987 CURRENT FILING DATE: 2002-06-17 NUMBER OF SEQ ID NOS: 3025 SOFTWARE: FastSeq for Windows Version 4.0 SEQ ID NO 1823
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; Sequence 194, Application.
; Sequence 194, Application.
; Applicant Carson-Walter, Eleanor
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Wogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
; GURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR PILING DATE: 2001-04-11
; PRIOR PAPLICATION NUMBER: 66/308,829
PRIOR FILING DATE: 2001-08-01
                                                                                                                                                                                                                                                                                                                                                                                Score 966; DB 7; Length 564;
Pred. No. 8.7e-89;
2; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 194
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Best Local Similarity 98.9%;
Matches 188; Conservative
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61 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
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APPLICANT: Theresa L. O'KEFFE
APPLICANT: Theresa L. O'KEFFE
APPLICANT: Theresa L. O'KEFFE
APPLICANT: Brigin OZRAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                   1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY
                                                                                                     Length 534;
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Pred. No. 1.1e-86;
2; Mismatches 0;
                                                                                                Score 945; DB 6;
Pred. No. 1.1e-86;
2; Mismatches 0
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Best Local Similarity 97.9%;
Matches 186; Conservative ;
                                                                                                    83.6%;
                                                                                                    Query Match 83.6
Best Local Similarity 97.9
Matches 186; Conservative
   ; LENGTH: 534
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-12
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ORGANISM: Homo sapiens
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KINDSVTLNE 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Sequence 12, Application US/10038307 | Sequence 12, Application US/10038307 | SEMERAL INFORMATION |
| APPLICANT: James B. ROTTMAN |
| APPLICANT: Theresa L. O'KEEFE |
| APPLICANT: Bigin OZKAYNAK |
| APPLICANT: Judith J. HEALEY |
| TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods |
| FILE REFERENCE: 7853-253-999 |
| CURRENT APPLICATION UMBER: US/10/038,307 |
| CURRENT FILIKO DATE: 2002-06-28 |
| NUMBER OF SEQ ID NOS: 26 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 562;
                                                                                                                                                                                                                         Sequence 301, Application PC/TUS0208253
GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Worlstein, Bert
APPLICANT: Winzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR PLILNG DATE: 2001-04-11
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 301
LENGTH: 562
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258 KINDSVTLNE 267
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Matches 187; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                 RESULT 12
PCT-US02-08253-301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US02-08253-301
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Query Match

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Gaps

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APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
TITE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
TITE REPERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2022-06-28
NUMBER OF SEQ ID NOS: 26
SOCTAME: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 543
TYPE: PRT PRESE PRESE APPLICATION NOT 
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83.6%; Score 945; DB 6; Length 54:
Best Local Similarity 97.9%; Pred. No. 1.1e-86;
Matches 186; Conservative 2; Mismatches 0; Indels
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258 KINDSVTLNE 267
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Search completed: August 9, 2002, 10:35:59 Job time: 357 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

9, 2002, 10:35:57; Search time 98.32 Seconds August Run on:

(without alignments) 593.720 Million cell updates/sec

8-920-026-60-SD

1728 1 MATAERRALGIGFQWLSLAT......TTHCSLHKIASGPTTAACME Perfect score:

333

Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

528882 seqs, 175299045 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptodata/2/paa/USO6\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/paa/USO6\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/paa/USO7\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/paa/USO8\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/paa/USO8\_NEW\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/paa/USO8\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptodata/2/paa/USO8\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ID Description	-2 Sequence 2,	US-10-038-307-20 Sequence 20, Appl	4 Sequence 24	2 Sequence	US-10-038-307-18 Sequence 18,	-187		823	e Sednence	4	9	US-10-038-307-10 Sequence 10,	94	PCT-US02-08253-301 Sequence 301,		US-09-629-469A-11706 Sequence 11706, P	Sednence	639 Sequence 2639	JS-10-038-307-6 Sequence 6, Appl	.0 Sequence 10	12	Sequence 8, 1	Sequence 4,	C	12-03-392-01/A-43
		DB	9	o	9	9	9	-	7	7	9	9	ø	9	-	7	9	Ŋ	9	9	9	7	9	9	9	ď	1
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		Score	1728	1728	1718	1713.5	1650.5	1649	1649	1649	1636	1628	1628	1618	1553	1553	1487	996	903	800.5	800.5	800.5	785.5	771	699	2 45	
	Result	No.		7	٣	4	S	9	7	æ	D	10	11	12	13	14	15	16	17	18	19	. 50	21	22	23	2.4	

301

Sequence 22380, A Sequence 1, Appli	Sequence 33525, A	Sequence 257, App	Sequence 61, Appl	Sequence 63, App.	Sequence 61, Appl	Sequence 63, Appl	Sequence 5866, Ap	Sequence 2, Appli	Sequence 3, Appli	Sequence 59, Appl	Sequence 4, Appli	Sequence 1591, Ap	Sequence 28757, 1	Sequence 34, Appl	Sequence 294, App	Sequence 294, App	Sequence 294, Apl
US-10-155-881-22380 US-09-805-354-1	US-10-155-881-33525	PCT-US02-08253-257	PCT-US02-19669-61	PCT-US02-19669-63	US-10-177-293-61	US-10-177-293-63	US-60-360-039-5866	US-09-805-354-2	US-09-805-354-3	US-09-592-617A-59	US-10-150-821-4	US-60-389-987-1591	US-10-155-881-28757	US-09-904-920A-34	US-10-121-049-294	US-10-121-050-294	US-10-121-053-294
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646	460	3063	3063	3063	3063	3063	3051	191	191	187	3594	1207	682	915	915	915	915
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134.5	132	131	131	131	131	131	128	125.5	124.5	121.5	118.5	117.5	114	114	114	114	114
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## ALIGNMENTS

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                    GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: James B. FOTTMAN
APPLICANT: Engin OZKAYNAK
APPLICANT: Endith J. HEALEY
TILE OF INVENTION: Tango 10 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASELEQ FOR WINDOWS VERSION 4.0
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Pred. No. 1.7e-154;
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100.0%; Pred. No. 1...
0; Mismatches
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US-10-038-307-2
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1
US-10-038-307-2
                                                                                                                                                                                                             LENGTH: 333
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Theresa L. O'KEEFE
APPLICANT: Brid OZKAYNAK
APPLICANT: Brid OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: TANDOR, TANDOR
                                                                APPLICANT: James E. ROTTMAN
APPLICANT: James L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Joidth J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-553-999
CURRENT APPLICANT: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
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100.0%; Pred. No. 3.6e-154;
iive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: James B. ROTIMAN
                  Sequence 20, Application US/10038307 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 333; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-038-307-20
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LENGTH: 345
US-10-038-307-20
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                                                                                                                                                                                                                                                                                                          241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
                                                                                                                                                                                                                                           181 KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
                                                                                                                                                                                                                                                                                                                             61 EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                                                                            61 BIXYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                                                                                                                         HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                                                                                          Gaps
                                         1 MATABRRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
                                                         APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
FILE REFERENCE: 7853-253-999
FURRENT APPLICATION NUMBER: US/10/038,307
CURRENT PILLING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOGTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 342
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Pred. No. 4.2e-153;
0; Mismatches 0;
pred. No. 1.6e-153;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                DGLSFISSSVIITTTHCSLHKIASGPTTAACME 333
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 99.78;
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Best Local Similarity 97.4
Matches 333; Conservative
 Best Local Similarity 99.7
Matches 332; Conservative
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US-10-038-307-22
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US-10-038-307-22
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Length 345;

DB 6;

Score 1718;

Query Match

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Query Match
Best Local Similarity
            ; LENGTH: 564
; TYPE: PRT
; ORGANISM: HOMO S
PCT-US02-08253-187
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SEQ ID NO 187
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Pred. No. 6.9e-147;
2; Mismatches 2; Indels 5;
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GENERAL INFORMATION:
APPLICANT: CATSON-Walter, Eleanor
APPLICANT: St. COTAX, Brad
APPLICANT: St. COTAX, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
TILE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/388,829
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
PRIOR PELICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
SOFTWARE: FastSEQ for Windows Version 4.0
              301 KAALQVSMNDGLSFISSSVIITTTHCSLHKIASGPTTAACME 342
292 KAALQVSMNDGLSFISSSVIITTHCSLHKIASGPTTAACME
                                                                                                                                                APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Con
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
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                                                                        RESULT 5
US-10-038-307-18
: Sequence 18, Application US/10038307
; GENERAL INFORMATION:
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Best Local Similarity 97.3%;
Matches 320; Conservative
                                                                                                                                     APPLICANT: James B. ROTTMAN
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US-10-038-307-18
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GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Wogelstein, Bert
TILE OF INVENION: Renoeth
TILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-10
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                                                 Pred. No. 9.9e-147; ; Mismatches 0.
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100.0%; Pred. No. 9.9e-147;
ive 0; Mismatches 0;
                                                           95.4%; Score 1649;
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PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                            Best_Local Similarity 100.0%; P:
Matches 318; Conservative 0;
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Matches 318; Conservative
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181 KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
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100.0%; Pred. No. 7.8e-146;
live 0; Mismatches 0;
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94.2%; Score 1628; DB 6;
Best Local Similarity 99.4%; Pred. No. 9e-145;
Matches 316; Conservative 0; Mismatches 0;
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US-10-038-307-14
Sequence 14, Application US/10038307
Sequence 14, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Judith J. HEALEY
TILE OF INVENTION: Tango 197 and Tango 216 COMPLE OF INVENTION: Tango 197 and Tango 216 COMPLERENT FILLS OF TREAT ST83-35-3-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILLING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENTH: S43
                               APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKANUAK
APPLICANT: Judith J. HEALEY
ITLE OF INVENTION: Tango 197 and Tango 216
FILE REPERBENCE: 7863-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
SEQ ID. NO 266
Sequence 26, Application US/10038307 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 316; Conservative
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GRGANISM: Homo sapiens
US-10-038-307-14
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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                                     KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEFSTICAGESFQVV
                                                                                                            HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGALVYCVGV
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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Abang, Bing
APPLICANT: Glang, Bing
APPLICANT: Glann, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnorck, Dale E.
APPLICANT: Warnorck, Dale E.
TILE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088 465P2
CURRENT APPLICATION NUMBER: US/60/389,987
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SEQ ID NO 1823
SEQ ID NO 1823
LENGTH: 564
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95.4%; Score 1649; DB 7; Length 564;
Best Local Similarity 100.0%; Pred. No. 9.9e-147;
Matches 318; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                         Sequence 1823, Application US/60389987 GENERAL INFORMATION:
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US-60-389-987-1823
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US-60-389-987-1823
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US-10-038-307-26
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                                                   HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
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                                                                                                                                                                                                                                                                                                     APPLICANT: James B. ROTTWAN
APPLICANT: James B. ROTTWAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
SUFFRENT FILING DATE: 2002-06-28
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                            KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
MATAERRALG1GFQWLSLATLVL1CAGQGGRREDGGPACYGGFDLYF1LDKSGSVLHHWN
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Pred. No. 9e-145;
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Matches 316; Conservative
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US-10-038-307-16
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241 VRGNGFRHARNYDRYLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS--EANRSRDLGAIVXCVGV
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: SHOOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1618; DB 6;
Pred. No. 7.8e-144;
                                              APPLICANT: Theresa L. O'KEEFE
APPLICANT: Finersa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NOS: 26
SEQ ID NOS: 26
FENOME: FASLSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                Tango 216
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CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 194
LENGTH: 562
Sequence 10, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
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Best Local Similarity
Matches 315; Conserv
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al Similarity 94.5
293; Conservative
                                                                                                                                                                                                                                                          TYPE: PRT; ORGANISM: Homo sapiens US-10-038-307-12
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he: 356 sec
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US-10-038-307-12
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                                                                                                    LAHKEISPOLRMSFIVESTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERAS 128
                                                                                                               9 LGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIXYFVEQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 LGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQ
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pred, No. 1.1e-137;
5; Mismatches 7;
                               Score 1553; DB 1;
Pred. No. 1.1e-137;
5; Mismatches 7;
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ilarity 96.1%;
Conservative 5
                                 89.9%;
ilarity 96.1%;
Conservative
; ORGANISM: Mus musculus PCT-US02-08253-194
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298; Conserv
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                                             Similarity
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; ORGANISM: Mouse
pcr-us02-08253-301
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                                  Query Match
Best Local Simi
Matches 298;
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Matches 298;
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249 ARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISS 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||: | ::| || SGRREDGGPACYGGFDLYFILLHIHHHHHHHHHHH || 59
                                                                                                                                                                                                                                                                        APPLICANT: Theresa L. O'KBEFE
APPLICANT: Theresa L. O'KBEFE
APPLICANT: Engin OZKAYUAR
APPLICANT: Engin OZKAYUAR
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REPERENT (1853-253-99)
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 LGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 534;
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94.5%; Pred. No. 1.7e-131;
tive 3; Mismatches 8;
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                                                                                                                                                                                                                                 Sequence 12, Application US/10038307; GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

Search time 507.33 Seconds August 9, 2002, 10:44:31

(without alignments) 231.032 Million cell updates/sec

Perfect score:

US-09-970-076-8 1728 1 MATAERRALGIGFOWLSLAT......TTHCSLHKIASGPTTAACME 333

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

3502263 segs, 351980561 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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/cgn2\_6/ptodata/2/pea/US06\_COMB.pep:\*
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/cgn2\_6/ptodata/2/pea/US08\_COMB.pep:\*
/cgn2\_6/ptodata/2/pea/US081\_COMB.pep:\*
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/cgn2\_6/ptodata/2/pea/US086\_COMB.pep:\*
/cgn2\_6/ptodata/2/pea/US080\_COMB.pep:\*
/cgn2\_6/ptodata/2/pea/US090\_COMB.pep:\*
/cgn2\_6/ptodata/2/pea/US091\_COMB.pep:\*
/cgn2\_6/ptodata/2/pea/US091\_COMB.pep:\* Pending\_Patents\_AA\_Main:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2\_6/ptodata/2/paa/USO99\_COMB.pep:\*/cgn2\_6/ptodata/2/paa/USO99\_COMB.pep:\*/cgn2\_6/ptodata/2/paa/USIO0\_COMB.pep:\*/cgn2\_6/ptodata/2/paa/USIO1\_COMB.pep:\*/cgn2\_6/ptodata/2/paa/USiO1\_COMB.pep:\*/cgn2\_6/ptodata/2/paa/USiO\_COMB.pep:\*

quence 61, A quence 621, advance 621, advance 621, advance 187, advance 620, advance 620, advance 620, advance 132, advance 132, advance 132, advance 105, advance 107, advanc	22, b,
PCT-USOD-30045-99 PCT-USOD-11988-6 US-09-918-715-16 US-09-918-715-16 US-09-918-715-16 US-09-918-715-16 US-09-918-715-16 US-09-918-715-17	6 US-60-318-905- 6 US-60-322-468- 6 US-60-322-733- 6 US-60-322-733- 6 US-60-323-790- 6 US-60-323-078-
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## ALIGNMENTS

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Length 333;
                                                                                                      APPLICANT: Millennium Pharmaceticals, Inc.
APPLICANT: Millennium Pharmaceticals, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: ENCODING THEM
FILE REFERENCE: 783-173-228
CURRENT APPLICATION NUMBER: PCT/US99/31025
CURRENT FILING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: 09/223,546
EARLIER PELING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SOCTUMARE: FASTERO for Mindows Version 4.0
                                                   Sequence 9, Application PC/TUS9931025 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Homo sapiens PCT-US99-31025-9
RESULT 1
PCT-US99-31025-9
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 333
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Gaps 1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60 Indels Query Match 100.0%; Score 1728; DB 1; Best Local Similarity 100.0%; Pred. No. 5.2e-168; Matches 333; Conservative 0; Mismatches 0;

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EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120

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RESULT 4
US-09-599-596-9
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Best Local
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09471179
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                    VRGNGFRHARNVDRYLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
                                                                                                               141 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
                                     APPLICANT: HOLIZAM, Douglas
APPLICANT: HOLIZAMA, Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 09404/066001
CURRENT APPLICATION NUMBER: US/09/223,546
CURRENT FILING DAFE: 1998-12-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV
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                                                                                                                                                       ; Sequence 9, Application US/09223546; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 333; Conservative
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US-09-223-546-9
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US-09-471-179-9
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US-09-223-546-9
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APPLICANT: Holtznan, Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FITER REFERENCE: 03404/06601
CURRENT PILICATION NUMBER: U5/09/599,596
CURRENT PILICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
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100.0%; Pred. No. 5.2e-168;
iive 0; Mismatches 0;
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100.0%; Pred. No. 5.2e-168;
ive 0; Mismatches 0;
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CURRENT FILING DATE: 1999-12-23
PALOR APPLICATION NUMBER: 09/223,546
PALOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9.
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Best Local Similarity 100.0
Matches 333; Conservative
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US-09-599-596-9
                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-471-179-9
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Best Local Similarity
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EIYYFVEOLAHKFISPOLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
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CURRENT PELLING DATE: 2001-03-01

PRIOR FILING DATE: 1998-10-30

PRIOR FILING DATE: 1998-110-30

PRIOR FILING DATE: 1998-10-30

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

PRIOR PELING DATE: 1999-03-01

PRIOR FILING DATE: 1999-06-18

PRIOR FILING DATE: 1999-06-19

PRIOR FILING DATE: 1999-06-19

PRIOR PELING DATE: 1999-06-29

PRIOR PELING DATE: 1999-06-30

PRIOR PELING DATE: 1999-06-30

PRIOR PELING DATE: 1999-06-30

PRIOR PELING DATE: 1999-06-30

PRIOR PELING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 09/342,64

PRIOR PELING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 09/342,64

PRIOR PELING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 09/342,404

PRIOR FILING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 09/344,071

PRIOR APPLICATION NUMBER: 09/44,071

PRIOR PELING DATE: 1999-07-20

PRIOR PELING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 09/44,071

PRIOR PELING DATE: 1999-07-20

PRIOR PELING DATE: 2000-02-25

PRIOR PELING DATE: 2000-02-25

PRIOR PELING DATE: 2000-06-19

PRIOR PELING DATE: 2000-07-31

PRIOR PELING DATE: 2000-07-31

PRIOR PELING DATE: 2000-07-31
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FILE REFERENCE: 78
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5.2e-168;
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100.0%; Pred. No. 5.2e-168;
ive 0; Mismatches 0;
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Pred. No. 5.26
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APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor FILE REFERENCE: 960296.97745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/970,076 CURRENT FILING DATE: 2001-10-03
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 12
LENGTH: 333
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Best Local Similarity 100.

Matches 333; Conservative
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US-09-796-753-12
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RESULT 9
PCT-US01-11988-621
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100.0%; Pred. No. 7.7e-160;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                    301 DGLSFISSSVIITTTHCS 318
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Best Local S1
Matches 318;
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Pred. No. 8.9e-160;
0; Mismatches 0;
RESULT 8

PCT-US00-30045-94

Sequence 94, Application PC/TUS0030045

Sequence 94, Application PC/TUS0030045

GENERAL INFORMATION:
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PS708PCT
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 201

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 94.
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Sequence 621, Application PC/TUS0111988
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Human Genome Sciences, Inc.
CURRENT PERENCE: PF546PCT
CURRENT APPLICATION NUMBER: PC7/US01/11988
CURRENT PILING DATE: 2000-101-12
PRIOR APPLICANION NUMBER: 60/226, 931
PRIOR PILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR PILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR PILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PARENTIN PUMBER: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
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100.0%; Pr
trive 0;
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Matches 318; Conservative
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ORGANISM: HOMO Sapiens
PCT-US00-30045-94
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61 EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRGGLEELQKVLPGGDTYM 120
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                          241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN
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Sequence INFORMATION:
Sequence INFORMATION:
APPLICAMT: Brad St. Croix
APPLICAMT: Bert Vogelstein
APPLICAMT: Bert Vogelstein
APPLICAMT: Bert Vogelstein
APPLICAMT: Reneth Kinzler
IIIE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT APPLICATION NUMBER: 00/222,599
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-01
PRIOR PLICATION NUMBER: 60/224,360
PRIOR PLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1.5e-159;
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100.0%; Pred. No. ...
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APPLICANT: Brad St. Croix
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318; Conservative
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US-09-918-715-232
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US-09-918-715-187
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Matches 318,
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181
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                                                                                                    Length 403;
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                                                                                               Score 1649; DB 1; I
Pred. No. 8.9e-160;
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100.0%; Pred. No. 8.9e-160;
iive 0; Mismatches 0;
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                                                                                                                       Best Local Similarity 100.0
Matches 318; Conservative
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  sapiens
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Matches 318; Conserv
; ORGANISM: HOMO PCT-US01-11988-621
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                                                                                                  Query Match
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Query Match
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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                               EXPRESSION PATTERNS
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Pred. No. 1.5e-159;
0: Mismatches 0;
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; Sequence 6, Application US/09970076
; GRERAL INFORMATION:
    APPLICANT: Pandley, Kenneth A. APPLICANT: Collier, Renneth A. APPLICANT: Collier, Robert J. APPLICANT: Mogridge, Jeremy S. TITLE OF INVENTION: Anthrax Toxin Receptor; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/09/970,076
; CURRENT FILING DATE: 2001-10-03
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PATENTIN VET. 2.1
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100.0%; Pred. No. ...
... 0; Mismatches
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTON: ENDOTHELIAL CELL EXPRESSI
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-02
PRIOR PLING DATE: 2000-08-11
PRIOR PLING DATE: 2000-08-11
PRIOR PLING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FESSES for Windows Version 3.0
SEQ ID NO 232
LENGTH: 564
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ORGANISM: Homo sapiens
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US-09-918-715-232
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Best Local Similarity
Matches 318; Conserv
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LENGTH: 564
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. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US00-30045-125
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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VOTER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME,KEY: SITE
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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                                                                  1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN
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Pred. No. 2.9e-159;
0; Mismatches 1;
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PCT-US00-30045-125
sequence 125, Application PC/TUS0030045
sequence 125, Application PC/TUS0030045
sequence 125, Application PC/TUS0030045
sequence 125, Application PC/TUS0030045
rTTLE OF INVENTION: 28 Human Secreted Proteins
rTLE OF INVENTION: PS708PCT
CURRENT APPLICATION NUMBER: PCT/US00/30045
CURRENT FILING DATE: 2000-11-01
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 201
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 125
LENGTH: 403
95.4%; Score 1649; DB 23;
100.0%; Pred. No. 1.5e-159;
iive 0; Mismatches 0;
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         Query Match 95.4 Best Local Similarity 100. Matches 318; Conservative
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LOCATION: (175)
OTHER INFORMATION: Xaa
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Job time: 870 sec
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LOCATION: (175)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE

LOCATION: (320)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE

LOCATION: (31)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE

LOCATION: (368)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT PAPLICATION NUMBER: PCT/US01/11988
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PALENTING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SEQ ID NO 620
                                                                                                                                                                                                                                                                                                                                     301 DGLSFISSSVIITTHCS 318
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Best Local Similarity 99.77
Matches 317; Conservative
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DGLSFISSSVIITTTHCS 318
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Sequence 620, App Sequence 194, App Sequence 301, App

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PCT-USO1-11988-620

1 US-09-918-715-301

3 US-09-918-715-301

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9 US-09-918-715-301

1 US-09-918-715-91

1 US-09-720-76-9

9 US-09-590-596-9

1 US-09-796-73-12

1 US-09-796-73-12

1 US-09-910-76-9

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1 US-09-471-179-30

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1 US-09-471-179-50

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1 US-09-916-745-107

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2 US-09-318-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-991-108-99
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Pred. No. 3.1e-179;
Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TILE PERERENEE: 960296, 97745
CURRENT APPLICATION NUMBER: 08/09/970, 076
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 60/251,481
SOFIWARE: PATENTING NOTE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
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ORGANISM: Homo sapiens
US-09-970-076-2
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Sequence 232, App
Sequence 6, Appli
Sequence 94, Appl
Sequence 621, App
Sequence 621, App
                                                                                                                                                                                                            (without alignments)
255.315 Million cell updates/sec
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(cgn2_6/ptodata/2/paa/US082_COMB.pep:*

(cgn2_6/ptodata/2/paa/US085_COMB.pep:*

(cgn2_6/ptodata/2/paa/US085_COMB.pep:*

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/cgn2_6/ptodata/2/paa/US60_COMB.pep:*
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./cgn2_o/ptodata/2/paa/PCTUS_COMB.pep:*
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.: /cgn2_o/ptodata/2/paa/USO7_COMB.pep:*
                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-918-715-187
US-09-918-715-232
US-09-970-076-6
PCT-US00-1908-621
PCT-US01-1908-621
US-09-833-245-621
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Best Local Similarity 100.0%; P.
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US-09-918-715-232
                                       ESEE 364
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US-09-970-076-6
                                                                                                                                                                                                                   SEQ ID NO 232
                                                                                                                                                                                                                                  TYPE: PRT
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100.0%; Pred. No. 5.4e-177;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 364; Conservative
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101 DGLSFISSSVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPAE 360
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Sequence 232, Application US/09918715

GENERAL INFORMATION:

APPLICANT: Brad 54. Croix

APPLICANT: Bert Vogelstein

APPLICANT: Renneth Kinzler

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REFERENCE: 1107.00134

CURRENT APPLICATION NUMBER: US/09/918,715

CURRENT FILING DATE: 2001-08-02

PRIOR PRIOR PLICATION NUMBER: 60/222,599

PRIOR PLICATION NUMBER: 60/224,360

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Pred. No. 5.4e-177;
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100.0%; Pred. No. 1e-176;
iive 0; Mismatches 0;
                                                 98.7%; Score 1889; DB 1;
100.0%; Pred. No. 1e-176;
iive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: PCT/US01/11988
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 66/229, 358
PRIOR APPLICATION NUMBER: 66/229, 358
PRIOR APPLICATION NUMBER: 66/229, 358
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-31
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SEQ ID NO 621
                                                                                    Conservative
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Best Local Similarity 100.
Matches 363; Conservative
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; ORGANISM: Homo
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   PCT-US00-30045-94
                                                                                    Matches 363;
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TILE OF INVENTION: 28 Human Secreted Proteins
FILE REFRENCE: PS708PCT:
CURRENT APPLICATION NUMBER: PCT/US00/30045
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR APPLICATION NUMBER: 60/215,133
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 200
SOFTWARE: PatentIn Ver. 2.0
                            APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TAPLICANT: Mogridge, Jeremy S.
TILE REFERENCE: 960296.97745
CURRENT APPLICATION NUMBER: 08/09/970,076
CURRENT FILING DATE: 2001-10-03
PRIOR PILING DATE: 2001-10-03
PRIOR FILING DATE: 2000-12-05
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PCT-USO0-30045-94
; Sequence 94, Application PC/TUS0030045
; GENERAL INFORMATION:
Sequence 6, Application US/09970076 GENERAL INFORMATION:
                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
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US-09-970-076-6
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ORGANISM: Homo sapiens
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LENGTH: 403
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LENGTH: 564
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100.0%; Pred. No. 1e-176;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                       PAPICANT Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546FCT
CURRENT APPLICATION UNMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-14-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN NOS: 2267
                                                                                                                                                                                                                                    ; Sequence 621, Application US/09833245
; GENERAL INFORMATION:
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US-09-833-245-621
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) NAME/KEY: SITE

LOCATION: (368)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
pcr-USO0-30045-125
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Pred. No. 7.7e-175;
0; Mismatches 3;
Sequence 125. Application PC/TUS0030045
Sequence 125. Application
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 28 Human Secreted Proteins
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PS708PCT
CURRENT PPLICATION NUMBER: PCT/US00/30045
CURRENT PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
NUMBER: PSEQ ID NOS: 201
SOFTWARE: PATENTIN VET: 2.0
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99.28;
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Best Local Similarity 99.2 Matches 360; Conservative
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NAME/KEY: SITE
                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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361 ESE 363
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LOCATION: (320)
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FEATURE:
NAME/KEY: SITE
LOCATION: (175)
OTHER INFORMATION: X
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LOCATION: (368)
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NAME/KEY: SITE

COTHER INFORMATION: (175)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

LOCATION: (120)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

LOCATION: (331)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-11988-620
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                                    APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FITLE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: PCT/USO1/11988
CURRENT FILING DATE: 2001-01-12
PRIOR PAPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR PILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR PILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SEQ ID NO 620
Sequence 620, Application PC/TUS0111988 GENERAL INFORMATION:
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Matches 360; Conservative
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US-09-833-245-620
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LOCATION: (320)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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99.2%; Pred. No. 7.7e-175;
ive 0; Mismatches 3;
TITLE OF INTENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-31
SPRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN Ver: 2.1
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GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
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Matches 360; Conservative
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; ORGANISM: Homo sapiens
PCT-US99-31025-9
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                                            Matches 342;
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Sequence 301, Application US/09918715
GENERAL INFORMATION:
APPLICANT: Bard St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Reneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-02
PRIOR PELICATION NUMBER: 60/222,599
PRIOR PELICATION NUMBER: 60/224,360
PRIOR PELICATION NUMBER: 60/224,360
PRIOR PELICATION NUMBER: 60/224,360
PRIOR PELICATION NUMBER: 60/282,850
PRIOR PELICATION NUMBER: 60/282,850
PRIOR PELICATION NUMBER: 60/282,850
SEQ ID NOS: 358
SOFTWARE: FastSEO for Windows Version 3.0
SEQ ID NO 3674: 562
                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 96.1%; Pred. No. 4.8e-167;
Matches 342; Conservative 6; Mismatches 8;
     EXPRESSION
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESS: FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: 05/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR PILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEC ID NOS: 358
SOFTWARE: FASTESQ for Windows Version 3.0
SSOFTWARE: 562
                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Mus musculus
US-09-918-715-194
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US-09-918-715-301
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                                                                                                                                                                                                                    ARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRH 248
                                                                                                                                                                                                                                                                                                                                         249 ARNVDRVICSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISS 308
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                                                                9 LGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEO
                                                                                  SVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPAEESEE 364
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| Sequence 3, Application PC/TUS9931025
| GENERAL INFORMATION:
| APPLICANT: Millennium Pharmaceticals, Inc.
| TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
| TITLE OF INVENTION: ENCODING THEM
| TITLE OF INVENTION: ENCODING THEM
| FILE REFERENCE: 7853-173-228
| CURRENT APPLICATION NUMBER: PCT/US99/31025
| CURRENT FILING DATE: 1999-12-23
| CARLIER APPLICATION NUMBER: 09/223,546
| EARLIER FILING DATE: 1998-12-30
| NUMBER OF SEQ ID NOS: 135
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 9
| LENCTH: 333
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                                  Indels
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100.0%; Pred. No. 3.5e-153;
iive 0; Mismatches 0;
Score 1793; DB 23;
Pred. No. 4.8e-167;
6; Mismatches 8;
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completed: August
ne: 867 sec
                Query Match
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Job time: {
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MATAERRALGIGFOWLSLATLVLICAGOGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
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Sequence 9, Application US/09471179
Sequence 9, Application US/09471179
Sequence 9, Application US/09471179
GENERAL INFORMATION:
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 7853-173
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                Sequence 9, Application US/09223546
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REPERENCE: 09404/066001
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
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100.0%; Pred. No. 3.5e-153;
tive 0; Mismatches 0;
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                            301 DGLSFISSSVIITTHCS 318
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Best Local Similarity 100.
Matches 318; Conservative
                                              301 DGLSFISSSVIITTHCS
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                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-09-223-546-9
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                                 Gaps
                                                                         1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN
                                                                                                                                                                    HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV
                                                                                                                                                                                                                        KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
       Length 333;
        Score 1649; DB 18;
Pred. No. 3.5e-153;
86.2%; Sco. 100.0%; Pred. No. 3... 100.0%; Pred. No. 3... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 DGLSFISSSVIITTHCS 318
                                   Matches 318; Conservative
                      Best Local Similarity
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sequence 99, Applisequence 2, Applisequence 2, Applisequence 99, Applisequence 99, Applisequence 2, Applisequence 2, Applisequence 2, Applisequence 3, Applisequence 43, Applisequence 43, Applisequence 3, Applisequence 4, Applis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 46, Application US/08286889

Patent No. 5470953

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
STREET: 233 South Wacker Drive, 6300 Sear Tower
CONFORT: Illinois
COMPUTE: Illinois
COMPUTE: Readable FORM:
MEDUM TYPE: Blopy disk
COMPUTE: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: A.25
FILING DATE:
FILING DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 TIMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 70
Sequence
Sequence
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28.9%; Pred. No. 6.8e-06;
tive 31; Mismatches 69
                   US-08 485-618-2
US-08 485-618-9
US-08 485-618-99
US-08 605-672-2
US-08 605-672-99
US-08 605-672-99
US-08 943-343-2
US-08 943-363-2
US-09 193-043-2
US-09-193-043-2
US-09-193-043-2
US-08-1476-062A-43
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US-08-286-889-3
US-08-485-618-3
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PRIOR APPLICATION DATA:
PRILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 27866/32168
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
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Best Local Similarity 28.9%;
Matches 50; Conservative
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linear
TOPOLOGY:
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1 MSFIVFSTRGTTLMKLTEDR.....STSGFKEGNSHPCLPARPHT 218
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Sequence 46
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Sequence 46
Sequence 53
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Sequence 53
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                                           Compugen Ltd
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US-08-365-446
US-08-605-672-46
US-08-643-36-46
US-08-443-36-46
US-09-193-043-46
US-08-618-618-53
US-08-618-618-53
US-08-618-618-37
US-08-943-363-53
US-08-943-363-37
US-08-943-363-37
US-08-943-363-37
US-08-943-363-37
US-08-482-293A-37
US-08-482-293A-37
US-08-618-55
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US-08-482-55
US-08-483-37
US-08-482-55
US-08-483-618-55
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                             GenCore version 4.5 Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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260 DGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVFK 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 TLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 70
260 DGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVFK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 Integrin Alpha Subunit
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                                                                            122 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 174
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTONEY/AGENT INPORMERTOR)
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTONEY/AGENT INPORMATION:
ANALY. ATTORNEY/AGENT ATTORNEY/A
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28.9%; Pred. No. 6.8e-06;
tive 31; Mismatches 69
                                                                                                                                                                                                                                                                                                                                        Sequence 46, Application US/08362652
Sequence 46, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5766850el Human
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1155 amino acids
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STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                    RESULT 3
US-08-362-652-46
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                                                                                                                                                                                                        260 DGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALGELNTIGSAPSQDHVFK 316
                                                    205 TEFKSSLSPOSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVIT 259
                                                                                                                                                            71 DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 46, Application US/08485618
Sequence 46, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE: ADSRESSE: AD
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                                                                                                                                                                                                                                                                                                                122 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 174
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
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28.9%; Pred. No. 6.8e-06;
tive 31; Mismatches 69
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US APPLICATION NUMBER: US PRIOR APPLICATION NUMBER: US 08/286,889
FRICK APPLICATION NUMBER: US 08/286,889
FRICK APPLICATION NUMBER: S-ANG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
APLICATION NUMBER: 21-DEC-1994
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 50; Conserva
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STATE: Illinois
COUNTRY: United S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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US-08-485-618-46
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205 TEFKSSLSPOSLVDAIVQLQ----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVIT 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 TLMKLTEDREQIROGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 70
    APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 Integrin Alpha Subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1155;
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Patent No. 5837478
GENERAL INFORMATION:
GABLatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha
NUMBER OF SEQUENCES:
ADDRESSEE: ADARESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69; Indels
                                                                                                                                                                                                         ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 128.5; DB 2
Pred. No. 6.8e-06;
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                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 530
PRIOR PAPLICATION 530
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
APLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 38,659 REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
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Best Local Similarity 28.9%
Matches 50; Conservative
                                                                                                                                                          STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-482-293A-46
                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                    Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 TLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 70
                                                                                                                                       2 Integrin Alpha Subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1155;
                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago, CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                       STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.4%; Score 128.5; DB 2; 28.9%; Pred. No. 6.8e-06; tive 31; Mismatches 69;
                  Sequence 46, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human
UNMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PELLING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-MG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC 1994
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC 1994
APPLICATION NUMBER: US 08/362,652
FILING DATE: 31-DEC 1994
ATTORNEY,AGENT INFORMATION:
NAME: WILLIAMS JT., JOSEPH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECHONE: 312-474-0448
TELECEN : 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERSTICS:
LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-482-293A-46; Application US/08482293A; Sequence 46, Application US/08482293A; Patent No. 5831029; GENERAL INFORMATION: APPLICANT: Gallatin, W. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 50; Conserva
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US-08-605-672-46
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71 DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFP 121
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                                                                                                                                                                                                                                                                                                                                                               12 TLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
TITLE OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
CORRESPONDENCE MATSHAII, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : | | : | | : | | : | | | : | | | 364
                                                                                                                                                                                                                                                                          11.4%; Score 128.5; DB 4; Length 1155; 28.9%; Pred. No. 6.8e-06;
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 6666-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                               31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMONICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPAX: 312-474-0448
TELERAX: 25-3856
TELERAX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
NAME: WILLIAMS JR., NUMBER: 38,654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/485,618
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN VEY. 2.0
SEQ ID NO 46
FEWART: 115
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US-08-485-618-53
Sequence 53, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
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APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28.9%
Matches 50; Conservative
                                                                                                                                                                          TYPE: PRT ORGANISM: Mus musculus US-09-193-043-46
                                                                                                                                                         LENGIH: 1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 TEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVIT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 DGELHEDLFFYSE--REANRSRDLGALVYCVGVKD-FNE-TQLARI-----ADSKDHVFP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 TLMKL/TEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 1155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
                                      233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.4%; Score 128.5; DB 2
28.9%; Pred. No. 6.8e-06;
tive 31; Mismatches 69
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Sequence 46, Application US/09193043
Sequence 46, Application US/09193043
SERENT INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Morica
TITLE OF INVENTION: No. 6251395el Human 2
TITLE REPERBNCE: 27866/35004
CURRENT FILIMO DATE: 1998-11-16
CURRENT FILIMO DATE: 1993-12-23
EARLIER FILING DATE: 1993-12-23
SERLIER APPLICATION NUMBER: 08/13,497
SERLIER APPLICATION NUMBER: 08/266,889
SERLIER RILING DATE: 1994-08-05
SERLIER APPLICATION NUMBER: 08/362,652
                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION UNBER: US 08/286,889
FILING DATE: 5-AUG-1994
FILING DATE: 5-AUG-1994
FILING DATE: 1-DEC-1994
ATORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
NAME: Williams Jr., Joseph A.
REFERENCE/DOCKET UNMBER: 38,659
RECISTRATION NUMBER: 31,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27866/32684
                                                                                                                                         ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.4%
Best Local Similarity 28.9%
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 312-474-0448
                                                                                                                 COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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                                                                                        Illinois
                               STREET: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
US-09-193-043-46
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                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 Integrin Alpha Subunit
                                                                                                                                                                                        23;
                                                                                                                                          11.4%; Score 128.5; DB 1; Length 1161; 28.9%; Pred. No. 6.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                             122 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 174
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 53, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. 5766850e1 Human 2 Integrin Alpha
TITLE OF ENVENTION: No. 5766850e1 Human 2 Integrin Alpha
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
COUNTRY: United States
COUNTRY: United States
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BE PC compatible
SOFTWARE: PSTEM: PC-DOS/MS-DOS
SOFTWARE: PSTEMIN Rolease #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/362,652
                                                                                                                                                                                      31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
1161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1161 amino acids
                                                                                                                                                                                    50; Conservative
                   ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-618-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                  Best Local Similarity
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  LENGTH:
                                                                                                                                             Query Match
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                         23; Gaps
                                                                        12 TLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 301/21.
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
ATTLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
TITLE OF INVENTION: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
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                                                                                                                                                                                                                                                                                                    | : | | | : | | : | | : | | | : | | 317 VGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STATE: Illinois STATE: Illinois COUNTRY: United States Ill: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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Best Local Similarity 28.9%; Pred. No. 6.9e-06;
Matches 50; Conservative 31; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 53, Application US/08605672 Patent No. 5817515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-605-672-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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205 TEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVIT 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 TLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 70
                                                                                                                                                                                                                                                                                             APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADRESSE:
ADRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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llarity 28.9%; Pred. No. 6.9e-06;
Conservative 31; Mismatches 69
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FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION
ATTORNEY/AGENT
ATTOR
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COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659 REFERENCE/POCKET NUMBER: 27866 TELECOMMUNICATION INFORMATION: TELECHHONE: 312-474-6300
                                                                                                                                                                                                              Sequence 53, Application US/08943363 Patent No. 5837478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312-474-0448
TELEX: 25-3856
INPERMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 50; Conserva'
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STATE: Illino
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                                                                                                                                                                            RESULT 12
US-08-943-363-53
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                                                                                                       205 TEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVIT 259
                                                                 DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFP 121
                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-08-482-293A-53
Sequence 53, Application US/08482293A
SEQUENCES 103
SUBPRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 133 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1161;
                                                                                                                                                                                     122 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 174
                                                                                                                                                                                                                           Indels
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MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
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ilarity 28.9%; Pred. No. 6.9e-06;
Conservative 31; Mismatches 69
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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PRICASSIFICATION DATA:
APPLICATION NUMBER: US APPLICATION NUMBER: US BPILOW DATA:
FILING DATE: 23-DEC-1993
PRICA APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 53:
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LENGTH: 1161 amino aci
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COUNTRY: United States
ZIP: 60606-6402
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Matches 50; Conserv
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Length 1161;

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FILING DATE: 23-DEC-1993 ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 27.77
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-889-37
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 TLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 174
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ADDRES
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                                                                                                                                                                                                                 APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
TITLE COF INVENTION: NO. 62513551 Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1997-10-03
NUMBER: OF SEQ ID NOS: 114
SEGOID NO 53
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APPLICATION NUMBER: US 08/173,497
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                                                                                                          Sequence 53, Application US/09193043 Patent No. 6251395
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US-09-193-043-53
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Best Local Similarity
Matches 50; Conserva
                                                                                                                                                                                             GENERAL INFORMATION:
                                                                          US-09-193-043-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SFIVESTRGTTLMKLTE----DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYEN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                Length 1151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
                                                                                                                                                                                                                                                                                                                                                                                                                   10.8%; Score 122; DB 1;
27.7%; Pred. No. 3.9e-05;
tive 32; Mismatches 76;
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 37, Application US/08485618; Patent No. 5728533; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS
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INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
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CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 27.7%; Pred. No. 3.9e-05;
Matches 52; Conservative 32; Mismatches 76; Indels 26
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/COCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
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Search completed: August 9, 2002, 10:33:12 Job time: 191 sec

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09ff49 arabidopsis

09f2v10 arabidopsis

091311 salmonella

0912f5 caenorhabdi

04285 arabidopsis

04286 arabidopsis

04286 arabidopsis

04286 arabidopsis

096781 bacilus su

074080 pyrococcus

09400 oryza sativ
                                                               O9sg86 arabidopsis
O9cyzl mus musculu
O43981 elmeria ten
O9aiu3 ehrlichia p
         019319 caenorhabdi
096ft5 homo sapien
09p218 homo sapien
09bqu7 homo sapien
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096191 homo sapien
P89140 pseudorabie
                                                                                                                    Q9sz38 arabidopsis
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097566 canis famil
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EMBL; AF421380; AAL26496.1; -.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Last sequence update)
Last annotation update)
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NCBI_TaxID=9606;
Receptor.
SEQUENCE
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09gye7 rattus norv
043853 homo sapien
070350 mus musculu
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Ogygc3 homo sapien
Ogyj130 rattus norv
0971t1 clostridium
Qye03 schizosacch
Og6hx6 homo sapien
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                                                                                          9, 2002, 10:46:26 ; Search time 102.68 Seconds
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1 MSFIVFSTRGTTLMKLTEDR.....STSGFKEGNSHPCLPARPHT
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Copyright (c) 1993 - 2000 Compugen Ltd
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NCBI_TaxID=7729;
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SEQUENCE 245 AA: 26111 MW; BIAE6EBOA2EBEEGG CRC64;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Last Sequence update)
CDNA FL031074 FIS, CLONE HSYRA2001476.
HOMO Sapiens (Human).
Edwaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.7%; Score 506; DB 4; Length 245; 53.4%; Pred. No. 1.1e-38; tive 37; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-BREAST, AND MAMMARY ADENOCARCINOMA;
Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; BC012475; AAH12475.1; -.
NON-TER 1
SEQUENCE 97 AA; 10453 WW; 14F475F0B170E71A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  096EC6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:4705862) (FRAGMENT).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.49
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TVNETYTTS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 KINDSVTLS 189
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
260 KINDSVTLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 096EC6
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                                                                                                                                     096NC7
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Q96EC6
                                                                                         RESULT 1096 NO. 1096 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCV 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 KLTEDREQIRQGLEELQXVLPG------GDTYMHEGFERASEQIYYENRQG 59
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miyazawa S., Azumi K., Nonaka M.;
Miyazawa S., Azumi K., Nonaka M.;
"Cloning and characterization of integrin alpha subunits from the
"Cloning and characterization of integrin alpha subunits from the
solitary ascidian, Halozynthia roretzi.";
J. Immunol. 166:1710-1715(2001).
EMBL, ABO86261; BAB21479.1;
INSP. 11215; 1A8X.
INTERPO, IPR000413; Integrin_alpha.
Interpo; IPR000413; Integrin_alpha.
From: PF01839; FG-GBP; 5.
Pfam: PF001857; integrin_A; 1.
Pfam: PF00092; vwa: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.9%; Score 123; DB 5; Length 1332; 25.7%; Pred. No. 0.02; Live 29; Mismatches 67; Indels 4
97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
INTEGRIN ALPHA HR1.
WW; 0D9108D2B05CFFAE CRC64;
                                     2; Indels
Length
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Query Match
Best Local Similarity 87.9%; Pred. No. 1.6e-06;
Matches 29; Conservative 2; Mismatches 2
                                                                                                                                                                                                                     PRT; 1332 AA.
                                                                             158 FQVVVRGNGFRHARNVDRVLCSFKINDSVTLSK 190
                                                                                                    TISSUE=HEMOCYTE;
MEDLINE=21103187; PubMed=11160215;
                                                                                                                                                                                                                                                                                                                                                           Halocynthia roretzi (Sea squirt).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145852 MW;
                                                                                                                                                                                                                                                                                                                     INTEGRIN ALPHA HR1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS, PRODIJĖS; INTEGRINA.
PRINTS; PROD453; VWFADOMAIN.
SMART; SM00191; INT_alpha; 5
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 10.9%
Best Local Similarity 25.7%
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50234; VWFA; 1
                                                                                                                                                                                                                         PRELIMINARY;
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1332
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31 133
1332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -YEMHFGENGF 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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93 GAIVYCVGVKD-FN----ETQLARIADSK--DHVFPVNDGFQALQGIIHSILKKSCIEIL 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 GDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHEDLFFYSE--REANRSRDL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 TLMKLTEDREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYRT--ASVII 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98003048; PubMed=9344363;
Messel H., Anderson S., Fite D., Halvas E., Hempel J., SundarRaj N.;
Messel H., Anderson S., Fite D., Halvas E., Hempel J., SundarRaj N.;
Type XII collagen contributes to diversities in human corneal and
limbal extracellular matrices.,
Invest Ophthalmol. Vis. Sci. 38:2408-2422(1997).
EMBL: 068139; AACOISO6.1; -.
Interpro; IPR003651; FN_III.
Interpro; IPR003651; WFA.
Pfam; PF00041; fn3; 3.
Pfam; PF00042; vwa: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 920;
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                                                                                                                                                                                                                                                                                                                                                             102440 MW; E96CC51E350DD5AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56727 MW; 9B6972F44A1BD88F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04383;
01-JUN-1998 (TEMBLrel. 06, Created)
01-JUN-1998 (TEMBLrel. 06, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
TYPE XII COLLAGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 9.6%; Score 109; DB 6
1 Similarity 29.0%; Pred. No. 0.24;
42; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.5%; Score 107.5; Di
26.0%; Pred. No. 0.15;
tive 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      517 AA.
HSSP; P11215; 1A8X.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vwFA.
Pfam; PF01839; FGAP; 4.
Pfam; PF00092; vwa; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00185; VWADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; vwa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 AAEPSTICAGESFQVVVRGNGFRHA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 AIEGTQTGSTSSFECEMSQEGFSAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00453; VWFADOMAIN.
SMART; SM00060; FN3; 3.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                             920 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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NON_TER
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SEQUENCE
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043853
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                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 I----ADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 LNTIGSAPPODHVFKVGN-FAALRSIQRQLQEK----IFAIEGTQSRSSSSFQHEMSQEG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 RQGYRTA-SVIIALTDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLAR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 NGSRKSAKKILLVITDGQKYRDPLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFIVESTRGTTLMKLTE-----DREQIRQCLEELQKVLPGGDTYMHEGFERASEQIYYEN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.8%; Score 122; DB 11; Length 1161; 27.7%; Pred. No. 0.021; tive 32; Mismatches 76; Indels 28
                                                                                                                                                                                                                                                                                                                                                                                     O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G.,
Gallatin W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2258491A984A705E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of rat alpha D, a novel beta 2 integrin.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF021334; AAF21241.1;
HSSP; 11215; 1ABX.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vWFA.
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Lee J.-K., Schook L.B., Rutherford M.S.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U40072; AAB16869.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                           Last sequence update)
Last annotation update)
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      PRT; 1161 AA
                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1161 AA; 126600 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01839; FG-GAP; 5.
Pfam; PF00357; integrin_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00092; vwa; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SWART; SW00191; Int_alpha; 4.
SWART; SW00327; VWA; 1.
                                                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, 01-FEB-1997 (TrEMBLrel. 02, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 27.7%
Matches 52; Conservative
      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 FRHARNVD 174
                                                                                                                                                  ALPHA D INTEGRIN.
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Q28984;
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                                                                                                FOALOGIIHSILKKSCIEI---LAA-----EPSTICAGESFQVVVRGNGFRHARNVDR 175
                                                                                                                            303 FDAFQRISFELTQSICLRIEQELAAIKKKAYVPPKDLSFSEVTSYGFKTNWSPAGENVFS 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rowen L., Madan A., Qin S., Hall J., Dahl T., James R., Dickhoff R., Schaffer T., Ratcliffe A., Abbasi N., Loretz C., Lasky S., Hood L.; Sequence of the mouse MHC class III region."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                        68 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDG 125
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/ENDBJ databases.
ITRIBILIARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
TRYPSIN FAMILY.
EMBL; AF049850; AAC84162-1; -.
EMBL; AF049850; AAC10284-1; -.
EMBL; BC011086; AAH11086.1; -.
                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                           .
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                                                                                                                                                            176 VLCSFKI---NDSVTLSKSLQSP------WVSSTSGFKEGNSHP 210
                                                                                                                                                                                                                                                                                                           01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
COMPLEMENT FACTOR C2 (COMPLEMENT COMPONENT 2) (WITHIN H-2S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEGUENCE OF 291-760 FROM N.A. Rowen L., Qin S., Lasky S.R., Loretz C., Dors M., Mahairas Rowen L., Qin S., Lasky S.R.,
                                                                                                                                                                              363 YHITYKEAAGDDEVIVVEPASSISVVLNSLKPETLYLVNVTAEYEDGFSIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                      760 AA.
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MGD; MGI:88226; G2.

InterPro; IPR0001314; Chymotrypsin.
InterPro; IPR000136; Sushi_SCR_CCP.
InterPro; IPR00135; vWFA.
InterPro; IPR00135; vWFA.
Pfam; PP00084; sushi; 2.
Pfam; PP00089; trypsin; 2.
Pfam; PP00089; trypsin; 2.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00723; CHYMOTRYPSIN.
PRINTS; PR00723; CHYMOTRYPSIN.
PRINTS; SN00323; CCP; 2.
SMART; SN00032; CCP; 2.
SMART; SN00032; VWFA.
PROSITE; PS00134; TRYPSIN_LIS; UNKNOW!
PROSITE; PS00134; WPA; 2.

Hydrolase; Serine Protesse.
                                                                                                                                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, Created)
                                                                                                                                                                                                                                                                       PRELIMINARY;
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TISSUE=BREAST TUMOR;
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01-DEC-2001
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SEQUENCE FROM N.A.

MEDLINE-93149203; PubMed-8426611;

Reguence of a major Einmeria maxima antigen homologous to the Einmeria acquence of a major Einmeria maxima antigen homologous to the Einmeria arguence of a major Einmeria maxima antigen homologous to the Einmeria arguence of a major Einmeria maxima antigen homologous to the Einmeria arguence of a major Einmeria Explo.";

Mol. Biochem. Parasitol. 57:171-174(1993).

ENELL, M990858; AAA29076.1;

ENELL, M99088; AAA29076.1;

InterPro; IPR00084; TSP1.

NR PRINTS; PR00099; twa; 1.

RART; SM00099; TSP1. 6.

NR SMART; SM0029; TSP1. 6.

NR SMART; SM0029; TSP1. 6.

NR PROSITE; PS50092; TSP1; 5.

NR PROSITE; PS50094; WFRA; A. ACAARATERE CRC64:
                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 GYR--TASVIIALTDGELHEDLFFYSERE-----ANRSRDLGAIVYCVGV-KDFNETQL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 GGRDNAPKMILVMTDGA-----SSRRSQTLSAAEKLRNRGVIIVVLGVGTGVNSAEC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 VGLVTFGTSAVTRWDLSDSRAQNADLLAAAAKKLPYAAGSTYTHLGLAKA-BEILFSFQK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRO 58
                                                                                                                                                                                                                                                                       ---VYCVGV-----KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEIL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 ARIA--DSKDHV-FP--VNDGFQALQGIIHSILKKSCIEI----LAAEPSTI--CAGE 156
                                                                                                                                                                                                            354 YSWMQSQMDRLGMETRHTILLTDGK--SNMGDSPKKAVTRIRELLSIEQNRDD 411
                                                                                                                                                                                                                                                                                                           412 YLDIYAIGVGKLDVDWKELNE--LGSKKDGERHAFILQDA-KALQQIFEHMLDVSKL--- 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 VAIITEASQPKTIMSILSERSQ-----DVTEVITSLDSASYKDHENATGTNTYEVLIRV 353
                                              Gaps
                                                                                                                                                                               ------ NRQGYRTAS------ VIIALTDGELHEDLFFYSEREANRSRDLGAI----- 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriidae; Eimeriidae;
                                                                                     1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE----
                                                                                                                                                                                                                                                                                                                                                                                                 466 ---TDTICG------VGNMSANASDQERTPWQVTFKPKSKETCQGSLISDQWV 509
                                                                                                                                                                                                                                                                                                                                                                 146 AAEPSTICAGESFQVVVRGNGFRHARNVDRV--LCSFKINDSVTLSKSLQS-PWV 197
                                              63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 724;
Length 760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TIEMBLEEL. 01, Created)
01-NOV-1996 (TIEMBLEEL. 01, Last sequence update)
01-DEC-2001 (TIEMBLEEL. 19, Last annotation update)
MAJOR ANTIGEN HOMOLOGOUS SEQUENCE (EMP100).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.3%; Score 105.5; DB 5;
27.0%; Pred. No. 0.37;
iive 28; Mismatches 71;
       DB 11;
                                              77;
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    9.4%; Score 106.5; DE 24.3%; Pred. No. 0.32; Live 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               724 AA; 75808 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 27.09
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
         Query Match
Best Local Similarity 24.3%
watches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5804;
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Q63001
ID Q63001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q63001
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PROSITE; PS50234; VWFA;
                         999
                                     660 AA;
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           Collagen.
NON_TER
SEQUENCE
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                                                                                                                                STRAIN-WISTAR KYOTO;

C STRAIN-WISTAR KYOTO;

A Nablika T., Ito T., Kitada H., Serikawa T., Mahimo T., Soubrier F.,

A Nablika T., Ito T., Kitada H., Serikawa T., Mahimo T., Soubrier F.,

A Julier C., Masuda J., Yamori Y., Nara Y.;

Comparative mapping of a hypertension-related region on rat

T "Comparative mapping of a hypertension-related region on rat

C Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; U59801; AAB03226.1; -.

R HSSP; P11215; 1A8X.

R HSSP; P11215; 1A8X.

R TREPTO; IRRO02932; vWFA.

PRINTS; PR00453; VWFADOMAIN.

SMART; SM00327; VWA; 1.

PRINTS; PR00453; VWFADOMAIN.

SMART; SM00327; VWA; 1.

PRINTS; PR00453; VWFADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 VYCVGVKD-FNETQLARIAD-----SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAE 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                 GDTYMHEGFERASEQIYYE-NRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.2%; Score 104; DB 11; Length 205; Best Local Similarity 28.2%; Pred. No. 0.094; Matches 40; Conservative 24; Mismatches 64; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith M.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO80250; CAB65984.1; -.
HSSP; P11215; 1BHQ.
                                                                                                                                                                                                                                                                                                                                           205 AA; 22922 MW; C8C2D9395008DA36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ234P15.1 (COLLAGEN, TYPE XII, ALPHA 1) (FRAGMENT)
         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTECRIN ALPHA-W (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 PSTICAGESFQVVVRGNGFRHA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 GTQTGSTSSFEHEMSQEGFSAA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00041; fn3; 2.
Pfam; PF00092; vwa; 2.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00060; FN3; 2.
SMART; SM00327; VWA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003961; FN_III. InterPro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                               205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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01-07-2000 (TrEMBLrel. 15, Last sequence update)
01-05C-2001 (TrEMBLrel. 15, Last sequence update)
10-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTEGRIN BETA 2 ALPHA SUBUNIT.
Rattus norveques (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522 TLKKFTKVEDII-----EAINTFPYRGGSTNTGKAMTYVREKIFVPSK-GSRSNVPKVMI 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                              12 TLMKLTEDREQIRQCLEELQKVLP -- GGDTYMHEGFERASEQIYYENRQGYRT -- ASVII 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Gaps
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                                                                                                                                                                                                                                                                        20;
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28.2%; Pred. No. 1.2;
Live 24; Mismatches 64; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fathallah D.M. Str., Zerria K. Jr.;

Rathallah D.M. Str., Zerria K. Jr.;

"Cloning of the rat CDllb CDNA sequence.";

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF26859; AAR81280.1;

R HSPS; Pil215; 1A8X.

InterPro; IPR000413; Integrin_alpha.

R InterPro; IPR000413; VWFA.

R Pfam; PF001839; FG-GAP; 5.

R Pfam; PF001839; FG-GAP; 5.

R Pfam; PF00092; VWex. 1.

R PRINTS; PR01185; Integrin_A; 1.

R PRINTS; PR01092; VWex. 1.

R SMART; SM00191; Int_alpha; 5.

R SMART; SM00191; Int_alpha; 5.

R SMART; SM00192; VWA; 1.

R PR0SITE; PS50224; VWFR.

R PROSITE; PS50244; VWFR.

R PROSITE; PS50244; VWFR.

R PROSITE; PS50244; VW
                                                                                                                                                  Query Match 9.1%; Score 103; DB 4; Length 660; Best Local Similarity 31.0%; Pred. No. 0.55; Matches 45; Conservative 22; Mismatches 58; Indels
72523 MW; 3E3A10A285ECAA51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 FQALQGIIHSILKKSCIEI---LAA 147
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Best Local Similarity 28.29
Matches 40; Conservative
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696HX6;
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                                                                                                                                                                                                                                                                                                                                          1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60
                                                                                                                                                                                                                                                                                                                    Gaps
                                01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DNAK PROTEIN (HEAT SHOCK PROTEIN), C-TERMINAL REGION HAS VWA TYPE
                                                                           Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                  8.8%; Score 99; DB 16; Length 698; ilarity 27.0%; Pred. No. 1.4; Conservative 28; Mismatches 45; Indels
                                                                                                                                                                                                                                                                       Heat shock; Complete proteome.
SEQUENCE 698 AA; 78064 MW; B7FE2625B90013DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPAC664.10.
Schlzosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi; Ascomycota; Schlzosaccharomycetes;
Schlzosaccharomycetales; Schlzosaccharomycetaceae;
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Last sequence update)
Last annotation update)
                   698 AA.
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                    PRT;
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01-MAY-2000 (TEMBLEEL: 13,
01-MAY-2000 (TEMBLEEL: 13,
01-DEC-2001 (TEMBLEEL: 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                     PRELIMINARY;
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NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=972H-;
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                                                                                                       NCBI_TaxID=1488;
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EN 659
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Q9US03
                     Q97LT1
Q97LT1;
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      RESULT 13
              097LT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --ELHEDLFFYSEREANRSRDLGAIVYCVG--VKDFNETQLARIADSKDHVFPVNDGFQA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 DGELHEDLFFYSE------REANRSRDLGAIVYCVGVKDFNETQLARIADSKDH--V 119
                                                                                                                                                                                                                                                                                                                                                                                                            F-----PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFR-HARNV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                          31; Gaps
                                                                                                                                                                                                                                                                                                                       11 TTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          402 IDEIRDLLYIGKDRKNPREDYLDVYVFGVGPLVNQVNINALASKKDNEQHVFKVKD-MEN
Cadieu E., Lelaure V., Galibert F., McDougall R.C., Rajandream M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64;
                                                                                                                                                                                                                                                           3; Length 817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.4%; Score 95; DB 4; Length 764; 20.3%; Pred. No. 3.7; tive 32; Mismatches 69; Indels
                              24 RQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC007990; AAH07990.1; - 7574383E5FF7CC95 CRC64;
SEQUENCE 764 AA; 85563 MW; 7574383E5FF7CC95 CRC64;
                                                                                                                                                                                                                                                                                              Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                              88;
                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        764 AA
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Best Local Similarity 25.1%; Pred. No. 2.9;
Matches 51; Conservative 33; Mismatches
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TISSUE=COLON ADENOCARCINOMA;
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Matches 42; Conserv
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Search completed: August 9, 2002, 10:46:28 Job time: 851 sec

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August 9, 2002, 10:47:07; Search time 31.3 Seconds (without alignments) 269.676 Million cell updates/sec
                                                                                                                                                                                                                      1131
1 MSFIVFSTRGTTLMKLTEDR......STSGFKEGNSHPCLPARPHT 218
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                          105224 seqs, 38719550 residues
                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000 SwissProt\_40:\* Database :

105224

Total number of hits satisfying chosen parameters:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	0916x2 homo sapien 09c252 mus musculu 198335 homo sapien 013349 homo sapien 193944 gallus gall 190555 mus musculu 190555 mus musculu 091145 notophthalm 06041 mus musculu 190715 homo sapien 192018 qallus gall 192018 qallus gall 1921941 homo sapien 192018 pallus gall 1921941 homo sapien 028902 oryctolagus 190751 homo sapien 1921941 homo sapien 042401 gallus gall 191111 homo sapien 191111 homo sapien 19456 caenorhabdi 067016 aquifex aeo 008746 mus musculu 194677 streptococc 008746 mus musculu 194677 streptococc 008746 mus musculu 194677 streptococc 00876 mus musculu 194677 streptococc 09676 oryza sativ 066507 oryza sativ 066507 oryza sativ 066300 arabidopsis 1915989 gallus gall
SUMMARIES	ATR HUMAN ATR HUMAN ATR MOUSE ITAM HUMAN CAIC_CHICK ITAM HUMAN CAIC_HUMAN ATN3_CHICK CAMA_HUMAN CAIC_HUMAN ATN3_CHICK CAMA_HUMAN CAIC_HUMAN CAIC_HUMAN CAIC_HUMAN CAIC_HUMAN INX3_CAEEL MAN3_CAEEL MAN3_CAEEL ATN3_CAEEL ATN3_CAECJ ATN
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P05099 gallus gall P23231 neurospora P43247 mus musculu P29305 hordeum vul 060677 mus musculu P38570 homo sapten Q550105 pyrococcus O50105 pyrococcus Q58192 methanococc P12109 homo sapten P49702 gallus gall	TS 4 AA. ate) pdate) endothellal marker 8). Vertebrata; Euteleostom1; 1; Hominidae; Homo.	erso G., Romans K.E., auer C., Vogelstein B., um."; lier R.J., Young J.A.T.; for anthrax toxin."; , AND SEQUENCE FROM N.A.	jaki H., Ikema Y., Okamoto S., 4., Nishi T., Shibahara T., 5.S.;  'DDBJ databases.  'DDBJ databases.  'OpbJ databases.  'Shown here', 2, 3 and 4; seem  'Shown here', 2, 3 and 4; seem  'In tumor endothelial cells  'In tumor endothelial cells  'In tumor endothelial cells  'Spowded through the VWA domain.  'Sproduced through a collaboration  'And the EMBL outstafion -  'And the EMBL outstafion.	atics and the Embi Outstation here are no restrictions on it as its content is in no wa
CAMA_CHICK OM70_NEUCR MSH2_MOUSE 143A_HORVU ITAE_HOWAN DP03_STAAU 1433_LILLO DHYS_PYRHO TF2B_METJA CALG_HUWAN ARF5_CHICK	ALIGNMEN' PRT; 566 updaction uportation uportation correction uportation upor	1). 947988; lescu V., Trav ins G.J., Leng umor endotheli. 2). 2). Mourez M., Col ular receptor	ake N., Inage, Obayashi hid. T., Sugancara, Sugancara, CanBank, Obayashi hid.	or stoinford institute. J ions as long
493 1 6193 1 262 1 1179 1 1436 1 1028 1 179 1 179 1 179 1 179 1 179 1 179 1 179 1 179 1 179 1 179 1 179	RD; Crea Last Last prec prec	ISOFORM bMed=100 , Velcu., Rigg human ti 2(2000) ISOFORM ge J.,   ge J.,   fe celli.	1ji T., Kobe T., Suzuki ) ura Y., Iso Sequencing 000) to the A. (ISOFORM A. (ISOFORM A. to the pi LOCATION: Ty PRODUCTS: 4 ed by alter FICITY: High ormal endothing to PA Se BELONGS TO: CONTAINS IV	nstics instit
0.7.7.0 0.7.7.0 0.0.7.0 0.0.0	TANI . 4 . 4 . 4 . 4 . 6 . 1 . 1 . 1 . 1 . 1 . 1 . 1 . 1 . 1	EROM N.A. (ISOFO 20407466; Pubmed-B., Rago C., Vel Y. E., Lal A., Ri. W. W.; E., Lal A., Ri. W. W.; E., Lal A., Ri. W.; E., Lal A., Ri. W.; E., Lal A., Ri. M.; Manan 289:1197-1202(200 FROM N.A. (ISOFO FROM Of the cellarists of t	Hi John Name Name Name Name Name Name Name Name	SW1 Bio -pro
79.5 79.5 79.5 79.5 78.5 78.5 77.5 77.5	HUMAN X2; Q AR-20 AR-20 AR-20 AR-20 AR-20 AR-20 Sapi Sapi	[1] MEDLINE=20407466; E St Croix B., Rago C Montgomery E., Lal Kinzler K.W.; Genes expressed in Science 289:1197-12 [2] SEQUENCE FROM N.A. PubMed=11700562; Bradley K.A., Mogri "Identification of Nature 414:225-229([3])	(ISOFORM 3).  Kawabata A., Hik  Kawabata A., Hik  Ckitani R., Ota  Tanaka T., Nakam  "NEDO human cDNA  Submitted (AUG-2  Strausberg R.;  Strausberg R.;  Strausberg R.;  Strausberg R.;  Strausberg R.;  Strausberg R.;  Submitted (AUG-2	sen the European by non
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(See http://www.isb-sib.ch/announce/
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
EDDD -> NKIK (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
NEKPEYUEDYLLCPAPILKEYGMARALQV.-> SKSLQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
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                                                                                                  MIM; 6064L0; -.
InterPool IPR002035; vWFA.
InterPool IPR00327; VWA; 1.
PROSITE; PS50224; VWFR; 1.
PROSITE; PS50224; VWFR; 1.
                                                                                                                                                                                                                                                                                                                    MISSING (IN ISOFORM 3).
DGSILAIALLILFLL -> LHKIASGPTTAACME (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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0
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Antrax town receptor precursor (Tumor endothelial marker 8).
ATR OR TEM8.
                                                                                                                                                                                                                                                                                                                                                                                            Score 966; DB 1; Length 564;
Pred. No. 4e-76;
2; Mismatches 0; Indels
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SEQUENCE FROM N.A. (ISOFORM 1).
SEQUENCE-21443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.)
                                                                                                                                                                                                                 ASP/GLU-RICH (HIGHLY ACIDIC).
                                                                                                                                                         POIENTIAL.
ANTRAX TOXIN RECEPTOR.
EXTRACELLULAR (POIENTIAL).
                                                                                                                                                                                                                                                                                                                                                   MISSING (IN ISOFORM 4).
B118A00AD5DF2233 CRC64;
                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           562 AA.
  modified and this statement is not removed. entities requires a license agreement (See h or send an email to license@isb.sib.ch).
                                                                                                                                                                                                                                                                                                                                           ISOFORM 4)
                                                                                                                                                                                     POTENTIAL.
                                                        EMBL; AK025429; BAB15128.1; ALT_INIT.
EMBL; AK001463; BAA91707.1; ALT_FRAME.
EMBL; BC012074; AAH12074.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                           VWFA
                                                                                                                                                                                                                                                                                                                                                                  62789 MW;
                                                  EMBL; AF279145; AAK52094.1; -
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 85.4%;
Best Local Similarity 98.9%;
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                              2564
2015
3068
1166
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297
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564 AA;
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                                                                                               MIM; 606410;
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ID ATR_MOUSE
AC Q9CZ52;
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DOMAIN
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CARBOHYD
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                                                                  RR SEQUENCE OF 88-562 FROM N.A. (ISOFORM 2).

RX KAWAIN-C57BL/G1; TISSUB-EMDYYO;

RX KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara M., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M. Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Reole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
GRCINFTRVKNSOPAKYPLNNTYHPSSPPRAPIYTPPPPAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCPPPAPSAPTPFIPSPPSTLPPPPQAPPPNRAPPPSRPPP
RPSV -> RFRGWRLTICLGSKHVHPGRHDKGPETPLLKQA
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AK013005; BAB28591.1; ALT_INIT.
MGD; MGI:1919432; Atr.
InterPro; IPR002035; VWFA.
PROSITE; PS50234; VWFA.
Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
SIGNAL
St Croix B.; tumor endothelial markers are conserved in mice and tumor endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASP/GLU-RICH (HIGHLY ACIDIC).
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6AC92049B4BB4F7C CRC64;
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ANTRAX TOXIN RECEPTOR
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Pred. No. 1.3e-75;
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                                                 Cancer Res. 61:6649-6655(2001).
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98.4%;
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        Kinzler K.W., "Cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Best Local Similarity

LSFIVESSQATIILPLTGDRGKISKGLEDLKRVSPVGETYIHEGLKLANEQI--QKAGGL 137

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21539596; PubMed=11683410;
Bell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S.,
Maxwell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S.,
Maxwell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S.,
Maxwell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S.,
Toliferential gene expression during capillary morphogenesis in 3D
collagen matrices: regulated expression of genes involved in basement
membrane matrix assembly, cell cycle progression, cellular
differentiation and G-protein signaling.";
T. Cell Sci. 114:2755-2773(2001).
Seems to bind to collagen type IV and laminin.
Subgelicitar Location: Type I membrane protein (Probable).
SIMILARITY: GONTAINS I VWFA DOMAIN.
                                                                                                                                                Gaps
                             MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAPILLARY MORPHOGENESIS PROTEIN-2. EXTRACELLULAR (POTENTIAL).
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 Indels
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0F9B2D6688EAB17A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                              Capillary morphogenesis protein-2 precursor (CMG-2).
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                                                                                                                                                                                                                                                                                                                                               01-WAR-2002 (Rel. 41, Created)
01-WAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                      386 AA
 Mismatches
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POTENTIAL.
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57.0%; Pred
tive 26; 1
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5
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 Conservative
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                            KINDSVTLSK 190
                                                                                                                                                                                                                               258 KINDSVTLNE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211
386 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                    CMG2_HUMAN
P58335;
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SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A. MEDLINE-96257236; PubMed-8666289; Wong D.A., Davis E.M., LeBeau M., Springer T.A.; "Cloning and chromosomal localization of a novel gene-encoding a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERACTION WITH VCAMI.
MEDLINE-99059842; PubMed-9841932;
Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W., Hoffman P.A., Staunton D.E., Bochner B.S.;
"alphadbeta2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE OF 1-235 FROM N.A.
MEDLINE-20187620; PubMed-10722744;
Noti J.D., Johnson A.K., Dillon J.D.;
Structural and functional characterization of the leukocyte integrin gene CD11d. Essential role of Sp1 and Sp3.";
J. Biol. Chem. 275:8959-8969(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nunton D.E., Gallatin W.M.;
novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
     RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
                                     197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99370002; Pubmed-10438935; Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A., Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.; "The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a binding integrine between I domain and VCAM-1."; J. Immunol. 163:1984-1990(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: INTEGRIN ALPHA-D/BETA-2 IS A RECEPTOR FOR ICAM3 AND VCAM1. MAY PLAT A ROLE IN THE ATHEROSCILENTIC PROCESS SUCH AS CLEARING LIPOPROTEINS FROM PLAQUES AND IN PHAGOCYTOSIS OF BLOODBORNE PATHOGENS, PARTICULATE MATTER, AND SENESCENT ERYTHROCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASSOCIATES WITH BETA-2.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: EXPRESSED MODERATELY ON MYELOMONOCYTIC CELL
                                                                                                                                                                                                                                                                                             D) (CD11d) (ADB2).
                      Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             St John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., Staunton D.E., Gallatin W.M.;
                                                                                                                                                                                                   ITAD_HUMAN STANDARD; PRT; 1162 AA. 013349; 015575; 015576; 016-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last annotation update) 01-MAR-2002 (Rel. 41, Last annotation update) Integrin alpha-D precursor (Leukointegrin alpha I
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96111956; PubMed=8777714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exp. Med. 188:2187-2191(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  beta 2-integrin alpha subunit.";
Gene 171:291-294(1996).
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunity 3:683-690(1995).
                                                                           PVNDGFQALQGIIHS 135
                                                                                                 INTERACTION WITH VCAM1.
                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM THE BLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Spleen;
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Gaps

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Indels

30;

Score 373; DB 1; Length 386;

Pred. No. 4.7e-25;

Mismatches

Conservative

Best Local Similarity

Query Match

77;

Matches

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1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60

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2846-2873
      CONFLICT
CONFLICT
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CARBOHYD
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CA1C_CHICK
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                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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                                                                                                                                                                                                                                                                         Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                              POTENTIAL.
INTEGRIN ALPHA-D.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                    POTENTIAL. CYTOPLASMIC (POTENTIAL).
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GFFKR MOTIF.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
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N-LINKED
                                                                                                                                                                                                                                                                                                                                 FG-GAP 1.
FG-GAP 2.
                                                                                                                                                                                              nterPro: IPR000413; Integrin_alpha.
InterPro: IPR002035; vWFA.
Pfam; PF01839; FG-6AP; 5.
Pfam; PF00357; integrin_A; 1.
Pfam; PF0092; vwa; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; vWFADOMAIN.
SMART; SM00391; Int_alpha; 4.
SMART; SM00307; vW#; 1.
                                                                                                                                                                                                                                                             PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                        EMBL; U37028; AAB38547.1; --
EMBL; U40274; AAB60634.1; --
EMBL; U40275; AAB60635.1; --
EMBL; U40277; AAB60637.1; --
EMBL; U40277; AAB60637.1; --
EMBL; U40278; AAB60638.1; --
EMBL; U40278; AAB60638.1; JOINED.
EMBL; AF187881; AAF62875.1; --
HSSP; P11215; 1A8X.
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Magnesium. 1 17
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STRAIN-WHITE LEGHORN;

MEDLINE-92011862; PubMed=1918137;

Yamagata M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka H.,

Nishida Y., Obara M., Kimata K.,

"The complete primary structure of type XII collagen shows a chimeric

"The complete primary structure of type III motifs, von Willebrand

molecule with reiterated fibronectin type III motifs, von Willebrand

factor A motifs, a domain homologous to a noncollagenous region of

fype IX collagen, and short collagenous domains with an Arg-Gly-Asp

site.":
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Gallus Abtazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 IIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLAR-----IADSKDH 118
                                                                                                                                                                                                                                                                                                                                                                                  : |:|:
193 SNLLKIHFTFTQFRTSPSQQSLVDPIVQLKGLTFTATGILTVVTQLFHHKNGARKSAKKI 252
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                                                                                                                                                                                                                                                                                                                           11 TTLMKLJEDREQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYENRQGYRTA-SV 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 2456-3124 FROM N.A., AND SEQUENCE OF 2772-2794 AND
. (POTENTIAL)
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"Type XII collagen: distinct extracellular matrix component discovered by cDNA cloning.";
Proc. Natl. Acad. Sci. U.S.A. 84:6040-6044(1987).
                                                                                                                                                                                                                  10.1%; Score 114; DB 1; Length 1162; 27.3%; Pred. No. 0.043; tive 27; Mismatches 83; Indels 18
                                                                                       L -> V (IN REF. 2).
V -> A (IN REF. 2).
WW: F296AlA35455D77D CRC64;
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P13944; Q04509;
01.JAN-1990 (Rel. 13, Created)
01.NOV-1997 (Rel. 35, Last sequence update)
01.MAR-2002 (Rel. 41, Last annotation update)
COLIGAN (Fibrochimerin).
  MISSING (IN REF. 2).
GHPW -> AIP (IN REF. 2).
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MEDLINE=93042014; PubMed=1420368;
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MEDLINE=87317590; PubMed=3476925;
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[2]
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Best Local Similarity
Matches 48; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINAL TISSUE FORM OF COLLAGEN XII MAY CONTAIN HOMOTRIMERS OF EITHER THE LONGER OR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTEOGLYCAN. THE LARGE ISOFORM HAS MORE RESTRICTED EXPRESSION IN EMBRYONIC TISSUE THAN
ALTERNATIVE SPLICING.

MEDLINE-95370352; PubMed-7642694;

MEDLINE-95370352; PubMed-7642694;

Mcoch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;

"Large and small splice variants of collagen XII: differential
expression and ligand binding.";

-1. FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
CONTAINING FIBRILS, THE COLL DOWNIN COULD BE ASSOCIATED WITH THE
SURFACE OF THE FIBRILS, AND THE COLL AND NC3 DOMAINS MAY BE
LOCALIZED IN THE PERIFIBRILLAR MATRIX.

-1. SUBUNIT: TRIMER. OF IDENTICAL CHAINS EACH CONTAINING 190 kDa OF
                                                                                                                                                                                                                                                                                                                DOMAIN: THIS SEQUENCE DEFINES FIRE DISTINCT DOMAINS, TWO TRIPLE-
HELICAL DOMAINS (COLI AND COL2) AND THREE NONTRIPLE-HELICAL
HELICAL DOMAINS (COLI, NC2, AND NC3).
PUMAINS (NC1, NC2, AND NC3).
PTW: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT
EACH BND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
SIGNAL 1 24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                          PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. PTM: GLYCOSYLATED, CHONDROITIN'-SULFATED (BY SIMILARITY). SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY. SIMILARITY: CONTAINS 4 VWFA DOMAINS. SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: TYPE XII COLLAGEN IS PRESENT IN TENDONS, LIGAMENTS, PERICHONDRIUM, AND PERIOSTEUM, ALL DENSE CONNECTIVE TISSUES CONTAINING TYPE I COLLAGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLLAGEN ALPHA 1(XII) CHAIN. FIBRONECTIN TYPE-III 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INCEPTO: IPRO00087; Collagen.
InterPro: IPRO0361; FN_III.
InterPro: IPRO0361; FN_III.
InterPro: IPRO0362; FNIII_repeat.
InterPro: IPRO02035; VWFA.
Pfam: PF00131; Collagen; 4.
Pfam: PF00131; Collagen; 4.
Pfam: PF00041; fn; 17.
Pfam: PF00092; vwa: 4.
Pfam: PF00092; vwa: 4.
PRINTS: PRO0044; FNNTPEIII.
PRINTS: PRO0045; VWA: 4.
PRINTS: PRO0045; VWAPADOMAIN.
SWART; SW00210; TSPN: 1.
SWART; SW00210; TSPN: 1.
PRINTS: PRO0051; VWA: 4.
PROSITE; PS50234; VWFA.
PROSITE; PS50234; VWFA.
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                                                                                                                                                                     NONTRIPLE-HELICAL SEQUENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, D00824, BAA00701.1, --
EMBL, X61024; CAA43388.1; --
EMBL, M17375, AAA48718.1; --
EMBL, J05137; AAA48635.1, --
EMBL, X67327; CAA47744.1; --
PIR, A34485; A34485.
HSSP, P17301; IAOX
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114
311
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94 AIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPST 151
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TO CHOUNDROITIN SULEATE (POTENTIAL).
TO CHOUNDROITIN SULEATE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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TRIPLE-HELICAL REGION (COL1)
WITH 2 IMPERFECTIONS.
NONHELICAL REGION (NC1).
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TRIPLE-HELICAL REGION (COL2)
WITH 1 IMPERFECTION.
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AA; 340578 MW; 094285AFE7F346CF CRC64;
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FIBRONECTIN TYPE-III 10.
FIBRONECTIN TYPE-III 11.
FIBRONECTIN TYPE-III 12.
FIBRONECTIN TYPE-III 12.
FIBRONECTIN TYPE-III 14.
FIBRONECTIN TYPE-III 14.
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FIBRONECTIN TYPE-III 15.
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-III 16.
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ARG/LYS-RICH (BASIC).
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FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
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D -> E (IN REF. 4).
P -> A (IN REF. 2).
L -> F (IN REF. 2).
V -> F (IN REF. 2).
FIBRONECTIN TYPE-III
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Best Local Similarity
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MGD; MGI:96607; Itgam.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH LOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
-!- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
-!- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
                                   01-FEB-1991 (Rel. 17, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1).
                                                                                                                                                                                                                                         "Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willebrand factor.";
                                                                                                                                                                                                                                                                                                                                   STRAIN-BALB/C; TISSUE-Spleen;
MEDIJNE-86287312; PubMed-2942940;
Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,
Larson R.S., Roberts T.M., Springer T.A.,
"A partial genomic DNA clone for the alpha subunit of the mouse
complement receptor type 3 and cellular adhesion molecule Mac-1.";
Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASSOCIATES WITH BETA-2.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 17-28.
MEDLINE-85188276; PubMed=3887182;
Springer T.A., Teplow D.B., Dreyer W.J.;
Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
"Sequence homology of the LFA-1 and Mac-1 leukocyte interferon.";
glycoproteins and unexpected relation to leukocyte interferon.";
Nature 314:540-542(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. ALPHA-M
                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=88312584; Pubmed=3044779;
                               (Rel. 09, Created)
                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 11-45 FROM N.A.
                                                                                                                                                                                                                                                                                                EMBO J. 7:1371-1378(1988).
STANDARD;
                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRANULOCYTES.
                                                                                                                                                                      NCBI_TaxID=10090;
                               01-NOV-1988
 ITAM_MOUSE
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94 AIVYCVGVKD-FNETQLARIAD-----SKDHVFPVNDGFQALQGIIHSILKKSCIEILA 146
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                                       PRINTS; PROLISS; INTEGRINA.
PRINTS; PROLISS; INTEGRINA.
SMART; SM00191; Int_alpha; 4.
SMART; SM00272; VWA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.98; Score 112; DB 1; Length 1153; 29.18; Pred. No. 0.064;
                                                                                                                                                                                                                                                                                                                                                                                                                                            178DB988AECB0343 CRC64;
                                                                                                                      INTEGRIN ALPHA-M.
EXTRACELLULAR (POTENTIAL)
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Interpro: IPR000413 Integrin_alpha. Interpro: IPR000413; Integrin_alpha. Pfam; PF01839; FG-GAP; 5. Pfam; PF00357; integrin_A; 1. Pfam; PF00992; vwa; 1.
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EMBL; X07640; CAA30479.1; -. EMBL; M14293; AAA39484.1; -. PIR; S00551; S00551. HSSP; P11215; 1ABX.

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Arnaout M.A., Remold-O'Donnell E., Pierce M.W., Harris P., Tenen D.G.; "Molecular cloning of the alpha subunit of human and guinea pig leukocyte adhesion glycoprotein Mol: chromosomal localization and homology to the alpha subunits of integrins."; Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93123748: PubMed-8419480;
Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;
"Structural analysis of the Collb gene and phylogenetic analysis of
the alpha-integrin gene family demonstrate remarkable conservation of
genomic organization and suggest early diversification during
                                                     01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha
subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1)
(Neutrophil adherence receptor).
ITGAM OR CR3A OR CD11B.
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-88257215; PubMed-2454931;
Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
Annio acid sequence of the alpha subunit of human leukocyte adhesion
receptor Mol (complement receptor type 3).";
J. Cell Biol. 106:2153-2158(1988).
                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-88131603; Pubmed-2457584;
MEDLINE-88131603; Pubmed-2457584;
Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;
"The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins, von Millebrand factor and factor B.";
J. Biol. Chem. 263:12403-12411(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "cDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits."; Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).
                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 9-1153 FROM N.A.
MEDLINE-89098893; Pubmed-2563162;
Hickstein D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shelley C.S., Arnaout M.A.; "The promoter of the CD11b gene directs myeloid-specific and developmentally regulated expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE-92144986; PubMed-1346576;
Pahl H.L., Rosmarin A.G., Tenen D.G.;
"Characterization of the myeloid-specific CD11b promoter.";
                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
                        PRT; 1152 AA
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MEDLINE-87076671; PubMed=3539202;
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                                                 (Rel. 11, Created)
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                        STANDARD;
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                                                01-JUL-1989
                      ITAM_HUMAN
P11215;
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          ITAM_HUMAN
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-!- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
-!- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
-!- DATABASE: NAME-PROW; NOTE-CD guide CD11b entry;
WWW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd11b.htm".
                                                                                                                                                          Lee J.O., Rieu P., Arnaout M.A., Liddington R.; "Crystal structure of the A domain from the alpha subunit of integrin
                                                                                                                                                                                                                                                                                                                                            Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.; "Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A., Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L., Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E., Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.; "Cation binding to the integrin CD11b I domain and activation model assessment.";
"N-terminal sequence of human leukocyte glycoprotein Mol: conservation across species and homology to platelet IIb/IIIa."; Biochim. Biophys. Acta 874:368-371(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
MEDLINE=98362595; Pubmed=9687375;
                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
MEDLINE-96363671; Pubmed-8747460;
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Cell 80:631-638(1995).
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RESULT 8
CA1C_NOTVI
                                          7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 GRTHTATGIRKVVRELENITNGARKNAFKILVVITDGEKEGDPLGYEDVIPEADRE---G 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 VIRYVIGVGDAFKSEKSRQELNTIASKPPRDHVFQVNN-FEALKTIQNQLREK----IFA 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR002035; vWFA.

Interpro; IPR002035; vWFA.

Interpro; IPR002035; vWFA.

R pfam; PF01839; FG-GAP; 5.

R pfam; PF01837; Integrin_A; 1.

R pfam; PF00192; vwa: 1.

R PRINTS; PR01185; INTEGRINA.

R RNART; SM00191; INTEGRINA.

R SMART; SM00191; INTEGRINA.

R RNART; SM00191; INTEGRINA.

R RNART; SM00191; INTEGRINA.

R RNART; SM00191; INTEGRIN_ALPHA; 1.

R PROSITE; PS50234; VWFA: 1.

R PROSITE; PS50234; VWFA: 1.

R RNART; SM0191; INTEGRIN_ALPHA; 1.

R RNART; SM0191; INTEGRINA.

R SMART; SM01919; INTEGRINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 111; DB 1; Length 1152; Pred. No. 0.078;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FG-GAP 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEGTOTGSSSSFEHEMSQEGFSAA 358
          S52165, AAB24821.1; JOINED.
S52165, AAB24821.1; JOINED.
S52167, AAB24821.1; JOINED.
S52170, AAB24821.1; JOINED.
S52170, AAB24821.1; JOINED.
S52173, AAB24821.1; JOINED.
S52173, AAB24821.1; JOINED.
S52180, AAB24821.1; JOINED.
S52181, AAB24821.1; JOINED.
S52189, AAB24821.1; JOINED.
S52189, AAB24821.1; JOINED.
S52189, AAB24821.1; JOINED.
S52218; AAB24821.1; JOINED.
S52221; AAB24821.1; JOINED.
S52222; AAB24821.1; JOINED.
S52222; AAB24821.1; JOINED.
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, M84477; AAA51960.1;
A31108; RWHU1B.
A26091; A26091.
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11; Conservative
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31
 $52161; R$52164; R$52165; R$52167; R$52169; R$52170; R$52173; R$52174;
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COLLAND STANDARD: PRT: 929 AA.

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   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

STRAIN-SWISS WEBSTER, AND C57BL/6J; TISSUE-Skin;

MEDLINE-96170761; PubMed-8601036;

A Bochme K., Li Y., Oh P.S., Olsen B.R.;

Bochme K., Li Y., Oh P.S., Olsen B.R.;

Tolidagen XII and their tissue-specific expression during embryonic and evelopment. ";

Dev. Dyn. 204:432-445(1995).

TE CONTAINING FIBRILS, THE COLI DOMAIN COULD BE ASSOCIATED WITH THE SURFACE OF THE FIBRILS, AND THE COLZ AND NO3 DOMAINS MAY BE LOCALIZED IN THE PERIFIBRILLAR MATRIX (BY SIMILARITY).

CONTAINING THE PERIFIBRILLAR MATRIX (BY SIMILARITY).

CONTAINING THE DEBNITCAL CHAINS EACH CONTAINING 190 KDB OF NOWIRIDEL-HELICAL SEQUENCES (BY SIMILARITY).

CONTAINING FIBRILS, AND THE COLZ AND NO3 DOMAIN HERE) AND A SHORT FORM; ARE RRODUCED BY ALTERNATIVE SPLICING: THE FIRAL TISSUE FORM OF COLLAGEN XII MAY COMPAIN HOPPRIMERS OF EITHER THE LONGER OR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT STREAM OF THE SHORTER ISOFORM CHAIRS. ONLY THE LONG FORM. MASSON CHAIRS. ONLY THE DANG VARIANT IS A PROPECLIVATOR.

"TESTED FORM OF COLLAGEN XII MAY COMBINATION OF LONG AND SHORT STREAM OF THE SHORTER ISOFORM. CHAIRS. ONLY THE DANG VARIANT IS A PROPECLIVATOR.

"THE SHORTER EDEVICE WAS THE DANG VARIANT IN MEMORY. DEPLICATION."

"THE SHORTER EDEVICE WE WAS CONTAIN HOPPORTECTIVE OF THE SHORTER EDEVICE WAS THE WAS T
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                                                                                                                                                                                                                                                                                                                                               655 FISRVVEVFDIGSDRVQIAVSQYSGDPRTEWQLNTHKTKKSLMDAVANLPYKGGNTNTGS 714
                                                                                                                                                                                                                                                                                                                                                                                             100 GVKDFNETQLARIADSKDHVFPVN-DGFQALQGIIHSILKKSCIEILAA----EPSTICA 154
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                               6 FSTRGTTLMKLTEDREQI-------ROGLEELQKVLP--GGDTYMHE 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                            44 GFERASEQIYYENRQGY----RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCV
                                                                                   (POTENTIAL).
                 VWFA 2.
FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 8.
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
                                                                                                                                                                                                                               42;
                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                Score 109; DB 1; Length 929;
Pred. No. 0.09;
                                                                                                                                                                                                                               73; Indels
                                                                                                                                                101647 MW; AE5D7485254FD954 CRC64;
   FIBRONECTIN TYPE-III 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                              Ouery Match 9.6%; Score 109; DB Best Local Similarity 24.2%; Pred. No. 0.09 Matches 46; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collagen alpha 1(XII) chain precursor.
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                                  907
>929
231
324
415
98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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                                                                                                                                 929
929 AA;
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                                                                                               415
98
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15-JUL-1998
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Q60847;
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CA1C_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R InterPro; IPR003129; TSPN.
R InterPro; IPR003129; TSPN.
R InterPro; IPR003035; WWFA.
R Pfam; PF00139; Collagen; 4.
R Pfam; PF00139; Collagen; 4.
R Pfam; PF00041; fin3; 18.
R PRIMTS; PR00014; FWPPEIII.
R PRIMTS; PR00014; FWPPEIII.
R PRIMTS; SM00050; FN3; 16.
R SMART; SM00210; TSPN; 1.
R SMART; SM00327; VWA; 4.
R PROSITE; PS5034; VWFA; 
PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT EACH END (BY SIMILARITY).
                                                                          PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-x-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
                                                                                                                                                    NONHELICAL REGION (NC1).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WITH 1 IMPERFECTION.
NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION (COL1)
WITH 2 IMPERFECTIONS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 4.0.0.6
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FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 6
FIBRONECTIN TYPE-III 7
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FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
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FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:88448; Coll2al.
InterPro; IPR000087; Collagen.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FnIII_repeat.
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PROSITE; PS50240; TRYPSIN_DOM; PROSITE; PS00134; TRYPSIN_HIS;
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AAA37381.1;
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AAA37380.1;
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M60568;
M60569;
M60569;
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M60573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 LKKSCI-----EILAAE----PSTICAGESFQVVVRGNGFRHARNVDRVLCSFKIND 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 REDLLAAVKKIPYKGGNTMIGDAIDYLVKNIFTESAGSRAGFPKVGIII--TDGKSQDEV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 9.6%; Score 109; DB 1; Length 3067;
1 Similarity 22.8%; Pred. No. 0.38;
51; Conservative 38; Mismatches 69; Indels 66; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQGLEELQKVLP--GGDTYMHEGFERASEQIYYE---NRQGYRTASVIIALTDGELHEDL 78
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Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Musmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
TO CHONDROITIN SULFATE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
HYDROXILATION (BY SIMILARITY).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
MISSING (IN SHORT ISOSPORM).
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1-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Complement C2 precursor (EC 3.4.21.43) (C3/C5 convertase).
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22951
22960
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P21180;
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         12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---VYCVGV------KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEIL 145
                                                            Plasma; Glycoprotein; Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.4%; Score 106.5; DB 1; Length 760; 24.3%; Pred. No. 0.12; Live 38; Mismatches 77; Indels 63
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COMPLEMENT C2A FRAGMENT.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                         SERINE PROTEASE
                                                                                        Sushi; Alternative splicing
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                                                                                                                                                                                                                                                                             SUSHI 2.
SUSHI 3.
                                                                                                                                                                                                                                                 SUSHI 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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                               PROSITE; PS50234; VWFA; 1
Complement pathway; Plasma
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY.
-:- SIMILARITY: CONTAINS 4 VWFA DOMAINS.
-:- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                              SMART: SM00060; FN3; 17.
SMART: SM00210; TSPN; 1.
SMART: SM00127; VWA: 4.
PROSTIE: PS50234; VWFN: 4.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EACH END (BY SIMILARITY).
-!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
"Complete primary structure of two splice variants of collagen XII, and assignment of alpha 1(XII) collagen (COL12A1), alpha 1(IX) collagen (COL9A1), and alpha 1(XIX) collagen (COL19A1) to human chromosome 6q12-q13.";
                                                                                                                                                                                                                                LOCALIZED IN THE PERIFIBRILLAR MATRIX (BY SIMILARITY)
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Interpro; IPR003961; FN_III.
Interpro; IPR003962; FnIII_repeat.
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InterPro: IPR002139; TSPN.
InterPro: IPR002139; VWFA.
Pfam; PF02110; Collagen; 4.
Pfam; PF02210; TSPN; 1.
Pfam; PF00210; TSPN; 1.
PRINTS; PR00014; FNTYPEIII.
PRINTS; PR00453; VWFADOMAIN.
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FIBRONECTIN TYPE-III 3 FIBRONECTIN TYPE-III 5 FIBRONECTIN TYPE-III 5 FIBRONECTIN TYPE-III 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 20-43.

MEDLINE-87167596; PubMed-3549901;

Miller L.J., Wiebe M., Springer T.A.;

J. Immunol. 138;2381-2383(1987).

J. SEBUNIT. ALPHA-X

ASSOCIATES WITH BETA-2.

ASSOCIATES WITH BETA-2.
                                                                                                                                                                                                                                                                                           Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.; and complete primary structure of the alpha subunit of a leukocyte adhesion glycoprotein, p150,95."; EMBO J. 6:4023-4028(1987).
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
1ntegrin alpha-x precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c) (Leu M5).
ITGAX OR CD11C.
                                                                                                                                                                       Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=90153906; PubMed=2303426;
Corbi A.L., Garcia-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.";
J. Biol. Chem. 265:2782-2788(1990).
                                                                                                                                           Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corbi A.L., Garcia-Aguilar J., Springer T.A.;
J. Biol. Chem. 265:12750-12751(1990).
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EMBL; M29487; AAA51620.1; ALT_SEQ.
EMBL; M29483; AAA51620.1; JOINED.
EMBL; M29484; AAA51620.1; JOINED.
EMBL; M29485; AAA51620.1; JOINED.
EMBL; M29485; AAA51620.1; JOINED.
EMBL; M29485; AAA51620.1; JOINED.
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MEDLINE=88166645; PubMed=3327687;
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EMBL; Y00093; CAA68283.1; -.
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HSSP; P11215; 1A8X.
CarbBank; CCSD:33581;
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             12;
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                                                                                                                                                                                                                                                                                                                                                            WALTH A INTERACTORY
NONHEDICAL REGION (NC2).

TRIPLE-HELICAL REGION (COL1)
WHITH 2 INDERESTONS.
NONHEDICAL REGION (NC1).
TO CHONDROITIN SULEATE (POTENTIAL).
TO CHONDROITIN SULEATE (POTENTIAL).
TO CHONDROITIN SULEATE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
HYDROXYLATION (BY SIMILARITY).
HYDR
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W; 75FEA78FA8E48293 CRC64;
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NONHELICAL REGION (NC3)
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FIBRONECTIN TYPE-III 10
FIBRONECTIN TYPE-III 11
FIBRONECTIN TYPE-III 11
FIBRONECTIN TYPE-III 13
FIBRONECTIN TYPE-III 14
FIBRONECTIN TYPE-III 16
FIBRONECTIN TYPE-III 16
FIBRONECTIN TYPE-III 16
FIBRONECTIN TYPE-III 16
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                      FIBRONECTIN TYPE-III
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26.0%; Pred. No. 0.75;
cive 34; Mismatches
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Matches 60; Conserv
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                                                                                                                                                                                                                       PRINTS, PRO1185; INTEGRINA.
PRINTS, PRO0453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA: 1.
PROSITE; PS50234; VWFA; 1.
PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
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EXTRACELLULAR (POTENTIAL).
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WWFA.
WG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 7.
POTENTIAL.
POTENTIAL.
GOTENTIAL.
GFFKR MOTIF.
                                                                           InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vWFA.
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                                                                                                                                        Pfam; PF01839; FG-GAP; 5.
Pfam; PF00357; integrin_A; 1.
Pfam; PF00092; vwa; 1.
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                           CarbBank; CCSD: 33584; -.
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                                                   MIM; 151510;
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-:- SUBURIT: HOMOTRIMER (PROBABLE).
-:- SUBURIT: HOMOTRIMER (PROBABLE).
-:- SUBCELLULAR LOCATION: Extracellular matrix.
-:- SUBCELLULAR LOCATION: Extracellular matrix.
-:- PTW: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-x-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
-:- PTW: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
-:- PTW: MAY CONTAIN CYSTEINE RESIDUES INVOLVED IN INTER- AND INTRAMOLECTUAR DISULETIDE BONDING.
-:- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTRAMOLECTUAR DISULETIDE PAMILS.
-:- SIMILARITY: CONTAINS 2 WERA DOMAINS.
-:- SIMILARITY: CONTAINS 2 WERA DOMAINS.
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                                           01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(XIV) chain precursor (Undulin).
COL14A1.
Gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99280705; PubMed-10350466; Montserret R., Aubert-Foucher E., McLeish M.J., Hill J.M., Ficheux Jaquinod M., van der Rest M., Deleage G., Penin F.; Structural analysis of the heparin-binding site of the NCI domain collagen XIV by CD and MRR ".
                                                                                                                                                                                                                                                                       Waelchii C., Trueb J., Ressler B., Winterhalter K.H., Trueb B.; "Complete primary structure of chicken collagen XIV."; Eur. J. Biochem. 212:483-490(1993).
                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 402-1549 FROM N.A.
MEDLINE-92339443; PubMed=1339349;
Trueb J., Trueb B.;
"Type XIV collagen is a variant of undulin.";
1888 AA
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                                                                                                                                                                                                                                         TISSUE=Embryo;
MEDLINE-93185668; PubMed-8444186;
                                  (Rel. 26, Created)
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 STANDARD;
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PDB; 189Q; 25-FEB-99
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                  01-JUL-1993
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467
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TRIPLE-HELICAL REGION 2.
POLY-THR.
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
MW; 39915BB9746DB973 CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                         tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1888;
                                                                                                                                                            PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00060; FN3; 7.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 2.
PROSTITE; PSS20234; VWFA; 2.
Extracellular matrix; Connective tissue; Repeat; Hydroxylaticell adhesion; Collagen; Glycoprotein; Signal; 3D-structure.
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                                                                                                                                                                                                                                                                                          COLLAGEN ALPHA 1(XIV) CHAIN.
                                                                                                                                                                                                                                                                                                          VWFA 1.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 5.
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NONHELICAL REGION (NC4).
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01-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cartilage matrix protein precursor (Matrilin-1).
MATNI OR CRIM OR CMP.
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                 InterPro; IPR003962; FnIII_repeat.
InterPro; IPR003129; TSPN.
InterPro; IPR02035; VWFA.
Pfam; PF01391; Collagen; 4.
Pfam; PF01210; TSPN: 1.
Pfam; PF02210; TSPN: 1.
Pfam; PF00220; VWA; 2.
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                                                                                                                                            PR00014; FNTYPEIII.
PR00453; VWFADOMAIN.
          InterPro; IPR003961; FN_III
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1010
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1468
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Best Local Similarity
Matches 49; Conserv
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SEQUENCE FROM N.A.
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P21941;
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CARBOHYD
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CAMA_HUMAN
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Interproj IPR002035; vWFA.
Interproj IPR002035; vWFA.
Interproj IPR002035; vWFA.
Interproj IPR002035; vWFA.
Interproj IPR00092; vW3: 2.
IPR00137; SMO0137; VWA; 2.
IPR0SITE; PS010027; VWA; 2.
IPR0SITE; PS01186; EGF_1; FALSE_NEG.
IPR0SITE; PS01186; EGF_2: 1.
IPR0SITE; PS01034; VWFA; 2.
IPR0SITE; PS01034; VWFA; 2.
IPR0SITE; PS01034; VWFA; 2.
IPR0SITE; PS01034; SUMA; 2.
IPR0SITE; PS01034; SUMA; 2.
IPR0SITE; PS01034; VWFA; 2.
IPR0SITE; PS01034; SUMA; SU
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N-LINKED (GLCNAC. ) (POTENTIAL).
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.5%; Score 96.5; DB
29.7%; Pred. No. 0.51;
Live 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: HOMOTRIMER.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 2 VWFA DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M55602; AAB38702.1; --
EMBL; M55675; AAB38702.1; JOINED.
EMBL; M55676; AAB38702.1; JOINED.
EMBL; M55677; AAB38702.1; JOINED.
EMBL; M55679; AAB38702.1; JOINED.
EMBL; M55680; AAB38702.1; JOINED.
EMBL; M55681; AAB38702.1; JOINED.
EMBL; M55681; AAAB38702.1; JOINED.
EMBL; M55681; AAA63904.1; ALT_SEO.
PIK, A37979; A37979.
MIM; 115437; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53700 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STICAGES---FQVVVRG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222
263
453
495
76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
496
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                                                                                                                                                                                                                                                                                                                                                                                               CONTAINING FIREILS, THE COLI DOMAIN COULD BE ASSOCIATED WITH THE SURFACE OF THE FIREILS, AND THE COLL AND NC3 DOMAINS MAY BE COCALIZED IN THE PERFIFIBILIAR MATRIX (BY SIMILARITY).

SUBUNIT: TRIMER OF IDEMTICAL CHAINS EACH CONTAINING 190 KDa OF NONTRIPLE-HELICAL SEQUENCES (BY SIMILARITY).

PAR THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT PECH END (BY SIMILARITY).

PART PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (C-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Sukaryota Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
--- PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
--- INTERRUPTED HELICES (FACIT) FAMILY.
--- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR00361; FN_III.
InterPro: IPR00361; FN_III.
InterPro: IPR002035; vwFA.
InterPro: IPR004035; vwFA.
Pfam: PF000402; vwa: 1.
SMART: SM00050; FN3: 5.
SMART: SM00377; vwA: 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; cell adhesion; Collagen; Glycoprotein.
                                                                                                                                                                                                                                                                                                                             "Localization of type XII collagen in normal and healing rabbit cornea by in situ hybridization."; Exp. Eye Res. 60:551-551(1995).
-i- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71032 MW; 162C6A923F551E6C CRC64;
                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(XII) chain (Fragment).
                                     639 AA
                                     PRT;
                                                                                                                                                                                                                                                                                           MEDLINE-95339912; PubMed-7615021;
                                                                                                                                                                                                                                                                                                                Zhan Q., Burrows R., Cintron C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; S78179; AAB34889.2; -. HSSP; P02751; 1TTF.
                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          TISSUE-Cornea
                                   CA1C_RABIT
RESULT 15
CA1C_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 .
```

6

Gaps

24;

8.4%; Score 95; DB 1; Length 639; 26.1%; Pred. No. 0.93; tive 29; Mismatches 60; Indels

Best Local Similarity 26.18 Matches 40; Conservative

Query Match

Search completed: August 9, 2002, 10:47:09 Job time: 832 sec

LTINLCNSVKGPGDLEAPSNLVISERTHRSFRV 146

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
```

9 10:56:55 2002

Fri Aug

OM protein - protein search, using sw model

August 9, 2002, 10:34:21; Search time 61.73 Seconds Run on:

(without alignments)
339.340 Million cell updates/sec

US-09-970-076-10 1131 1 MSFIVFSTRGTTLMKLTEDR......STSGFKEGNSHPCLPARPHT 218 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\* Database

pir1:\*
pir2:\*
pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	collagen alpha 1(X	leukocyte surface	cell surface alvco	collagen alpha 1(X	type XII collagen	classical ·compleme	antiqen Em100 - Ei	cell surface glyco	collagen alpha 1(X		_	cartilage matrix p	kinesin-like prote	complement factor	cartilage matrix p	hypothetical prote	immunodominant mic	hypothetical prote	undulin 1 - human	sensor kinase phoQ	collagen alpha 1(V	probable retroelem	sensor protein Pho	hypothetical prote	collagen alpha 3(V	hypothetical prote	transcription regu	hypothetical prote	
SUMM	ID	A40020	S00551	RWHU1B	A45974	151027	CZMS	A48569	RWHU1C	S31212	S78476	B96958	A37979	T50240	ввни	866522	T20721	A45638	T04822	A40970	VZEBPT	A54849	F84811	AG0646	н96798	CGHU3A	S42373	E69838	G71227	E70373
	DB	-	~	٦	۲	N	7	ď	1	~	~	~	~	~		~	~	~	~	7	•	~	•	•		Н	~	7	7	-
	Length	3124	1153	1153	1747	929	160	724	1163	1857	1888	698	496	817	764	200	4307	712	537	843	487	2944	689	487	453	3176	3051	237	240	432
æ	Query	10.1	6.6	9.6	9.7	9.6	9.4	9.3	9.1	9.1	9.1	8.8	8.5	8.5	8.4	8.3	8.2	8.0	7.9	7.9	7.8	7.8	7.7	7.6	7.6	7.6	7.5	7.5	7.5	7.4
	Score	114	112	111	109.5	109	106.5	105.5	103	102.5	102.5	66	96.5	96.5	95	93.5	ď	90	88	89	88.5	88	87	9	85.5	S	85	84.5	84.5	83.5
	Result No.	-	7	m	4	S	Q	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59

hypothetical prote	nypornetical proce transcription regu	conserved hypothet hypothet	hypothetical prote	complement factor	hypothetical prote	hypothetical prote	penicillin-binding	hypothetical prote	penicillin-binding	penicillin-binding	penicillibinding p	DNA polymerase I -	spore coat peptide
T21280	T51512 AF1166	.B71257	D59092	BBMS	T13530	T19173	S16629	AG2285	F95039	S06726	н97909	F71816	н69605
~	7 7	90	1 (1)	Н	7	N	7	0	7	~	7	7	7
1107	334	448	230	761	853	1027	675	710	750	750	750	897	189
7.4	7.3	7.3	7.3	7.3	7.3	7.3	7.2	7.2	7.2	7.2	7.2	7.2	7.2
83.5	82.5	82.5 82.5	82	82	82	82	81.5	81.5	81.5	81.5	81.5	81.5	81
30	31 32	33	32	36	37	38	39	40	41	42	43	44	4.5

## ALIGNMENTS

_	RESULT 1
_	A40020
_	collagen alpha 1(XII) chain precursor – chicken
_	N;Alternate names: fibrochimerin
_	C;Species: Gallus gallus (chicken)
_	C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
	C; Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811
	R;Yamaqata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida
	J. Cell Biol. 115, 209-221, 1991
	A; Title: The complete primary structure of type XII collagen shows a chimeric of
	nous region of type IX collagen, and short collagenous domains with an Arg-Gly
	A; Reference number: A40020; MUID:92011862
_	A:Accession: A40020

1, Y.; 0

-Asp st molecul

A; Molecule type: mRNA A; Residues: 1-3124 <7WAN A; Residues: 1-3124 <7WAN A; Cross-references: GB:D00824; NID:g222810; PIDN:BAA00701.1; PID:g222811 A; Note: in the authors' translation residues 1216-1219 are shown after residue 1235 a R; Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R. J. Biol. Chem. 264, 19772-19778, 1989 A; Title: Type XII collagen. A large multidomain molecule with partial homology to typ A; Reference number: A34485; MUID:90062079

A;Accession: A34485 A;Molecule type: mRNA A;Residues: 2456-2758, A',2760-2802, F',2804-2976, F',2978-3124 <GOR> A;Cross-references: EMBL:J05137; NID:9211284; PIDN:AAA48635.1; PID:9211285 A;Accession: B34485

A.McdecsLauris 1972-2792;2846-2873 <GOR2>
A.Rocaton, M.K.; Gereck, D.R.; Olsen, B.R.
R.Sordon, M.K.; Gereck, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.5A. 84, 6640-6044, 1987
A.Title: Type XII collagen: distinct extracellular matrix component discovered by CDN
A.Refedence number: A28037; MUID:87317590
A.Molecule type: mRNA
A.Mo

A; Accession: 523814
A; Molecule type: protein
A; Rocieule type: protein
A; Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-251
A; Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-251
B; Dublet, B:, van der Rest, M.
B; Dublet, B:, van der Rest, M.
B; Dublet, B:, van der Rest, M.
A; Ritle: Type XII collagen is expressed in embryonic chick tendons. Isolation of peps A; Reference number: S22254; MUID:88087065
A; Reference number: S22254
A; MulD:88087065
A; Residues: 2831-2832,'T', 2834,'R', 2836-2843; 3002-3014 <DUB>
B; Trueb, J; Trueb, B.

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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1153 <COR>
A; Coss-references: GB:103925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A; Cross-references: GB:103925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A; Orce: part of this sequence was confirmed by protein sequencing
B; Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
J. Cell Biol. 106, 2153-2158, 1988
A; Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion recepto
A; Reference number: A28915; MUID:88257215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: Mac-1
A;Gene: Mac-1
A;Gene: Mac-1
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat h
C;Superfamily: cell adhesion; glycoprotein; transmembrane protein
C;Keywords: cell adhesion; glycoprotein; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;1-16/Domain: signal sequence #status predicted Nac-1 alpha chain #status experimen
F;148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F;1106-1129/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-1153 (PYT>
A; Residues: 1-1153 (PYT>
A; Residues: 1-1153 (PYT>
A; Cross-references: EMBL: X07640; NID: 952982; PIDN: CAA30479.1; PID: 952983
A; Cross-references: EMBL: X07640; NID: 952982; WJJ; Gee, C.E.; Larson, R.S.; Rober R; Sastre, L.; Roman, J.M.; Teplow, D.B.; Droger, W.J.; Gee, C.E.; Larson, R.S.; Rober R; Sastre, L.; Roman, J.M.; Teplow, D.B.; Droger, W.J.; Gee, C.E.; Larson, R.S.; Rober A; Title: A partial genomic DNA clone for the alpha subunit of the mouse complement re A; Reference number: 159078; MUID: 86287312
A; Reference number: 159078; MUID: 86287312
                                                                                                                                   A;Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with th A;Reference number: S00551; MUID:88312584
A;Accession: S00551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 AIVYCVGVKD-FNETQLARIAD-----SKDHVFPVNDGFQALQGIIHSILKKSCIEILA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1233 GRIKTASGIRKVVRELEHKINGARENAAKILVVITDGEKEGDPLDYKDVIPEADRA---G 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 VIRYVIGVGNAFNKFQSKRELDTIASKPAGEHVFQV-DNFEALNTIQNQLQEK----IFA 334
                       22-0ct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 GDTYMHEGFERASEQIYYE-NRQGYRTASVIIALTDGELHEDLFFYSE--REANRSRDLG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB:M14293; NID:g198993; PIDN:AAA39484.1; PID:g554193
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.9%; Score 112; DB 2; Length 1153; .29.1%; Pred. No. 0.14; attive 26; Mismatches 56; Indels 11
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change
C;Accession: S00551; I59078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-499,501-965,'P',967-1153 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A31108; MUID:88315033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEPSTICAGESFQVVVRGNGF 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 IEGTOTGSTSSFEHEMSQEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 29.1
Matches 41; Conservative
                                                                                                                   R;Pytela, R.
EMBO J. 7, 1371-1378, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A31108
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A. Thtrons. 2865/3; 2863/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3; 2869/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALIDGELHEDLFFYSEREANRSRDLG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                 end.
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                             Biochim. Biophys. Acta 1171, 97-98, 1992
A;Title: The two splice variants of collagen XII share a common 5'
A;Reference number: S28811; MUID:93042014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukocyte surface glycoprotein Mac-1 alpha chain precursor N;Alternate names: complement-3 receptor alpha chain
                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
A;Residues: EMBL:X67327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 ICAGESFQVVVRGNGFRHARNV---DRVLCSFKINDSVTLSK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
Matches 45; Conserv
                                                                                                                                                 Accession: S28811
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Gaps

18;

Length 1153; 58; Indels

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Ascession: A45974 AND:93280195
Ascession: A45974 AND:93280195
Ascession: A45974
Ascession: A55974
Ascession: A45974
Ascession: A45974
Ascession: A57974
Ascession: A57974
Ascession: Ascession: A57
                        F;1135-1153/Domain: intracellular #status predicted <INT>
F;86,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collagen alpha 1(XIV) chain precursor, short form 2 - chicken
N;Alternate names: undulin
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A45974; S30085; S22916; S17035; S20833
R;Gerecke, D.R; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; A. Biol. Chem. 268, 12177-12184, 1993
A;Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 AIVYCVGVKDFNETQLAR-----IADS--KDHVFPVNDGFQALQGIIHSILKKSCIEILA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 GDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHEDLFFYSE--REANRSRDLG 93
                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                           Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                             27; Mismatches
                                                                                                                                                                                                               Query Match 9.8%; Score 111;
Best Local Similarity 28.5%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 AEPSTICAGESFQVVVRGNGFRHA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335 IEGTQTGSSSSFEHEMSQEGFSAA 358
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                             41;
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A.Map position: 16p1.2-16p1.2
C.Superfamily: call surface glycoprotein CD11b; von Willebrand factor type A repeat home C.Keywords: alternative splicing, calcium; call adhesion; glycoprotein; heterodimer; mag F:1-16/Domain: signal sequence #status predicted <SIG>
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-1153/Product: call surface glycoprotein CD11b #status experimental <AMAT>
F:17-1108/Domain: extracellular #status predicted <AMAT>
F:148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F:465-473/Region: calcium/magnesium binding #status predicted
F:530-518/Region: calcium/magnesium binding #status predicted
F:593-601/Region: calcium/magnesium binding #status predicted
F:1109-1134/Domain: transmembrane #status predicted <IMM>
A;Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594 A;Note: the authors translated the codon TAC for residue 1129 as Thr A;Note: part of this sequence, including the amino end of the mature protein, was confir R;Shalley, C.S.; Arnacut, M.A. Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991 Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991 A;Title: The promoter of the CD11b gene directs myeloid-specific and developmentally reg A;Reference number: A41600; MUID:92073318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 9-1153 <HIC.>
A; Residues: 9-1153 <HIC.>
A; Cross-references: GB.J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A; Oross-references: GB.J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A; Note: part of this sequence was confirmed by protein sequencing
R; Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
A; Timmunol. 150, 480-490, 1993
A; Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in during evolution.
                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-9 <SHE>
A; Cross-references: GB:M76724; NID:g180018; PIDN:AAA58410.1; PID:g553215
A; Cross-references: GB:M76724; NID:g180018; PIDN:AAA58410.1; PID:g553215
B; Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.
Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988
Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988
A; Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesi
A; Reference number: A94193; MUID:88190151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M18044
R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
A;Teroc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A;Tetle: CDNA sequence for the alpham subunit of the human neutrophil adherence receptor A;Reference number: A3218; MUID:89098893
A;Accession: A32218
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C;Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not all mature
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A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-499,501-1153 <FLE>
A;Cross-references: GB:S52227; NID:g263047; PIDN:AAB24821.1; PID:g263049
A;Oross-references: GB:S52227; NID:g263047; PIDN:AAB24821.1; PID:g263049
A;Note: the last three bases of intron 13, CAG, are included in some but not all matural A;Note: sequence extracted from NCBI backbone (NCBIP:121963)
R;Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
Biochim: Biophys. Acta 874, 368-371, 1986
A;Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across : A;Reference number: A90664; MUID:87076671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Characterization of the myeloid-specific CD11b promoter. A,Reference number: 152567; MUID:92144986
A,Accession: 152567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reference number: A46526; MUID:93123748
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R:Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
Blood 79, 865-870, 1992
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A; Residues: 917-1042 <AR2>
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Residues: 17-31 <PIE>
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Residues: 1-9 <RES>
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Ξ

Colten,

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N; Alternate names: C3 convertase; C5 convertase; complement C2
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
C; Accession: A38876; B36593; I54429
R; Ishikawa, N.; Nonaka, M.; Wetsel, R.A.; Colten, H.R.
Submitted to GenBank, January 1991
A; Reference number: A38875
A; Accession: A38876
A; Recidues: 17760 < L152>
A; Residues: 1760 < L152>
A; Title: Murine complement C2 and factor B genomic and cDNA cloning reveals different A; Reference number: A36593; MUID:91035430
A; Reference number: A36593; MUID:91035430
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A; Molecule type: mRNA
A; Residues: 660-677, R., 679, 681-723, 'G', 725 <RES>
A; Molecule type: mRNA
A; Residues: 660-677, R., 679, 681-723, 'G', 725 <RES>
A; Cross-references: GB:M16271; NID:g199289; PIDN:AAA39562.1; PID:g199290

B; Cromplex: The proenzyme forms a complex with C4a and is activated by cleavage into C C; Complex: The proenzyme forms a complex with C4a and is activated by cleavage into C; Complement C3: complement C3 and complement C3 alpha chains
A; Description: cleaves complement C3: complement factor H repeat homology; trypsin homology; C; Superfamily: complement C2: complement factor H repeat homology (FH1)

E; 10-18/Domain: signal sequence #status predicted <C18>
E; 10-18/Domain: complement factor H repeat homology <FH2>
E; 10-19/Domain: complement factor H repeat homology <FH3>
E; 10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. Molecule type: mRNA
A. Residues: 1-760 < LSH>
A. Residues: 1-760 < LSH>
A. Cross-references: ERBL:MS7891; NID:9192436; PIDN:AAA63294.1; PID:9192437
A. Cross-references: ERBL:MS7891; NID:9192436; Jeff. J. S. Gitlin, J.; Whitehead, A.S.; C. R. Fallus, A.; Waterland, E.K.; McConnell, T.J.; Gitlin, J.; Whitehead, A.S.; C. R. Timunogenetics 25, 290-298, 1987; Inmunogenetics 25, 290-298, 1987; MRC III genes in inbred and wild mouse strains. A. Faference number: 154429; MUID:87192938
A. Accession: 154429
A. Status: preliminary; translated from GB/EMBL/DDBJ
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24.3%; Pred. No. 0.26;
iive 38; Mismatches
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R;Wei, Y.; Yang, E.V.; Klatt, K.P.; Tassava, R.A.
R;Wei, Y.; Yang, E.V.; Klatt, K.P.; Tassava, R.A.
A.Title: Monoclonal antibody MT2 identifies the urodele alpha 1 chain of type XII
A.Title: Monoclonal antibody MT2 identifies the urodele alpha 1 chain of type XII
A.Reference number: 151027; MUID:95246925
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F;631-795/Domain: von Willebrand factor type A repeat homology <VWA3>
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C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C;Accession: I51027
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                                                                               F;716-798/Domain: fibronectin type III repeat homology <FN3F>F;806-893/Domain: fibronectin type III repeat homology <FN3G>F;924-1089/Domain: von Willebrand factor type A repeat homology <F;1111-1352/Domain: non-collagenous NC4 #status predicted <NC4>F;1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>F;1554-1659/Domain: non-collagenous NC2 #status predicted <NC2>F;1554-1659/Domain: triple helical domain COLI #status predicted
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-929 <WEL>
                                                                                                                                                                                                                                                                                                                                                                                                        9.7%; Score 109.5; DE 22.9%; Pred. No. 0.41; ative 37; Mismatches
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C; Genetics:
A; Gene: GDB:ITGAX; CDILC
A; Gross-references: GDB:119758; OMIM:151510
A; Gross-references: GDB:110758; OMIM:151510
A; Gross-references: GDB:110.2-16611.2
C; Superfamily: cell surface glycoprotein (DDID; von Willebrand factor type A repeat h
C; Superfamily: cell surface glycoprotein; heterodimer; magnesium; tandem repe
C; Reywords: calculum; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repe
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-1167/Domain: extracellular #status predicted <SIG>
F; 20-1107/Domain: transmembrane #status predicted <TWM>
F; 1108-1133/Domain: intracellular #status predicted <TWM>
F; 1184-1163/Domain: intracellular #status predicted <TWM>
F; 1184-1163/Domain: intracellular #status predicted <TWM>
F; 1189, 392, 697, 735, 899, 939, 1050/Binding site: carbohydrate (Asn) (covalent) #status
C; Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collagen alpha 1(XIV) chain precursor, short form - chicken
C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 RQGYRTAS-VIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV------KDFN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 ETQLARIAD--SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 9.1%; Score 103; DB 1; Length 1163; Best Local Similarity 24.5%; Pred. No. 0.91; Matches 45; Conservative 33; Mismatches 72; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: S31212
Biv. 1. Sessler, B.; Winterhalter, K.H.; Truek Bur. J. Blochem. 212, 483-490, 1993
A; Title: Complete primary structure of chicken collagen XIV.
A; Reference number: S31211; MUID:93185668
A; Accession: S31212
A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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Best Local Similarity
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                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: nucleic acid
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-74 <PARS-
A;Cross-references: GB:M99058; NID:q158890; PID:g158891
A;Cross-references: GB:M99058; NID:q158890; PID:g158891
A;Note: sequence extracted from NCBI backbone (NCBIN:123776, NCBIP:123777)
C;Superfamily: thrombosopondin type I repeat homology cTHR2>
F;308-734/Domain: thrombospondin type I repeat homology cTHR2>
F;308-31/Domain: thrombospondin type I repeat homology cTHR3>
F;308-31/Domain: thrombospondin type I repeat homology cTHR3>
F;308-31/Domain: thrombospondin type I repeat homology cTHR3>
F;433-493/Domain: thrombospondin type I repeat homology cTHR3>
F;404-556/Domain: thrombospondin type I repeat homology cTHR6>
                                                                                                 R;Pasamontes, L.; Hug, D.; Humbelin, M.; Weber, G.
Mol. Biochem. Parasitol. 57, 171-174, 1993
A;Title: Sequence of a major Eimeria maxima antigen homologous to the Eimeria tenella mi
A;Reference number: A48569; MUID:93149203
A;Accession: A48569
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A; Molecule type: DNA
A; Molecule type: DNA
A; Rostoues: 1-1163 octors
A; Note: this revision to the sequence from reference A35543 includes the carboxyl end
R; Corbi, A.L.; Garcia-Aguilar, J; Springer, T.A.
B; Blol. Chem. 265, 2788, 1990
A; Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.
A; Reference number: A35543; MUID:90153906
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A;Reference number: S00864; MUID:88166645
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A:Cross-references: GB:M81695; EMBL:Y00093; NID:g487829; PIDN:AAA59180.1; PID:g487830
A:Note: part of this sequence was confirmed by protein sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....cll surface glycoprotein CDIIc precursor - human
N:Alternate names: leukocyte adhesion receptor p150,95 alpha chain
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: A36584, A35543; S00864
R;Corbi, A.L.; Garcia-Aquilar, J.; Springer, T.A.
J; Bill. Chem. 265, 12750-12751, 1990
A;Reference number: A36584
                          Species: Elmeria maxima
Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYR--TASVIIALTDGELHEDLFFYSERE-----ANRSRDLGAIVYCVGV-KDFNETQL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: this sequence has been revised in reference A36584
R;Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
EMBO J. 6, 4023-4028, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 ARIA--DSKDHV-FP--VNDGFQALQCIIHSILKKSCIEI----LAAEPSTI--CAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 724;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 105.5;
Pred. No. 0.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.3%;
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Best Local Similarity 27.0'
Matches 48; Conservative
  antigen Em100 - Elmeria maxima
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A; Molecule type: DNA
A; Residues: 1-834 <CO2>
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                                                                                     Accession: A48569
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--GFKMMEMF 1246

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C;Species: Hono saplens (man)
C;Species: Hono saplens (man)
C;Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 21-Jul-2000
C;Accession: A37979; B37979 B37979
C;Accession: A37979; B37979 B37979 S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.;
R;Jenkins, R.N.; Osborne-Lawarence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.;
A;Title: Structure and chromosomal location of the human gene encoding cartilage matr
A;Reference number: A37979; MUID:91060568
                                                                                                                                                                                                               c;Superfamily: unassigned EGF-related proteins; EGF homology; von Willebrand factor C;Reywords: glycoprotein; homotrimer F;1-22/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;MOJECULE TYPE: MRNA
A;Residues: 157-290, TL', 292-496 <JE2>
A;Residues: 157-290, TL', 298-496 <JE2>
A;Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
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A; Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RTASVIIALTDGELHEDLFFYSER----EANRSRDLGAIVYCVGVKDFNETQLARIADSK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    605 GDCEVVV-LIDGQ-----WYGKKDIMAEVNKCKEYEIBIAAIGFGNAKKDFLDKIATCE 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY
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1194 PSERHVFFVDD-FDAFTKIEDELITFVCETASATCPLVFKDGDKLA---
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                                                                                                       1271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.8%; Score 99; DB .27.0%; Pred. No. 1.1; tive 28; Mismatches
                                                      174 DRVLCSFKINDSVTLSKSLQSPWVSSTSGFKEGNSHPC
                                                                                                          -TFNVYPC
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A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1;
C;Complex: homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:127280; OMIM:115437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cartilage matrix protein precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: A37979
A,Molecule type: DNA
A,Residues: 1496 <JENA
A,Cross references: GB:J05667
A,Accession: B37979
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                                                                                                                1247 GLVEKEFSAIDGVSMEPG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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A; Residues: 1-698 <KUR>
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EN 659
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Best Local Sim:
Matches 33;
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A;Gene: CAC0473
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mLochem. 12, 483-490, 1993
B; Cross-references: EMBL:X70793; NID:9288872; PIDN:CCAA50064.1; PID:9288873
R; Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
R; Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
R; Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
R; Molecule type: mRNA
A; Reference number: S31211; MUD:9318568
A; Accession: S31211
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-416; 1466-1811, 1843-1888 < WAE>
A; Cross-references: EMBL:X70793
A; Cross-references: EMBL:X70793
A; Cross-references: EMBL:X70793
C; Genetics:
A; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 1(XIV) chain precursor, long form - chicken
C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Aug-1999
C;Accession: S78476; S31211
R;Trueb, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 GYRTA--SVIIALTDGELHEDLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD- 114
                                                                                                                                                                                                                                                                                                                                  1194 PSERHVFFVDD-FDAFTKIEDELITFVCETASATCPLVFKDGDKLA-----GFKNMEMF 1246
                                                                                                                             1082 VAIIQFSDDPRTEFKLNAYKTKETLLEAIQQI--AYKGGNTKTGKAIKHARE-VLFTGEA 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                      115 -SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNV 173
                                                                                                                                                                                 GYRTA--SVIIALTDGELHEDLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD- 114
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSFIVESTRGTTLMKLT--EDREQIRGGLEELQKVLPGGDTYMHEGFERASEQIYYENRQ
                                                                                                                                                                                                                     MSFIVFSTRGTTLMKLT - - EDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQ
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                                   35;
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                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98;
                                   .86
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TENVYPC 1271
                                                                                                                                                                                                                                                                                                                                                                                              174 DRVLCSFKINDSVTLSKSLQSPWVSSTSGFKEGNSHPC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.1%; Score 102.5; D
22.5%; Pred. No. 1.9;
tive 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, January 1993
A; Reference number: $78476
A; Accession: $78476
                                      Mismatches
                                        36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 22.5%
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1247 GLVEKEFSAIDGVSMEPG---
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
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                                              Matches
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C;Date: 19-Feb-1984 #sequence_revision 05-Aug-1994 #text_change 08-Dec-2000
C;Accession: SAU75; AM522; AN0934; A19947; B19947; B25971; S14339; A44628;
R;Wejia, J.E.; Jahn, I.; de la Salle, H.; Hauptmann, G.
A:Reference number: Sal075
A;Reference number: S34075
A;Reference number: S34075
A;Reference number: S14075
A;Reference number: S14075
A;Residues: 1-764
A;Residues: 467
A;Reference number: A19188
A;Reference number: A1948
A;Reference number: A194
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A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: MNA
A; Molecule type: MINA
A; MI
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A;Residues: 270-329 <NIE>
A;Note: binding site for carbohydrate to lysine under artificial conditions
E,Morley, B.J.; Campbell, R.D.
EMBO J. 3, 153-157, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:MI5082; NID:g187699; PIDN:AAA59625.1; PID:g553534 R;Niemann, M.A.; Bhown, A.S.; Miller, E.J. Blochem. J. 274, 473-480, 1991 A;Title: The principal site of glycation of human complement Factor B. A;Reference number: S14339; MUID:91174758
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A;Molecule type: mRNA
A;Residues: 16-225,'F',227-259 <MOR>
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A; Residues: 1-99 <WUL>
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N.Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; heat-
N.Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragment
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinesin-like protein [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C;Accession: T50240
R;Cadieu, E.; Lelaure, V.; Galibert, F.; McDougall, R.C.; Rajandream, M.A.; Barrell, S. Submitted to the EMBL Data Library, January 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL136235; PIDN:CAB65811.1; GSPDB:GN00066; SPDB:SPAC664.10 A;Experimental source: strain 972h(-); cosmid c664 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGAIVYCVGVKDFNETQLARIADS--KDHVFPVNDGFQALQGIIHSILKKSCIEILAAEP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F----PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFR-HARNV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 TILMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 TYMHEGFERASEQIY----YENRQGYRTAS--VIIALTDGELHEDLFFYSEREANRSRD 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: | |: :: | |: :: | 360 SAIQPLQEENNSLKQQIEQLQEEN-ASETVVKENLKSSLDQ-QSANVQKLESTNRALEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;23-496/Product: cartilage matrix protein *status predicted <MAT>
F;39-206/Domain: von Willebrand factor type A repeat homology <VWAI>
F;227-262/Domain: EGF homology <EGF>
F;273-437/Domain: von Willebrand factor type A repeat homology <VWA2>
F;273-437/Domain: von Willebrand factor type A repeat homology <VWA2>
F;76,344/Binding site: carbohydrate (Asn) (covalent) *status predicted F;221-238,234-247,249-262/Disulfide bonds: *status predicted
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                                                                                                                                                                                                                                                                                                                                                            Length 496;
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                                                                                                                                                                                                                                                                                                                                                            DB 2;
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A;Accession: T50240
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-817 <CAD>
                                                                                                                                                                                                                                                                                                                                                        8.5%; Score 96.5; Di
29.7%; Pred. No. 1.2;
tive 19; Mismatches
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 29.7%
Matches 41; Conservative
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A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                            Query Match
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evid

EGF homology; von Willebrand factor

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Gaps

23;

55; DB 2;

Length 500; Indels

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C; Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: $6622
R;Ascodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.; Bosze, Z.
Eur. J. Blochem. 236, 970-977, 1996
Eur. J. Blochem. 236, 970-977, 1996
A;Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein A;Accession: $66522; MUID: 96270751
                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-500 <ASZ>
A; Cross-references: EMBL:U35035; NID:g1163178; PIDN:AAB06521.1; PID:g1163179
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGAIVYCVGVKDFNETQLARIADS--KDHVFPVNDGFQALQGIIHSILKKSCIEILAAEP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 TYMHEGFERASEQIY----YENRQGYRTAS--VIIALTDGELHEDLFFYSEREANRSRD 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 SYMEKGIMIGAALKYLIDNSFIVSSGARPGAQKVGIVFIDGRSQD----YINDAARKAKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assertion of the control of the cont
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29.0%; Pred. No. 2.1;
tive 20; Mismatches
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Best Local Similarity 29.09
Matches 40; Conservative
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Job time: 262 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
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C; Superfamily: complement C2; complement factor H repeat homology; trypsin homology; von
C; Superfamily: complement C2; complement alternate pathway; duplication; glycoprotein; hydrol
C; Keywords: acute phase; complement alternate pathway; duplication; glycoprotein; hydrol
C; Keywords: acute phase; complement factor B #status experimental <AAT>
F; 26-754/Froduct: complement factor B #status experimental <BAF>
F; 26-754/Froduct: complement factor H repeat homology <FH1>
F; 10-98/Domain: complement factor H repeat homology <FH2>
F; 10-154/Froduct: C3/C5 convertase Bb fragment #status experimental <BBF>
F; 260-764/Froduct: C3/C5 convertase Bb fragment #status experimental <BBF>
F; 260-764/Froduct: C3/C5 convertase Bb fragment #status experimental <BBF>
F; 260-764/Froduct: C3/C5 convertase Bb fragment #status experimental <F; 260-764/Froduct c3/C5 convertase Bb fragment #status experimental <F; 200-764/Froduct c3/C5 convertase Bb fragment (AF) (Covalent) #status experimental <F; 200-765/Froduct c3/Froduct c3/Froduc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:119726; OMIM:138470
A;Gross-references: GDB:119726; OMIM:138470
A;Gross-references: GDB:13-6p21.3
A;Introns: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3; 69
A;Note: the list of introns may be incomplete
A;Note: gene is located in the major histocompatibility complex, class III region
C;Complex: complement factor B initially forms an inactive complex with complement factor
ment factor C3b forming active C3/C5 convertase; Ba is released
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTILE: Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic conv A;Reference number: 157824; MUID:94067177
A;Accession: 157824
                                                            zum Busche
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                                                                                                                   Title: Human complement factor B: functional properties of a recombinant zymogen of Reference number: 154409; MUID:94041399
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:S67310; NID:9452937; PIDN:AAD13989.1; PID:94261689
R;Horiuchi, T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Fujita, S.; Volanakis, J.E.
Mol. Immunol. 30, 1587-1592, 1993
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                                                                                E.H.; Meyer
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule trye: mRNA
A;Residues: 1-31, '0', 33-764 <RE2>
A;Cross-references: GB:L15702; NID:g291921; PIDN:AAA16820.1; PID:g291922
C;Comment: 292-Cys has a free sulfhydryl.
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                                                            R;Schwaeble, W.; Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, Immunobiology 188, 221-232, 1993
A;Title: Human complement factor B: functional properties of a rec
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20.3%; Pred. No. 2.7;
.ive 32; Mismatches 69; Indels
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A; Status: translated from GB/EMBL/DDBJ
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Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
Residues: 1-764 <RES>
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A;Gene: GDB:BF
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S66522 cartilage matrix protein precursor - mouse

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human protein segu	Human polypeptide	Human TANGO 197.	Human gene 4 encod	Human gene 4 encod	Amino acid sequenc	A human TANGO 216	A human TANGO 216	A human TANGO 216	Human novel extrac	Amino acid sequenc
QI	AAB92985	AAM38976	AAB01422	AAE01439	AAE01469	AAB18447	AAB18455	AAB18456	AAB18457	AAU19662	AAB18448
OB	22	22	21	22	22	21	21	21	21	22	21
Length	218	297	333	403	403	488	488	488	488	587	487
Query Query Match Length DB	100.0	100.0	85.4	85.4	85.0	44.7	44.7	44.7	44.7	44.7	43.8
Score	1131	1131	996	996	961	206	206	206	206	505	495
Result No.		7	m	4	ß	9	7	80	6	10	11

AAB18458	ALIGNMENTS  ; 218 AA. diagnosis; antisense therapy; gene therapy.  diagnosis autisense therapy; gene therapy.  6. 6. 7. 9
8.8.8.8.8.8.8.8.8.8.8.8.8.8.8.8.8.8.8.	dard; Protein; 218 (first entry) sequence SEQ ID N ; detection; diagn 2000EP-0116126. 99JP-0248036. 99JP-0348036. 2000JP-0118776. 2000JP-0118776. 2000JP-0118776. 2000JP-0118776. 2100JP-0118776. 2100JP-01187
495 43 112 495 43 114 495 43 115 128 15 128 15 128 15 128 15 111 128 111 138 111 148 111 158 111 168 111 178 111 188 188 111 188 111 188 111 188 111 188 111 188 111 188 111 188	T 1 985 AAB92985 standard AAB92985; 26-JUN-2001 (fir Human protein seq Human protein seq Human protein seq Human protein seq To remail to the sequent of the

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The present invention describes primer sets for synthesising 5602

(c) full-length cDNAs defined in the specification. Where a primer set

(c) comprises: (a) an oligo-dr primer and an oligonuclectide complementary

(c) comprises strand of a polynucleotide which comprises one of

(c) the 5602 nucleotide sequences defined in the specification, where the

(c) complementary strand of a polynucleotide which comprises one of

(c) of an oligonucleotide comprising a sequence complementary to the

(c) of an oligonucleotide comprising a sequence complementary to the

(c) oplynucleotide which comprises a 5'-end

(c) oplynucleotide which comprises a 1'-end sequence complementary to a

(c) sequence and an oligonucleotide comprising a sequence, where the

(c) oplynucleotide which comprises at least 15 nucleotides and the combination of

(c) oligonucleotide which comprises at least 15 nucleotides and the combination of

(c) oligonucleotide which captures at least 15 nucleotides and the combination of

(c) oligonucleotide of a primer sets can be used in antisense therapy and

(c) oligonucleotide of aliagnosis of the primers are also useful for the primers encoded by

(c) of an oligonucleotides of the primers and the combination of the full-length cDNAs. The primers allow obtaining of the proteins encoded by

(c) of an oligonucleotides of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length of AAH13628 and

(c) AAH13631 to AAH13742 represent human amino acid sequences; and AAH3629 to AAH13632

(c) AAB5893 represent human amino acid sequences; and AAH31823 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancel peripheral nervous system; cNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; DB 22; Length 218;
3e-124;
hes 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 KINDSVTLSKSLQSPWVSSTSGFKEGNSHPCLPARPHT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 kindsvtlskslqspwvsstsgfkegnshpclparpht 218
                                                                                       ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1131;
100.0%; Pred. No. 3e-
:ive 0; Mismatches
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                                                                                       2537pp + CD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the present invention.
                                                                                           Claim 8; SEQ ID 11706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 218; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic, cc immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotide or polynucleotide in gene therapy. A composition containing a polypeptide or polynucleotide or polynucleotide in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous coff the invention may be used to treat of diseases of the peripheral nervous coff collised neuropathies and central nervous system diseases, and sacrophic collised neuropathies and central nervous system diseases, and streat collised the activity, of the collised of the activity, cancer diagnosis and therapy, drug screening, cand thrombolytic activity, arthritis and inflammation, leukaemias and collised of the coll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1131; DB 22;
100.0%; Pred. No. 5e-124;
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0; Mismatches 0;
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Xu C, Xue AJ,
R, Drmanac RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 2121; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and polypeptides, us such as central nervous system injuries
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                                                                                                                                                                                                                                                                                                        Asundi V, Che
Wehrman T, Xu
Goodrich R,
                                                                                   2000US-052317.
2000US-0552317.
2000US-0598042.
2000US-0653450.
2000US-0653450.
2000US-0653450.
2000US-0653450.
                                             26-DEC-2000; 2000WO-US34263.
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Matches 218; Conservative
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                                                                                                                                                                                                                                                                                                              Liu C, P
Wang Z, F
Zhou P,
                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
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                                                                                                                                                                     13-AUG-2000; 2
14-SEP-2000; 2
19-OCT-2000; 2
29-NOV-2000; 2
                                                                                                                                  09-JUL-2000;
                                                                                                                                                      19-JUL-2000;
                                                                                                             25-APR-2000;
               26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                        J,
QA,
                                                                                                                                                                                                                                                                                                                Tang YT,
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                                                                                                                                                                                                                                                                                                                                        Wang
Zhao
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WO200153312-A1

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AAE01439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, postriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chisease, osteoarthritis, Lyme's disease, cachexia and autoimmune diseases e.g. myasthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial CTANGO-128, 140, 197, 213, 214, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, paramacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a clisorder associated with aberrant TANGO expression. A wide range of cellular disorders can be treated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TANGO, 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; Crohn's disease; chronic myelogenous leukemia; cancer; liver disease; Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus erythematosus; transgenic animal; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
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pred. No. 1.5e-104;
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                                                                                                                                                                                                                          prognosis; prophylatic; therapeutic; human.
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98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                  98US-0223546.
                                                                                                                                                                                                                                                                                                                                                              99WO-US31025.
                                20-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-465743/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 AA;
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                                                                  Human TANGO 197.
                                                                                                                                                                                                                                                                                             WO200039284-A1.
                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                  30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                               23-DEC-1999;
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                                                                                                                                                                                                                                                                                                                             06-JUL-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holtzman DA;
AAB01422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Matches
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AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode. AAE01514-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes are described for gene amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the metations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the mutations, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AlbS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer; sidsease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; endocrine disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; chromosome 19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:94.
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/label- Signal_peptide
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                                                                                                                                                                                                                                                                                                                              AAE01439 standard; Protein; 403 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-2000; 2000WO-US30045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000; 2000US-0215133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0163581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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181 KINDSVTLSK 190
                                                                                    260 kindsvtlne 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
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"Encoded by

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skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, anglogenic disorders, kidney disorders, cardiovascular disorders, anglogenic disorders, kidney disorders, cardioratinal disorders, pregnancy-related disorders, and offertions. The proteins can also be used to aid wound cannot, to maintain organs before transplantation, for supporting cell sunburn, to maintain organs before transplantation, for supporting cell contains of primary tissues, to regenerate tissues, to identify their contains of primary tissues, to regenerate tissues, to identify their as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF 180
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                              1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:125.
                                                                                                                                                                                                                                                                                                               Score 966; DB 22; Length 403; Pred. No. 2e-104;
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   binding partner identification; chromosome 19
                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Unknown
/note= "Encoded by GKT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Signal_peptide
28. 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE01469 standard; Protein; 403 AA.
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                                                                                                                                                                                                                                                                                                                     85.4%;
98.9%;
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                                                                                                                                                                                                                                                                                                                                                       188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 KINDSVTLSK 190
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260 kindsvtlne 269
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                       403 AA;
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                                                                                                                                                                                                                                                                         Sequence
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AADD53100-AADD5379 represent cDNAs corresponding to 28 human secreted correcting genes, and AAED1436-AAED1513 represent the proteins they encode. protein genes, and AAED1436-AAED1513 represent the proteins they encode. CC AAED1514-AAED1544 represent human secreted protein fragments or variants. They genes and their secreted proteins are useful for preventing. They genes and their secreted proteins, e.g., by protein or gene treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the communition in the new genes. Specific uses are described for each of the much of the new genes. Specific uses are described for each of the include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental and include developing products for the diagnosis of the immune system, and include developing products for the dispass of the immune system, altory autoimmune diseases (e.g., rheumatoid arthritis), inflammation, alteryles, neurological disorders, schizophrenia, asthma, contractive in disorders (e.g., psorlasis), sepsis, diabetes, atheroselerosis, carteriar disorders (e.g., psorlasis), sepsis, diabetes, atheroselerosis, carteriar and developing representation and disorders, kidney disorders, endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  distributes that disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin adjung due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemicaris, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., redsint sequence represents a human secreted protein of the invention of nearly human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTASVIJALTDGELHEDLEFYSERBANKSRDLGAIVYCVGVKDFNETGLARIADSKDHVF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 961; DB 22;
Pred. No. 7.9e-104;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                               Ruben SM, 'Komatsoulis GA, Moore PA, Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 505-506; 562pp; English.
                                                                                                                    by WGC'
                                                          рy
                 /label- Unknown
/note= "Encoded
Misc-difference 368
                                                                                            /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.0%;
ilarity 98.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                              05-NOV-1999; 99US-0163581.
30-JUN-2000; 2000US-0215133.
                                                                                                                                                                                                                                          01-NOV-2000; 2000WO-US30045.
/note=
Misc-difference 331
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-308778/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 187; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD05334.
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                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                          cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectrasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
              140 rtasviialtdgelhedlffysereanrsrdlgaixycvgvkdfnetglariadskdhvf 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                                                                                                                                                                                                                                                                                                                           44.213
/note- "von Willebrand factor A domain"
                                                                                                                                                                                    TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
                                                                                                                                                                 Amino acid sequence of human TANGO 216 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                341
ote= "transnmembrane domain"
                                                                                                                                                                                                                                                                                                                                    "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                       "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser
                                                                                                                                                                                                                                                                                                                                                                                            /note= "cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                             35..488
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                  /note= "signal peptide"
                                                                                                                                                                                                                                                                                                 .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sharp JD,
                                                                                                               AAB18447 standard; Protein; 488 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Fig 1A-C; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2000; 2000WO-US05226.
                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "t
342..488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holtzman DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for treating cancer
                                                                                                                                                                                                                                                                                                                           34..79
/note=
                                                                                                                                                                                                                                                                                                                                                                                         /note-
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                                                             |||||||||:
260 kindsvtlne 269
                                                  KINDSVTLSK 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200052022-A1
                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1999;
                                                                                                                                                15-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barnes TM,
                                                                                                                                AAB18447;
                                                                                                                                                                                                                                                                                                   Key
Peptide
                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                             Domain
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                                                  181
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                                                                                                       AAB18447
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The present sequence represents a human TANGO 216 polypeptide. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. THE TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any won Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular interactions, modulate cell adhesion in proliferation, modulate cellular interactions, modulate the proliferation, differentiation, differentiation, differentiation, differentiation, differentiation, differentiation, differentiation, differentiation, differentiation of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematropoletic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disorders, treat cardiovascular disorders such as ischemic heart disorders, they may also be used to treat disorders associated with the covaries, cerebral oedema, bydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, latrogenic disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, disorders, hydrocephalus and encephalitis, and treat hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.7%; Score 506; DB 21;
53.4%; Pred. No. 3.3e-50;
iive 37; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A human TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB18455 standard; Protein; 488 AA.
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Best Local Similarity 53.4%
Matches 101; Conservative
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258 tynetytts 266
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AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 267, and TANGO 267. The TANGO CC describes TANGO 267, The TANGO CC pollypeptides can be used to medulate cellular adhesion. The cellular differentiation and/or modulate cellular adhesion, and the second and the cell trafficking and/or migration, modulate cellular interactions, and cell trafficking and/or migration, modulate cellular interactions, computate cell adhesion in proliferative disorders, such as cancer, that appear in the bone marrow, and leukocytes, treat bone marrow, blood conditions of cellular interactions, and hematopoietic associated diseases and disorders, atelectasis, and hematopoietic associated diseases and disorders, spheen associated associated diseases, modulate renal disorders, treat cardiovascular disorders as is schemic heart disorders, intestinal disorders, spheen associated diseases, modulate the proliferation, differentiation, and for treat bone and or cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to botten and viral menigitis, Alzheimer's Disease, inflammations, hadrochalus, brain herniations, introgenic disease, inflammations, hydrocephalus, brain herniations, introgenic disease, inflammations, hydrocephalus, brain herniations, and treat hepatic disorders. Hydrocephalus and encephalitis, and treat hepatic disorders. In once: the present sequence does not appear in the specification; it was consisted using information provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
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                                                                                                                                                                                                                                               Novel human and murine secreted proteins designated TANGO 216, 261, 265, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
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                                                                                                                                                     Fraser CC;
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                                                                                                                                                            Sharp JD,
                                                                                                                                                                                                                                                                                                                                       Disclosure; Page -; 175pp; English.
                                                                                                                 (MILL-) MILLENNIUM PHARM INC
                                        01-MAR-2000; 2000WO-US05226.
                                                                             99US-0122458.
                                                                                                                                                            Holtzman DA,
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08-SEP-2000
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ABB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 260 cellular differentiation and/or modulate proliferation, modulate polypeptides can be used to modulate cellular adhesion. The cellular differentiation and/or modulate cellular adhesion, disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, and cell trafficking and/or migration, modulate cellular interactions, condulate the proliferation of disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells cand hematopoietic associated diseases and disorders, atelectasis, bronchial pulmonary congestion or oedema, emphysema, chronic bronchial, bronchial cases, modulate renal disorders, spleen associated diseases, modulate the proliferation, differentiation, as ischemic heart disease, modulate the proliferation, differentiation, as ischemic heart diseases or disorder. They may also be used to cartilage associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, jatrogenic disease, cerebral concephalus, brain meningitis, Alzheimer's bisease, inflammations, bydrocephalus and encephalitis, and treat hepatic disorders. They may also be used to concert the present sequence does not appear in the specification; it was received with rich are all the present sequence does not appear in the specification; it was received.
                                                                             TANGO 266; TANGO 216;; TANGO 261; TANGO 267;
cellular proliferation; cellular differentiation; cellular adhesion;
von Willebrand factor-associated disorder; cell trafficking; cancer;
homatopoletic associated disease; atelectasis; pulmonary congestion;
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
intestinal disorder; spleen associated disease; renal disorder;
cardiovascular disorder; ischemic heart disease; hydrocephalus;
brain herniation; iatrogenic disease; inflammation; meningitis;
Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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                                                    A human TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC
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           15-JAN-2001 (first entry)
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Query Match Best Local Similarity 53.4%; Matches 101; Conservative 3

created using information provided.

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488 AA;

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AAU19662 standard; Protein; 587 AA.
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2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
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2000US-0184664
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258 tynetytts
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24 - FEB - 2000;
02 - MAR - 2000;
17 - MAR - 2000;
17 - MAR - 2000;
19 - MAY - 2000;
07 - JUN - 2000;
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cellular proliferation; cellular differentiation; cellular adhesion;
von Willebrand factor-associated disorder; cell trafficking; cancer;
hematopoletic associated disease; atelectasis; pulmonary congestion;
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
intestinal disorder; spleen associated disease; renal disorder;
cardiovascular disorder; ischemic heart disease; hydrocephalus;
brain herniation; iatrogenic disease; inflammation; meningitis;
Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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                                     61 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
                                                       Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
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N-PSDB; AAA75159.
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as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage earlis and to treat bone and/or treat disorders associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, bydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral menhapitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

once: the present sequence does not appear in the specification; it was created using information provided.
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PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-021515.
PR 10-JUL-2000; 2000US-021647.
PR 11-JUL-2000; 2000US-0214480.
PR 11-JUL-2000; 2000US-0214480.
PR 11-JUL-2000; 2000US-0214480.
PR 11-JUL-2000; 2000US-0222964.
PR 14-JUL-2000; 2000US-0222964.
PR 14-JUL-2000; 2000US-022296.
PR 14-JUL-2000; 2000US-0222513.
PR 14-JUC-2000; 2000US-022513.
PR 14-JUC-2000; 2000US-022513.
PR 14-JUC-2000; 2000US-022514.
PR 14-JUC-2000; 2000US-022513.
PR 14-JUC-2000; 2000US-022514.
PR 14-JUC-2000; 2000US-022914.
PR 14-JUC-2000; 2000US-022914.
PR 14-JUC-2000; 2000US-022914.
PR 14-SEP-2000; 2000US-022914.
PR 14-SEP-2000; 2000US-022914.
PR 14-SEP-2000; 2000US-023124.
PR 14-SEP-2000; 2000US-023124.
PR 14-SEP-2000; 2000US-023124.
PR 14-SEP-2000; 2000US-023124.
PR 14-SEP-2000; 2000US-023128.
PR 14-SEP-2000; 2000US-0
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PR 20-CGT-2000; 2000US-0241786.

PR 20-CGT-2000; 2000US-0241786.

PR 20-CGT-2000; 2000US-0241809.

PR 20-CGT-2000; 2000US-0246524.

PR 20-CGT-2000; 2000US-0248524.

PR 20-CGT-2000; 2000US-0248524.

PR 20-CGT-2000; 2000US-024821.

PR 20-CG
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e.g.

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be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynuclectides may also be used as DNA probes in diagnostic assays. The SPs may also be used as natigens to produce antibodies and to identify modulators and antagonists of the SPs. The anti-(SP) antibodies and antagonists and antagonists of the SPs. The anti-(SP) antibodies and antagonists and also be used to down regulate expression and activity of SP and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Caucher's disease), neurological diseases (e.g. Alzhaimer's disease, Parkinson's disease) neurological diseases (e.g. Alzhaimer's disease, e.g. Parkinson's disease) cardio-/cerabrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and hyberomy has incomed and maintenance of corneal infections.
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expression of SPs. The SP polynucleotide or a vector expressing them may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETOLARIADSKDHVF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hematopoietic associated disease; atelectasis; pulmonary congestion; oedema: emphysema: chronic bronchitis; bronchial sthma; bronchied; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflammation; meningitis; halzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                              include wound healing, maintenance of organs before transplantation,
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                           ; DB 22;
5.8e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 505;
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Matches 101; Conservative
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disorders, atclectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchicetasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's bisease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, bisean cancers, hydrocephalus and encephalitis, and treat hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a murine TANGO 216 polypeptide. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO DOLYPEPTIGES can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and
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                                                                                                                                                                                                                                                                                                  Fraser CC;
             318..341 /note= "transnmembrane domain"
                                                                        "extracellular domain"
"cytoplasmic domain"
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                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC.
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Best Local Similarity 53.7%,
Matches 102; Conservative
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Length 487;

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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 267, TANGO 262, and TANGO 267. The TANGO CC describes TANGO 267, TANGO 267, TANGO 267, TANGO 267, The TANGO CC polypeptides can be used to modulate cellular adhesion. The cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, compulate the proliferation proliferation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, compunenty congestion or oredema, emphysema, chronic bronchitis, bronchial confidency of associated diseases and disorders, sphen associated disease, and cardiovascular disorders such associated disease, the proliferation, differentiation, as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated disease, and cartilage cells and to treat bone and varies, and cerebral oedema, hydrocephalus, brain herniations, introgenic disease, inflammations, corpusamosis, parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

C toxplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

C created using information provided.
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                                                                             AAB18458 standard; Protein; 487 AA.
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                                                                                                                           61 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
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43.8%; Score 495; DB 21;
53.7%; Pred. No. 6.5e-49;
                                 Mismatches
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      43.
53.78; Fil
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(MILL-) MILLENNIUM PHARM INC.

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modulate cell adhesion in proliferative disorders, such as cancer, that appear in the broliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, blood asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as Ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral cedems, by disorders associated with the ovaries, and cerebral cedems, bacterial and viral meningitis, altrogenic disease, inflammations, bacterial and viral meningitis, and treat hepatic disorders.

Copplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

Coreated using information provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema: emphysema: chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; schemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                 43.8%; Score 495; DB 21; Length 487; 53.7%; Pred. No. 6.5e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Mismatches
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Matches 102; Conservative
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258 tanstytkse 267
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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO cellular believation and/or modulate cellular proliferation, modulate cellular adhesion. The proteins can be used to creat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell dimesion in proliferative disorders, such as cancer, and tappear in the bone marrow, and leukocytes, treat bone marrow, blood conditions to cedema, emphysema, chronic bronchitis, bronchial as the matopoietic associated diseases and disorders, spleen associated asthma and bronchiectasis, intestinal disorders, spleen associated associated diseases, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or and/or function of bone and cartilage cells and to treat bone and/or treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, bydrocephalus and encephalitis, and treat hepatic disorders.

Contribused associated with the ovaries, encebral cancers, bydrocephalus and encephalitis, and treat hepatic disorders.

Contribused associated does not appear in the specification; it was and and an analyzed of the and an analyzed of the and an analyzed of the analyz
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                                                                                                                                                                                            262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human and murine secreted proteins designated TANGO 216,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.8%; Score 495; DB 21;
53.7%; Pred. No. 6.5e-49;
iive 32; Mismatches 54;
                                               Fraser CC;
                                               Sharp JD,
                                                                                                                                                                                                                                                                       Disclosure; Page -; 175pp; English.
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Matches 102; Conservative
                                               DA,
                                                 Holtzman
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258 tanstytkse 267
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Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host disease, rheumatoid arthritis, psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachexia and autoimmune disease, e.g. myasthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial cransgenic animals and the TANGO polypeptides themselves. Partial for processic biology, for diagnostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic polypeptides are suitable for both prophylactic and therapeutic disorder associated with aberrant TANGO expression. A wide range cellular disorders can be treated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; crohn's disease; chronic myelogenous leukemia; cancer; liver disease; Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune disease; systemic lupus erythematosus; transgenic animal; diagnosis; prophylatic; therapeutic; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Fig 27; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                98US-0223546.
                                                                                                                                                                                                                                                                                      99WO-US31025
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N-PSDB; AAA47479.
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                                                                                                                                                                                                             WO200039284-A1.
                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                           23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                Holtzman DA;
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                                            108 QLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGF 167
                                                        Gaps
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0
Score 415; DB 21; Length 381;
Pred. No. 1.1e-39;
2; Mismatches 0; Indels C
                        2;
      36.7%;
97.6%;
                             Conservative
       Query Match
Best Local Similarity
                             81;
                   Best Loca
Matches
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<sup>168</sup> RHARNVDRVLCSFKINDSVTLSK 190

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<sup>64</sup> 

Search completed: August 9, 2002, 10:32:15 Job time: 134 sec

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Sequence 55, Appl
Sequence 2, Appl
Sequence 55, Appl
Sequence 56, Appl
Sequence 2, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 69, Appl
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Sequence 3, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.6%; Score 166; DB 1; Best Local Similarity 28.2%; Pred. No. 1.9e-09; Matches 66; Conservative 42; Mismatches 96
            US-08-605-672-55
US-08-605-672-99
US-08-482-293A-99
US-08-482-293A-99
US-08-943-363-99
US-08-943-363-99
US-09-193-043-55
US-09-193-043-55
US-09-193-043-99
PCT-US95-04439-1
US-08-476-062A-43
5424399-2
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US-08-286-889-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/POCKET NUMBER: 27866/32168
TELECOMMUNICATION:
TELEPHONE: 312-474-6300
TELEPRAS: 312-474-648
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 46, Application US/08286889 Patent No. 5470953 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 233 SOUTH Macker Drive
CITY: Chicago
STATE: 11inois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC COMPATIBLE
COMPUTER: PARPE PCOMPATIBLE
COMPUTER: PARPE PCOMPATIBLE
SOFTWARE: PATENTIN RELEASE #1
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-889-46
amino acid
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US-08-286-889-46
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178.842 Million cell updates/sec
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1 MATAERRALGIGFQWLSLAT......TTHCSLHKIASGPTTAACME 333
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Sequence
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2: /cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/iaa/6E_COMB.pep:*
5: /cgn2_6/ptcdata/2/iaa/FCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/iaa/FCTUS_COMB.pep:*
                                    Compugen Ltd
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US-08-362-652-46
US-08-605-672-46
US-08-943-363-46
US-08-943-363-46
US-08-943-363-46
US-08-943-363-45
US-08-852-53
US-08-943-363-53
US-08-943-363-37
US-08-85-618-37
US-08-943-37
                                                                                                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
                GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                      2002, 10:33:08
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length: 2000000000
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Match Length DB
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95 LTEDR-----EQIROGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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                                       95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
                                                                     149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, Vicole, Gerstein, Murray & Borun
ADDRESSEE: Marshall, Vicole, Gerstein, Murray & Borun
144 PECPEGGEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT
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                                                                                                                                                                                                       200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                 Length 1155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREM APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.6%; Score 166; DB 1;
ilarity 28.2%; Pred. No. 1.9e-09;
Conservative 42; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ir., 10.Seph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                      ; Sequence 46, Application US/08362652
; Patent No. 5766850
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-362-652-46
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Best Local Similarity
Matches 66; Conserv
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                                                                                                              149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                          2 Integrin Alpha Subunit
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                                                                                                                                                                                                                                                  200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                          9.6%; Score 166; DB 1; Length 1155;
28.2%; Pred. No. 1.9e-09;
Live 42; Mismatches 96; Indels 3
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233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
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Sequence 46, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 572853361 Human 2
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27866/32797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-ANG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
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Best Local Similarity 28.2<sup>3</sup>
Matches 66; Conservative
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COUNTRY: United States
ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
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CITY: Chicago
STATE: Illinois
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US-08-485-618-46
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95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                Sequence 46, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                     200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                 | : | | | : | | | : | | | : | | | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.6%; Score 166; DB 2; Length 1155;
28.2%; Pred. No. 1.9e-09;
Live 42; Mismatches 96; Indels 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: WIlliams Jr., Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chlcay-
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~~MPUTER: IBM PC compatible
~~MPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 27
ELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 28.29
Matches 66; Conservative
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                             RESULT 5
US-08-482-293A-46
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204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                         144 PECPGOEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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                                                                                                                                                                                                                                                                                   US-08-605-672-46
Sequence 46, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 581751561 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                            200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNYD 253
                                                                                                                                                                        | : | ||: | | : | | : | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.6%; Score 166; DB 2; Length 1155; 28.2%; Pred. No. 1.9e-09; tive 42; Mismatches 96; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOWMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPRAX: 312-474-0448
TELERAX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 28.2%
Matches 66; Conservative
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COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-605-672-46
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149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
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APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
APPLICANTON: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 PVNDGFQALQGIIHSILKKSCIBILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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                                                                                  Score 166; DB 4; Length 1155; Pred. No. 1.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUDICESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
FITLE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER PILING DATE: 1993-12-23
EARLIER PILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER PILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
NUMBER: OF SERIOR DATE: 1997-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 53, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
                                                                                                                                                                                                    Sequence 46, Application US/09193043
Patent No. 6251395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
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COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Ver. 2.0
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Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: MUS musculus US-09-193-043-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-485-618-53
                                                                                                                                                                                            US-09-193-043-46
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                                                 Sequence 46, Application US/08943363
Sequence 46, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                       PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                              9.6%; Score 166; DB 2; Length 1155;
28.2%; Pred. No. 1.9e-09;
tive 42; Mismatches 96; Indels 3
                                                                                                                                                                                                                                                                                                                                                           ANDMESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREE: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STATE: Illinoie
                          TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/943,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION UNDRER: US 08/286,889
FILING DATE: 5-AUG-1994
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORICY ACREST ACCOUNTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Illinois
COUNTRY: United States
ZIP: 60606 6402
ZIP: 60606 6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTING RAIDARCATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 28.2%
Matches 66; Conservative
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INFORMATION FOR SEQ ID NO:
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144 PECPGGEMDIAFLIDGSGSIDGSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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Patent No. 5817515
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTYON: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 10. 8817515el Human 2 Integrin Alpha Subunit
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STRREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATORS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.6%; Score 166; DB 1;
28.2%; Pred. No. 1.9e-09;
tive 42; Mismatches 96
                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR DATE: 03-DEC-1993
PRIOR DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
TELECOMMUNICATION:
                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312-474-6300
312-474-0448
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Best Local Similarity 28.2%
Matches 66; Conservative
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STATE: Illinois
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-362-652-53
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US-08-362-53
Sequence 53, Application US/08362652
Sequence 53, Application US/08362652
Sequence 53, Application US/08362652
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATSHALL, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42; Mismatches
                                                                                                                                                                                                                                                                                                                                                    PATION AND SERVICE TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27866/32797
                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25.3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1161 amino acids
                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 28.29
Matches 66; Conservative
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STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-618-53
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF ENQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, Orole, Gerstein, Murray & Borun
ADDRESSEE: Marshall, Orole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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9.6%; Score 166; DB 2; Length 1161;
Best Local Similarity 28.2%; Pred. No. 1.9e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMENT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
                              FILING DATE:
CLASSIFICATION DATA:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 3.0EC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-04G-1994
FILING DATE: 1-094
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
APTOCNEY AGENT INPORMATION:
NAME: Williams Jr. JOSEPh A.
REGISTATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REJECOMUNICATION INFORMATION:
TELECOMUNICATION FOR SEQ ID NO: 53:
SEQUEDRICE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                               27866/32684
APPLICATION NUMBER: US/08/482,293A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 53, Application US/08943363 Patent No. 5837478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-08-943-363-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DoS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.6%; Score 166; DB 2; Best Local Similarity 28.2%; Pred. No. 1.9e-09; Matches 66; Conservative 42; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 53, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029e1 Human 2
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                            FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-193
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-A0G-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38-659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECHOMNINGATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                     27866/32684
                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/605,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-605-672-53
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US-08-482-293A-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF 315
                                                                                                                                                                                                                                                                                                95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : | ||: | ||: | | :| | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
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                                                                                                                             Length 1161;
                                                                                                                                                                                          96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.2%; Score 159.5; DB 1;
27.9%; Pred. No. 1e-08;
tive 41; Mismatches 93;
                                                                                                                   ; Score 166; DB 4;
; Pred. No. 1.9e-09;
42; Mismatches 96;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: 312-474-630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/286,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicayor STATE: Illinois COUNTRY: United States ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk MEDIUM TYPE: Floppy disk MEDIUM TYPE: PLOPPY disk ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37, Application US/08286889 Patent No. 5470953 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37:
                                                                                                                          Query Match
Best Local Similarity 28.2%;
Matches 66; Conservative 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.2's
Best Local Similarity 27.9's
Matches 63; Conservative
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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; ORGANISM: Mus musculus US-09-193-043-53
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STREET: 231
-wv: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.6%; Score 166; DB 2; Length 1161; 28.2%; Pred. No. 1.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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APPLICAMT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/3504
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER PELING DATE: 1993-12-23
EARLIER PELING DATE: 1994-08-05
EARLIER PELING DATE: 1994-08-05
EARLIER PELING DATE: 1994-08-05
EARLIER PELING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER PELING DATE: 1994-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                  NAME: Williams Jr., Joseph A. RECISTRATION NUMBER: 38,659
REFENCE/DOCKET NUMBER: 27866/32684
TELECOMMINICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 53, Application US/09193043 Patent No. 6251395 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-943-363-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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Best Local Similarity
Matches 66; Conserv
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SEQ ID NO 53
LENGTH: 1161
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US-08-485-618-37
US-08-485-618-37
Sequence 37. Application US/08485618
Sequence 17. Application US/08485618
Sequence 17. Application
SPECIAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADPRESS:
ADDRESSEE: ABTSHAll, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                   157 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 207
                                                                                                                                                          98 DREGIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 156
                                                       DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 27.9%; Pred. No. 1e-08;
Matches 63; Conservative 41; Mismatches 93;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 23-DEC-1993
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
FILING DATE: 5-AUG-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
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Q91900 xenopus lae Q923k3 mus musculu Q18048 caenorhabdi O00816 toxoplasma

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Bradley K.A., Magridge J., Mourez M., Collier R.J., Young J.A.T.;
Bradley H.O. (2001).
Nature 414:0-0(2001).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Result Š HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180

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Rattus norvegicus
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NINOMINA K. Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Ninomiya K., Wagatsuma M., Kikkawa E., Omura Y., Abe K., Kamihara K., Furuya T., Takahashi M., Tanikawa B., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sudiyama T., Irie R., Kawai Hio Y., Saito H., Wakamatsu N., Ishii S., Yamamoto J., Isoo Y., Kawai Hio Y., Saito K., Nahikawa T., Kimura K., Yamashita H., Marakuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Yamanori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human CDNA sequencing project.";

"NEDO human CDNA sequencing project.";
Submitted (cor-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AROS5636; BAB70976 i.; "
SEQUENCE 245 AA, 26111 MW; BIABSEBEDOAZEBEEGO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 GYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDH 197
| :|:|:|||||||:|:||||||:
59 GLKTSSIIIALTDGKLDGLVPSYAEKEAKISRSLGASVYCVGVLDFEQAQLERIADSKEQ 118
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                                                                                                          241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Homo sapiens (Human).

Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   Ouery Match 33.7%; Score 582; DB 4; Length 245; Best Local Similarity 48.4%; Pred. No. 2.2e-42; Matches 124; Conservative 47; Mismatches 71; Indels 14;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:4705862) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                  301 DGLSFISSSVIITTHCS 318
                                                                                                                                                                                                                                                                          DGLSFISSSVIITTHCS 318
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230 CTFGLSGSGDPPTSAS 245
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SEQUENCE FROM N.A.
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096NC7;
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ID 099
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44 DLYFILDKSGSV-LHHWNEIYYEVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE---- 97
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G.,
O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G.,
O'Brien M.M.;

Gallatin W.M.;

I "Cloning of rat alpha D, a novel beta 2 integrin.";

Submitted (AuG-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AF021334; AAF21241.1; -.

EMBL; AF021334; AAF21241.1; -.

EMBL; AF03134; AAF21241.1; -.

EMBL; AF03134; AAF21241.1; -.

EMBL; AF001335; VWFA.

R Pfam; PF00189; FG-GAP; 5.

R Pfam; PF00189; FG-GAP; 5.

R Pfam; PF00189; Wax; 1.

R PRINTS; PR00189; Integrin.A; 1.

R SMART; SM00191; Int_alpha; 4.

EMBRT; SM00191; Int_alpha; 1.

R SMART; SM00191; Int_alpha; 1.
                                                                                                                                                                                                                                                                                                                    Score 467; DB 4; Length 97; Pred. No. 5.4e-33; 0; Mismatches 4; Indels
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                                                                                               [1]
SEQUENCE FROM N.A.
TISSUB-BREAST, AND MAMMARY ADENOCARCINOMA;
Strausberg R.;
Strausberg R.;
Stumitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012475;
AM112475.1;
NON_TER
                                                                                                                                                                                                                                                97 AA; 10453 MW; 14F475F0B170E71A CRC64;
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Last annotation update)
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9.2%; Score 159.5; DB 11;
Best Local Similarity 27.9%; Pred. No. 6.2e-05;
Matches 63; Conservative 41; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 VSMNDGLSFISSSVIITTTHCSLHKIASGPTTAACME 333
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01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 95.93
Matches 93; Conservative
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MEDILINE-93149203; PubMed-8426611;
Pasamontes L.E., Hug D., Huembelin M., Weber G.;
Pasamontes L.E., Hug D., Huembelin M., Weber G.;
Sequence of a major Eimeria maxima antigen homologous to the Eimeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 ---ANRSRDLGAIVYCVGV-KDFNETQLARIA--DSKDHV-FP--VNDGFQALQGIIHSI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eimeria tenella.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
Eimeria.
NCBI_TaxID~5802;
                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 VLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHEDLFFYSERE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75808 MW; AC2A0E7A346A7E9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            043981;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MICRONEME PROTEIN ETMIC-1 PRECURSOR.
                                                                      Q04588 PRELIMINARY; PRT; 724 AA. 004588; 01-NOY-1996 (TEMBLEL 01, Created) 01-NOY-1996 (TEMBLEL 01, Last sequence update) 01-DEC-2001 (TEMBLEL 19, Last annocation update) MAJOR ANTIGEN HOMOLOGOUS SEQUENCE (EMP100).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.7%; Score 150.5; DB 5; Best Local Similarity 25.9%; Pred. No. 0.0002; Matches 69; Conservative 45; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                    tenella microneme protein Etp100.";
Mal. Biochem. Parasitol. 57:171-174(1993).
EMBL; M99058; AAA29076.1; -
InterPro; IPR000884; TSP1.
InterPro; IPR00035; WFA.
Pfam: PF00090; tsp_1; 6.
Pfam: PF00092; vwa: 1.
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SMART; SM00209; TSP1; 6.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50092; TSP1; 5.
PROSITE; PS50234; VWFA; 1.
SEQUENCE 724 AA; 75808
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 NCBI_TaxID=5804;
                                                                                                                                                                                             Eimeria maxima
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043981
                                      RESULT
Q04588
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MEDLINE-21103187; PubMed-11160215;

MEDLINE-21103187; PubMed-11160215;

MINDAGAMA S. Azumi K., Nonaka M.;

MINDAGAMA S. Azumi K., Nonaka M.;

"Cloning and characterization of integrin alpha subunits from the solitary ascidian, Halocynthia roretzi.";

J. Immunol. 166:1710-1715(2001).

EMBL; AB048261; BA821479.1; -.

EMBL; AB048261; BA821479.1; -.

R HSSP; P11215; 1A8X.

InterPro; IPR0004315; NWFA.

R Pfam; PF01839; FG-GAP; 5.

R Pfam; PF01839; FG-GAP; 5.

R Pfam; PF01845; Integrin_A; 1.

R PRINTS; PR01185; INTEGRINA.

R PRINTS; PR01185; INTEGRINA.

R SMART; SM00191; Int.alpha; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 VFSTRGTTLAMKLTEDREQIRQGLEELQKVLPG-------GDTYMHEGFERAS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 ------AKLDIGKEIVRVGVVQYSHYVEGKSINKQKYITTEISIGEFKLLDNFENAV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQIYYENRQGYRT-------ASVIIALTDGELHEDLFFYSEREANRS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDLGAIVYCVGVKDFNETQLARIA---DSKDHVFPVNDGFQALQGIIHSILKKSCIEILA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 GGRREDGG-----PACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFI 83
                                                              157 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.9%; Score 153.5; DB 5; Length 1332; 24.1%; Pred. No. 0.00025;
live 42; Mismatches 81; Indels 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
INTEGRIN ALPHA HR1.
W; 0D9108D2B05CFFAE CRC64;
                                                                                                                                      208 LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                            Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTEGRIN ALPHA HRI PRECURSOR.
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SEQUENCE 1332 AA; 145852 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | | ::: | | | | 398 GGKSAKTAG--YEMHFGENGF 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEPSTICAGESFQVVVRGNGF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50234; VWFA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
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17;

Gaps

43;

712 AA

g

g õ g à g õ d ò

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Length 724; Indels

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Rowen L., Madan A., Oin S., Hall J., Dahl T., James R., Dickhoff R., Schaffer T., Ratcliffe A., Abbasi N., Loretz C., Lasky S., Hood L.; "Sequence of the mouse MHC class III region."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                              [2] SEQUENCE OF 291-760 FROM N.A. SEQUENCE OF 201. Jons M., Mahairas Rowen L., Qin S., Lasky S.R., Loretz C., Dors M., Mahairas
                                                                                                                                                                                   Hood L.; submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 765 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                            EMBL; APU9906; AAC84162.1; --
EMBL; APU9906; AAC85284.1; --
EMBL; APU49850; AAC65284.1; --
EMBL; DEOLIOBG6; AAH11086.1; --
HSSP; POO761; 1EPT.
MGD; MGI:88226; C2.
InterPro; IPR001344; Chymotrypsin.
InterPro; IPR001354; Trypsin.
InterPro; IPR001254; Trypsin.
InterPro; IPR002035; VRFA.
Pfam; PP00089; trypsin; 2.
Pfam; PP00089; trypsin; 2.
Pfam; PP00089; trypsin; 2.
Pfam; PP00089; trypsin; 2.
Pfam; PR00089; trypsin; 2.
Pfam; PR00032; VWFA.
PRNTS; PR00032; VWFA.
SMART; SM00020; Tryp_SP; 2.
SMART; SM00020; Tryp_SP; 2.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 MND----GLSFISSSVII 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               531 VGDPTSQHGKEFLVEDVII 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.8%
Best Local Similarity 23.5%
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9U8J9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
Q9U8J9
ID Q91
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                           SOW WHEN THE STATE OF THE SOUTH OF THE SOUTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 LQKVLPG-------GDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGEL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 HEDLFFYSEREANRSRDLGALVYCVGV-KDFNETQLARIADSKDHVFP-----VNDGFQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGSV-LHHWNEIYYFVEQLAHKF-ISPQ-LRMSFIVFSTRGTTLMKLTEDREQIRQGLEE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 PKATNPSLAISAARSLSYSTGVTYTHYGLQDA-KKLLYDTNAGARNNVPKLVLVMTDGA- 164
                                                                    MEDLINE-92131064; PubMed=1775171; Tomley F.M., Clarke L.E., Kawazoe U., Dijkema R., Kok J.J.; Tomley F.M., Clarke L.E., Kawazoe U., Dijkema R., Kok J.J.; Sequence of the gene encoding an immunodominant microneme protein of Eimeria tenella.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MATAERRALGIGFQWLSLATLVLICAG-----QGGRREDGG--PACYGGFDLYFILDK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C2.
Mus musculus (Mouse).
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                   A Relleher M., Tomley F.M.;

A Relleher M., Tomley F.M.;

Transient expression of beta-galactosidase in differentiating sporozottes of Elmeria tenefla.";

Mol. Biochem Parasicol. 97:21-31(1998).

E EMBL, AF032905; AAD03350.1; -. 31(1998).

R HSSP: P17301; 1AOX.

R Interpro; IPR000884; TSP1.

R Interpro; IPR000901; vwFA.

R Pfam; PF00090; vwa; 1.

R PRIMTS; PR00453; Vwa; 1.

R SMART; SW00209; TSP1; 6.

R SMART; SW00209; TSP1; 6.

R RRAT; SW0021; VWA; 1.

R PROSITE; PS50924; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.0%; Score 137.5; DB 5; Length 712; ilarity 24.7%; Pred. No. 0.0025; Conservative 43; Mismatches 108; Indels 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
COMPLEMENT FACTOR C2 (COMPLEMENT COMPONENT 2) (WITHIN H-2S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
MICRONEME PROTEIN ETMIC-1.
15B8F3C190B70F73 CRC64;
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                                                                                                                                                                       Mol. Biochem. Parasitol. 49:277-288(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 QVNGIIKAACKDLAKDAVCSEWSEYGPCVGE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 PO
712 MI
74777 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
37
712 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
STRAIN=129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
                                         SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                      STRAIN-HOUGHTON;
MEDLINE-99094493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
SEQUENCE
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070350
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                                              δ
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16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 FNETOLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430 INE--LGSKKDGERHAFILQDA-KALQQIFEHMLDVSKL-----TDTICG-----V 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 -----VIIALTDGELHEDLFFYSEREANRSRDLGAI------VYCVGV-----KD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE------NRQGYRTAS- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 GHINLYLLLDASQSVTEKDFDIFKKSABLMVERIFSFEVNVSVAIITFASQPKTIMSILS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 GGFDLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLRMS--FIVFSTRGTTLMKLTE 97
Strausberg R.; Submilted (JUL-2001) to the EMBL/GenBank/DDBJ databases. submitted (JUL-2001) to the EMBL/GenBank/IN S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.8%; Score 134; DB 11; Length 760; 23.5%; Pred. No. 0.0056; Live 55; Mismatches 115; Indels 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 TTLMKLTEDREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYRT--ASVI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 FILKKFIKVEDII-----EAINTFPYRGGSTNTGKAMTYVREKIFVPSK-GSRSNVPKVM 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVND 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  39 CYGGFDL---YFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFST---RG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chistar.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                              Query Match 7.6%; Score 131.5; DB 4; Length 517; Best Local Similarity 29.6%; Pred. No. 0.0054; Matches 61; Conservative 39; Mismatches 77; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Smith M.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALOBO256; CAB65984.1; -.
R HSSP: P11215; 1BHQ.
InterPro; IPR003961; FN_III.
R InterPro; IPR002035; vWFA.
R Pfam; PF00041; fn3; 2.
R Pfam; PF00042; vwa; 2.
R PRINTS; PR00453; VWFADOMAIN.
SMART; SM00066; FN3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 7.6%; Score 131; DB 4; Length 660; Best Local Similarity 29.8%; Pred. No. 0.0084; Matches 59; Conservative 38; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72523 MW; 3E3A10A285ECAA51 CRC64;
                                                                                                                                                                                                                                                                    56727 MW; 9B6972F44A1BD88F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
D234P15.1 (COLLAGEN, TYPE XII, ALPHA 1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               660 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 GFQALQGIIHSILKKSCIEI---LAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 -FDAFORISFELTOSICLRIEQELAA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                      Interpro; IPR003961; FN_III.
Interpro; IPR002053; WFPA.
Pfam; PF00041; fi3; 3.
Pfam; PF00092; vwa; 1.
PRINTS; PR004053; VWFADOMAIN.
SMART; SM00060; FN3; 3.
SMART; SM00327; VWA; 1.
EMBL; U68139; AAC01506.1; -. HSSP; P17301; 1AOX.
                                                                                                                                                                                      PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 660 AA;
                                                                                                                                                                                                                                                                    517 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                               \frac{1}{517}
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SEQUENCE
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NON_TER
SEQUENCE
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                                                                                                                                                                                                          Collagen.
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                                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 LMKL----TEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY-YENRQGYRTASVII 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HWSLRANNASDKETAMQ--DVLTIPYHGGTTNTAAGLQTCNOMLFDYPREERQTVPKLVI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDF-NETQLARIADSKDHVFP----V 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98003048; PubMed-9344363; Wessel H., Anderson S., Fite D., Halvas E., Hempel J., SundarRaj N.; "Type XII collagen contributes to diversities in human corneal and limbal extracellular matrices."; Innest. Ophthalmol. Vis. Sci. 38:2408-2422(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 CYGGFDLYFILDKSGSVLH-HWNEIYYFVEQLAHKFIS-----PQLRMSFIVFSTRGTT 91
                                                                                                                                                                                                                                          MEDLINE-20183852; PubMed-10717300;
MEDLINE-20183852; PubMed-10717300;
Molecular characterization of a LD.;
Molecular characterization of a LD.;
protein homologue in Neospora caninum.";
Mol. Biochem. Parasitol. 107:33-43(2000).
EMBL; AF001273; AAF01565.1;
InterPro; IPR001969; Asp.protease.
InterPro; IPR001969; Asp.protease.
PinterPro; IPR001969; Asp.
Pf00090; tspl.
Pfam; PF00090; tspl.;
Pfam; PF000902; vww; 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match '7.7%; Score 132.5; DB 5; Length 765; Best Local Similarity 25.1%; Pred. No. 0.0076; Matches 50; Conservative 35; Mismatches 89; Indels 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    765 AA; 82880 MW; 9727838CC1FE8CD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TYPE XII COLLAGEN (FRAGMENT).
                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
THROMBOSPONDIN-RELATED ADHESIVE PROTEIN HOWOLGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               517 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
PROSITE; PS50092; TSP1; 6.
PROSITE; PS50234; VWFA; 1.
SEQUENCE 765 AA; 82880 MM; 9727838CC1F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 NDGFQALQGIIHSILKKSC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 QTEWSQLLPSISPILKEVC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00453; WWFADOMAIN.
SMART; SM00209; TSP1; 6.
SMART; SM00327; VWA; 1.
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                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                    NCBI_TaxID-29176;
                                                                                                                            Neospora caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-CORNEA;
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9 9 9 3767 AA

PRT;

PRELIMINARY;

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(FRAGMENT)
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15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 -TASVIIALTDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FN----ETQLARIA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 THFTENDFKRNPSPKLLVRPIRQLL-----GRTHTATGIRKVVRELFH-SKSGARE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 NALKILVVITDGEKFGDPLGXEDVIPEADRK---GVIRYVIGVGDAFNSWKSREELNTIA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 DSK--DHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKPCGDHVFQVNN-FEAVKIIQNQLQEKT----FAIEGTQTGSTSSFECEMSQEGFSAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISP---QLRMSFIVFSTRGTTLMKLTED-- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469 DIVFLVDGSYSIGIANFVKVRAFLEVLVKSFEISPNRVQISLVQYSRDPHTEFTLKKFTK 528
                                   DREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYRT--ASVIIALTDGEL 153
                                                                                 154 HEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGI
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFST---RGTTLMKLTE
                                               Length 920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                            Lee J.-K., Schook L.B., Rutherford M.S.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U40072; AB16869.1; -
HSSP; P11215; 1A8X.
InterPro; IPR000413; Integrin_alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                     102440 MW; E96CC51E350DD5AC CRC64;
                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 7.6%; Score 130.5; DB 6; 1 Similarity 26.4%; Pred. No. 0.015; 63; Conservative 41; Mismatches 72;
                                                                                                                                                                            920 AA
                                                                                                                                                                                                 Created)
                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01839; FG-GAP; 4.
Pfam; PF00092; vwa; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; vWA; 1.
                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, 01-FEB-1997 (TrEMBLrel. 02, 01-DEC-2001 (TrEMBLrel. 19, CD11B (FRAGMENT).
                                                                                                               212 IHSILKKSCIEI---LAA 226
                                                                                                                                638 SFELTQSICLRIEGELAA 655
                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                        920 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              Sus scrofa (Pig).
                                                                                                                                                                                                                                                                       NCBI_TaxID=9823;
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NON_TER
SEQUENCE
                                                                                                                                                                                         028984;
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                                                                                                                                                               RESULT 12
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13

RESULT Q9UA13

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TRANSMEMBRANE CELL ADHESION RECEPTOR MUA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TRANSMEMBRANE CELL ADHESION RECEPTOR MUA-3 PRECURSOR (K08E5.3 PROTEIN)
                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF-like domain; Glycoprotein; Receptor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
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27.1%; Pred. No. 0.16;
tive 31; Mismatches 75; Indels 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8DA3AE5EA50AEB8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lu Z., Vogel B., Hedgecock E.; "uu Z., Nogel B."; "mua-3 mRNA Splicing Pattern Revealed."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kershaw J.K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases
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SMART; SM00179; EGF_CA; 1.

SMART; SM00179; EGF_CA; 1.

SMART; SM00019; EGF_LIKe; 45.

SMART; SM00200; SEA; 2.

SMART; SM00277; WAx; 1.

PROSITE; PS00010; ASX_HYDROXXL; UNKNOWN_32.

PROSITE; PS01186; EGF_1; UNKNOWN_1.

PROSITE; PS01186; EGF_2; 6.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01068; LDLRA_2; 2.
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Science 282:2012-2018(1998).
EMBL; AF139060; AAD29428.1;
EMBL; 230974; CAA83226.2; JOINED.
HSSP; P01130; 1LDL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00289; DISINTEGRIN. PRINTS; PR00261; LDLRECEPTOR. PRINTS; PR00453; VWFADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50024; SEA; 4.
PROSITE; PS50234; VWFA; 2
Calcium-binding; EGF-like
Signal.
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' AA;
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>3767
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Best Local Similarity
Matches 64; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 25
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3767
                                                                                                                                                                                                                                      MUA-3 OR K08E5.3
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
021340
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SEQUENCE
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TISSUE
                            RESULT 15
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                  ELFEIGRSKTRVGLIQYSDQIRHEFDLDQYGDRDSLLKGISETQ-YLTGLTRTGAAIQHM 1317
                                                                                                                                       1318 VQEGF-----SERRGARPQQSDIARVAIILTDGRSQDNV----TGPADSARKLSIN 1364
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                                                                                                                                                                                                                                                                                         01-077-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTEGRIN BETA 2 ALPHA SUBUNIT.
Rattus norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THFTFNDFKRNPDPKSHVRPIRQLNGRTKTASGIRKVVRELFQKINGARDNAAKILVVIT 257
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--- DLYFILDKSGSVLHH--WNEIYYFVEQLA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                  ::|| | ::| || |: | || || 1365 TFAIGVTDHVLASELESIAGSPNRWFYV-DKFKDLDTRLRSMIQK-----AACPS 1413
                                                      71 HKFI--SPQLRMSFIVFSTRGTTLMKLTE--DREQIRQGLEELQKVLPG----GDTYMH-
                                                                                                                                                                 175 VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 229
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23.9%; Pred. No. 0.088;
tive 46; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Fathallah D.M. Sr., Zerria K. Jr.;
"Cloning of the rat CDllb cDNA sequence.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF268593; AAF81280.1;
"HSSP; P11215; 1ABX.
Interpro; IPR000413; Integrin_alpha.
Interpro; IPR002035; wWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1151 AA; 126943 MW; 8F785695D4074CA5 CRC64;
                                                                                                                                                                                                                                                                  PRT; 1151 AA
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Pfam; PF00357; integrin_A; 1.
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Matches 70; Conservative
                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC003908; AAH03908.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 AA; 24505 MW; 31AB702E42E9CEB3 CRC64;
                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 24.5 KDA PROTEIN (FRAGMENT).
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44.0%; Pred. No. 0.014;
iive 11; Mismatches 1
221 AA
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       PRT;
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Best Local Similarity 44.09
Matches 22; Conservative
       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
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Job time: 849 sec
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SEQUENCE
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Search time 61.73 Seconds August 9, 2002, 10:34:18; Run on:

(without alignments)
518.350 Million cell updates/sec

08-920-076-80

1728 1 MATAERRALGIGFOWLSLAT......TTHCSLHKIASGPTTAACME 333 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 segs, 96089334 residues

Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SHIMMARTES

	Description	in a Description of the control of t	face glv	surface		leukocyte surface	immunodominant mic	collagen alpha 1(X	classical-compleme	collagen alpha 1(x	collagen alpha 1(X	hypothetical prote	cartilage matrix p	type XII collagen	complement factor	collagen alpha 1(V	complement factor	collagen alpha 2(V	cartilage matrix p	cartilage matrix p	complement factor	hypothetical prote	sporozoite surface	hypothetical prote	hypothetical prote		'	thrombospondin-rel	dnaK protein (heat	hypothetical prote
SUMMARIES	ID	A48569	RWHU1B	RWHU1C	A40020	S00551	A45638	A45974	C2MS	S31212	S78476	S42373	A37979	151027	ввни	A54849	BBMS	S21369	S66522	A33809	I51579	T28797	A46283	T23087	T04822	E70121	S33578	S04531	B96958	T46488
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	% Query Match	8.7	8	8.3				7.9						<u>.</u> ف		ė.	٠													
	Score	150.5	145.5	143.5	143		137.5	137	131	130	130	128	120.5	118	113.5	111.5	110.5	109.5	108.5	107.5	106.5	105.5	100.5	100	100	99.5	99.5	66	66	66
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229

RESULT

kinesin-like prote collagen alpha 2(V collagen alpha 2(V	collagen alpha 3(V imidazolonepropion dnak protein NMB05	collagen alpha 3(V hypothetical prote integrin alpha-1 -	probable retroelem transcription regu arginyl-tRNA synth	inter-alpha-inhibi integrin alpha-E c integrin alpha-I c undulin I - human	
T50240 S09646 CGHU2A	CGHU3A D87368 H81185	A37797 T47637 A55348	F84811 AF1166 E87665	JC5953 A53213 A45226 A40970	
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817 917 1018	3176 401 642	3137 676 272	689 334 600	932 1179 1151 843	
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30 31 32	33 34 35	36 37 38	30 4 10 10	4 4 4 4 2 6 4 7	!

## ALIGNMENTS

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Autoros Elmeria maxima
C; Species: Eimeria maxima
C; Date: 0.1-0ec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
C; Accession: 448569
R; Päsamontes, L.; Hug, D.; Humbelin, M.; Weber, G.
Mol. Biochem. Parasitol. 57, 171-174, 1993
A; Title: Sequence of a major Eimeria maxima antigen homologous to the Eimeria tenella A; Reference number: A48569; MuID: 93149203
A; Title: Sequence of a major Eimeria maxima antigen homologous to the Eimeria tenella A; Reference number: A48569
A; Accession: A48569
A; Status: preliminary
A; Molecule type: nucleic acid
A; Residues: 1-724 <PAS.
A; Cross-references: GB:M99058; NID: 9158890; PID: 9158891
A; Residues: 1-724 <PAS.
A; Cross-references: GB:M99058; NID: 9158890; PID: 9158891
A; Note: sequence extracted from NCBI backbone (NCBIN:123776, NCBIP:123777)
C; Superfamily: thrombospondin type I repeat homology <THR1>
F; 332-296, Domain: thrombospondin type I repeat homology <THR2>
F; 332-3432 Domain: thrombospondin type I repeat homology <THR4>
F; 494-556, Domain: thrombospondin type I repeat homology <THR4>
F; 560-610, Domain: thrombospondin type I repeat homology <THR6>
F; 560-610, Domain: thrombospondin type I repeat homology <THR6>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.7%; Score 150.5; DB 2; Best Local Similarity 25.9%; Pred. No. 0.00032; Matches 69; Conservative 45; Mismatches 109;
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A; Title: Characterization of the myeloid-specific CD11b promoter. A; Reference number: 152567; MUID:92144986
A; Accession: 152567
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A; Recession: A32218
A; Molecule type: mRNA
A; Residues: 9-1153 - 4160
A; Residues: 9-1153 - 4160
A; Residues: 69-1153 - 4160
A; Residues: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975
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A; Residues: GB:J04145; NID:g189068; PIDN:AA59903.1; PID:g386975
A; References: GB:J04145; NID:g189068; PIDN:AA59903.1; PID:g189068; PIDH: A; Thein, D.G.
A; Timunol. 150, 480-490, 1993
A; Timunol. 150, 480-490, 1993
A; Reference number: A46526; MUID:93123748
A; Reference number: A46526; MUID:93123748
A; Reference number: A46526; MUID:93123748
A; Residues: 1-499, 501-1153 - FIES
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: GB:S52277; NID:g263047; PIDN:AAB24821.1; PID:g263049
A; Cross-references: GB:S52277; NID:g263047; PIDN:AAB24821.1; PID:g263049
A; Residues: 1-499, 501-1153 - FIES
A; Note: sequence extracted from NCBI backbone (NCBIP:121963)
A; Note: sequence oxtracted from NCBI backbone (NCBIP:121963)
A; Note: sequence oxtracted from NCBI backbone (NCBIP:121963)
A; Note: sequence oxtracted from NCBIP: Totten A; Accession: A26091
A; Accession: A26091
A; Residues: 17-31 cPIE>
A; Residues: 17-31 cPIE>
A; Residues: 17-31 cPIE>
A; Repailmental source: granulocytes
B; R; Pahl, H.L.; Rosmarin, A.G; Tenen, D.G.
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 917-1042 <AR2>
A; Cross-references: GB:M18044
R; Hickstefn, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
R; Hickstefn, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
A; Title: ONA sequence for the alphaM subunit of the human neutrophil adherence receptor
A; Reference number: A32218; MUID:89098893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Residues: 1-499,501-965,'P',967-1153 <ARN>
A.Residues: 1-499,501-965,'P',967-1153 <ARN>
A.Residues: 1-499,501-965,'P',967-1153 <ARN>
A.Residues: 1-499,501-965,'P',967-1153 <ARN>
A.Rorosz-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594
A.Rorosz-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594
A.Rores: part of this sequence, including the amino end of the mature protein, was confined; S.Relein A. Acade Sci. U.S.A. B8, 10525-10529, 1991
Proc. Natl. Acad. Sci. U.S.A. B8, 10525-10529, 1991
A.Reference number: A41600; MUID:92073318
A.Recession: A41600
A.Moccosion: A41600
A.Residues: 1-9 CSHES
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R;Arnaout, M.A.; Remold-O'Donnall, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.
Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988
A;Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesi A;Reference number: A94193; MUD:88190151
A;Accession: A30892
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                                                                                                                   MΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell surface glycoprotein CDIlb precursor [validated] - human will the man complement receptor type 3 alpha chain; leukocyte adhesion protein 1 M.Alternate names: complement receptor type 3 alpha chain; leukocyte alpha chain; neutrophil adherence receptor alpha chain chain; neutrophil adherence receptor alpha chain c; species: Homo sapiens (man) c; species: Homo sapiens (man) c; bote: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 31-Dec-2000 c; bote: 31-Dec-1992; A2915; A41600; A30892; A32218; A46526; A26091; I52567 R; Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A,Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A31108; MUID: 88315033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A28915
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A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-1163 <COR>
A, Residues: 1-1163 <COR>
A, Note: this revision to the sequence from reference A35543 includes the carboxyl end
A, Note: this revision to the sequence from reference A35543 includes the carboxyl end
B, Corbi, A, L.; Garciar Aguilar, J.; Springer, T.A.
B, Sold C, A, The C, 265, 2782-2788, 1990
A, Title: Genomic Structure of an integrin alpha subunit, the leukocyte p150,95 molecu
A, Reference number: A35543; MUID:90153906
                                                                                                                                                                                                                                                                                                                                                              A, Gene: GDB: ITGAM; CR3A
A, Gene: GDB: L20599; OMIW: 120980
A, Gene: GDB: L20599; OMIW: 120980
A, Gross-references: GDB: L20599; OMIW: 120980
A, Wap position: 16p11.2-16p11.2
A, Wate: promoter contains a GATA motif and two Sp1 consensus binding sites
A, Note: promoter contains a GATA motif and two Nilebrand factor type A repeat h
A, Note: promoter contains a graph sequence #status predicted <51G>
C, Superfamily: cell surface glycoprotein CD11b *status experimental <AAT>
F; 1-16 Domain: signal sequence #status predicted <51G>
F; 1-16 Domain: status predicted <51G>
F; 1-108 A Domain: von Willebrand factor type A repeat homology <VWA2>
F; 148-318 A Domain: von Willebrand factor type A repeat homology <VWA2>
F; 539-601/Region: calcium/magnesium binding #status predicted
F; 530-538 A Region: calcium/magnesium binding #status predicted
F; 510-6118 A Domain: transmembrane #status predicted <TWA>
F; 1109-1134 A Domain: intracellular #status predicted <TWA>
F; 1153-1153 A Domain: intracellular #status predicted <INT>
F; 1153 A Domain: intracellular #status pred
                                                                                                                                             A; Cross-references: GB:M84477; NID:g180184; PIDN:AAA51960.1; PID:g553219
C; Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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NiAlternate names: leukocyte adhesion receptor pl50,95 alpha chain
NiAlternate names: leukocyte adhesion receptor pl50,95 alpha chain
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Date: 31-Dec-1992 #sagience_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Date: 31-Dec-1992 #text_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 DGEKFGDPLGYEDVIDEADRE---GVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQ 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 DLYFILDKSGSVL-HHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTED---- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: this sequence has been revised in reference A36584 R; Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
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nllarity 26.2%; Pred. No. 0.0015;
Conservative 45; Mismatches 81;
A; Status: translated from GB/EMBL/DDBJ
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Best Local Similarity
Matches 60; Conserva
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A; Residues: 1-834 <CO2>
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us-09-970-076-8.rpr

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C;Genetics:
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F;24-114/Domain: IIIA %status predicted <IIIA>
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F;24-116/Domain: fibronectin type III repeat homology <FN3A>
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F;247-108/Domain: fibronectin type III repeat homology <FN3D>
F;266-108/Domain: fibronectin type III repeat homology <FN3D>
F;261-108/Domain: fibronectin typ
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F;32,1006,1032,1044,1512,1767,2210,2273,2532,2683/Blnding site: carbohydrate (Asn) (c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: $23814
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 'X',1333,'O',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-251
R; Dublet, B.; van der Rest, M.
J. Blod. Chem. 262, 17724-17727, 1987
J. Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of peps
A; Reference number: $22254; MUID:88087065
R;Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A;Title: Type XII collagen: distinct extracellular matrix component discovered by cDN
A;Reference number: A28037; MUID:87317590
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                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 2960-2976, Fr. 2978-3074, AG' <GOR3>
A; Cross-references: EMBL:M17375; NID:g211649; PIDN:AAA48718.1; PID:g211650
A; Note: this sequence has been revised in reference A34485
R; Koch, M.; Bernasconi, C.; Chiquet, M.
Eur. J. Blochem. 207, 847-856, 1992
Bur. J. Blochem. 207, 847-856, 1992
A; Title: A major oligomeric fibroblast proteoglycan identified as a novel large form
A; Reference number: $23814; MUID:92362621
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A;Molecule type: protein
A;Residues: 2831-2832, T',2834, R',2836-2843;3002-3014 <DUB>
B;Trucb, J:;Trucb, B.
Biochim. Biophys. Acta 1171, 97-98, 1992
A;Title: The two splice variants of collagen XII share a common 5'
A;Reference number: $28811; MUID:93042014
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A;Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
A;Cross-references: EMBL:X67327
C;Genetics:
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A; Status: preliminary
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F; 2509-2750/Domain:
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                                                                                                                                                                                             A Molecule type: mRNA

A Residues: 1-752, L'. 757-1163 <CO3>

A) Residues: 1-755, L'. 757-1163 <CO3>

A) Residues: 1-755, L'. 757-1163 <CO3>

A) Note: part of this sequence was confirmed by protein sequencing

C) Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on my

A) Gene: GDB:ITGAX; CD11C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Across-references: GDB:119758; OMIM:151510
A:Wap position: 16p11.2-16p11.2
C:Superfamily: call surface glycoprotein CD11b; von Willebrand factor type A repeat home C:Reywords: calcium; call adhesion; glycoprotein; heterodimer; magnesium; tandem repeat; F:1-19/Domain: signal sequence #status predicted <SIC>
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F:20-1103/Domain: extracellular #status predicted <EXYN>
F:149-319/Domain: von Willebrand factor type A repeat homology <VWA4>
F:108-1133/Domain: transmembrane #status predicted <TWN>
F:1134-1163/Domain: thracellular #status predicted <INT>
F:61,89,392,697,735,899,939,1050/Binding site: carbohydrate (Asn) (covalent) #status predicted <INT>
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A; Molecule type: mRNA
A; Residues: 1-3124 < YAMS
A; Residues: 1-3124 < YAMS
A; Cross-references: GB: D00824; NID:g222810; PIDN:BAA00701.1; PID:g222811
A; Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and, B; Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
J. Biol. Chem. 264, 19772-19778, 1989
A; Title: Type XII collagen. A large multidomain molecule with partial homology to type I A; Reference number: A34485; MUID:90062079
                                                                     structure of the alpha subunit of a leukocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811
R;Yamagata, M.: Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Oba.
J. Cell Biol. 115, 209-221, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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A; Residues: 2456-2758, A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A; Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g211285
A; Accession: B34485
A; Molecule type: protein
A; Residues: 2772-2792; 2846-2873 <GOR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLYFILDKSGSV-LHHWWEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE-- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIVELIDGSGSISSRNFATMMNFVRAVISQFQRPSTQFSLMQFSNKFQTHFTFEEFRRTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTAS-VIIALTDGELHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---KDFNETQLARIAD--SKDHVFPVNDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | | : : | : : | | | : : | | | 319 FDALKDIQNQLKEK----IFAIEGTETTSSSSFELEMAQEGF 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 143.5; DB 1;
Pred. No. 0.0023;
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                                                            A, Title: CDNA cloning and complete primary A, Reference number: S00864; MUID:88166645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
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24.88;
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Best Local Similarity
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44 151 101

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Matches

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A45038
immunodominant microneme protein Etp100 - Eimeria tenella
C;Species: Eimeria tenella
C;Species: Eimeria tenella
C;Species: Eimeria tenella
C;Species: Eimeria tenella
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A45638
R;Tomley, F.M.: Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.
Mol. Biochem. Parasitol. 49, 277-288, 1991
A;Title: Sequence of the gene encoding an immunodominant microneme protein of Eimeria
A;Reference number: A45638
A;Accession: A45638
A;Accession: A45638
A;Accession: A45638
A;Accession: A45638
A;Accession: A45638
A;Acteria preliminary
A;Molecule type: DNA
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A;Residues: 1772 <TOM
A;Residues: Tractacted from NOBI backbone (NOBIN:77752, NCBIP:77756)
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A;Note: sequence extracted from NOBI repeat homology <THR2>
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F;39-372/Domain: thrombospondin type I repeat homology <THR3>
F;39-372/Domain: thrombospondin type I repeat homology <THR3>
F;444-556/Domain: thrombospondin type I repeat homology <THR3>
F;444-556/Domain: thrombospondin type I repeat homology <THR3>
F;560-610/Domain: thrombospondin type I repeat homology <THRA>
F;560-610/Domain: thrombospondin type I repeat homology <THRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 HEDLFFYSERBANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFP-----VNDGFQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 -SNLPSQTRSSAAALRDAGAIVVVLGVGSGVNSSECRSIAGCSTSNCPRYLOSNWSNVTQ 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGEL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGSV-LHHWNEIYYFVEQLAHKF-ISPQ-LRMSFIVFSTRGTTLMKLTEDREQIRQGLEE 108
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                                                                                                                                                                                                                                             VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFK 260
198 IHFTFNDFKRNPSPRSHVSPIKQLNGRTKTASGIRKVVRELFHKTNGARENAAKILVVIT 257
                                                                                                                               1 MATAERRALGIGFQWLSLATLVLICAG-----QGGRREDGG--PACYGGFDLYFILDK
                                                                                DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNETQLARIAD-----SKDHVFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 -SASITSN-------GPLLGSVGSFDWAGGAFLYTSKDKVTFINTT
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                                                                                                                                                                                                                                                                                                    ; Score 137.5; DB 2;
; Pred. No. 0.0036;
43; Mismatches 108;
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Local Similarity 24.7%;
nes 67; Conservative 4
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C; paceise Mas musculus (house mouse)
C; pate: 30.5ep-1989 seaquence_revision 30-Sep-1991 *text_change 22-Oct-1999
C; Accession: S00551; I59078
R; Pytela, R.
EMBO J. 7, 1371-1378, 1988
A; Reference number: S00551; MUD:88312584
A; Reference number: S00551; MUD:88312584
A; Residues: 1-1153 CPT
A; Molecule type: DNA
A; Residues: 1-1153 CPT
A; Molecule type: DNA
A; Residues: 1-1153 CPT
A; Roman, J. M.; Teplow, DB: Dreyer; W.J.; Gee, C.E.; Larson, R.S.; Roberts, R; Saster, L., Koman, J. M.; Teplow, DB: Dreyer; W.J.; Gee, C.E.; Larson, R.S.; Roberts, Proc. Natl: Acad. Scil. U.S.A. 83, 5644-5643, 1986
A; Reference number: 159078; MUD:86287312
A; Reference number: 159078; MUD:862802; PIDN:AAA39484.1; PID:9554193
A; Reference number: 159078; MUD:862802; PIDN:AAA39484.1; PID:9554193
A; References: Cichentiss:
A; Redentiss:
C; Genetiss:
A; Genetiss:
A; Genetiss:
C; Superfamily: cell surface glycoprotein CDID; von Willebrand factor type A repeat home C; Rewords: cell adhesion: glycoprotein; transmembrane protein
C; Rewords: cell adhesion: glycoprotein CDID; von Willebrand factor type A repeat home C; Rewords: cell adhesion: glycoprotein CDID; P:1-150/Domain: signal sequence **status predicted CDMA>
F; 1165/Domain: von Willebrand factor type A repeat home CDMA>
F; 1166-1129/Domain: transmembrane **status predicted CDMA>
F; 1166-1129/Domain: transmembrane #status predicted CDMA>
F; 1166-1129/Domain: Product PDMA>
F; 1166-1129/Domain: PDMA>
F; 1166-1129/Domain: PDMA>
F; 1166-1129/Domain: PDMA>
F; 1166-1129/Doma
                             F;2780,2789,2836,2842,2860,2866,2869,3004,3007/Modified site: hydroxyproline (Pro) #stat
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                                                                                                                                                                                                                                             14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 DIVFLIDGSGSI----NNIDF---QKMKEFVSTVMEQFKKSKTLFS-----LMQYSDEFR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                         DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDRE 100
                                                                                                                                                                                                                                                                                                                                                                                                 QIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHED 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIHS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             555 AF---KEPAIKLRDADVEIFAVGVKDAVRTELEAIASPPAETHVYTVED-FDAFQRISFE 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 ILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNV---DRVLCSFKINDSVTLNEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        497 NRVKDIIQAINTEPYRGGSTNTGKAMTYVREKVFVTSK-GSRPNVPRVMILLITDGK-SSD
                                                                                                                                                                                                                                                 36;
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                                                                                                                                                            Length 3124;
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                                                                                                                                                                ; Score 143; DB 1;
; Pred. No. 0.0093;
51; Mismatches 97.
                                                                                                                                                                                 8.3%;
26.1%;
                                                                                                                                                                                                                                                     Conservative
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---EKSYLI 663
                                                                                                                                                                                                                        Similarity
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component precursor

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A; Description: cleaves complement C3 and complement C5 alpha chains
A; Pathway: complement classical pathway
C; Superfamily: complement C2; complement factor H repeat homology; trypsin homology;
C; Superfamily: complement C2; complement classical pathway; duplication; glycopro
E;1-18/Domain: signal sequence #status predicted <SIG>
F;1-28/Domain: somplement C2b fragment #status predicted <C2B>
F;2-269/Domain: complement factor H repeat homology <FHI>
F;24-149/Domain: complement factor H repeat homology <FHI>
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F.156-210/Domain: Complement factor H repeat homology FF.251-760/Product: Complement C2a fragment long form #status predicted <C2s>F.251-760/Product: Complement C2a fragment short form #status predicted <C2s>F.251-469/Domain: von Willebrand factor type A repeat homology FF.478-747/Domain: trypsin homology #status atypical FF.22-6.49-89.94-136.122-149, 156-197, 182-210, 470-590, 499-515, 593-609, 647-674, 685-715/FF.27.117, 297, 340, 474.478, 663/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.514,570, 689/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A)Residues: 1-760 <1S2>
A)Cross-references: GB:M57891; GB:J05661; NID:g192436; PIDN:AAA63294.1; PID:g192437
B)Shikawa, N.; Nonaka, M.; Wetsel, R.A.; Colten, H.R.
J. Biol. Chem. 265, 19040-19046, 19990
A)Title: Murine complement C2 and factor B genomic and cDNA cloning reveals different A)Reference number: A36593; MUID:91035430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: EMBL:M57891; NID:g192436; PIDN:AAA63294.1; PID:g192437
R;Falus, A.; Wakeland, E.K.; McConnell, T.J.; Gitlin, J.; Whitehead, A.S.; Colten, Immunogenetics 25, 290-298, 1987
A;Title: DNA polymorphism of MHC III genes in inbred and wild mouse strains.
A;Reference number: 154429; MUID:87192938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; introns: 16/1; 91/1; 153/1; 212/1; 245/3; 290/3; 337/1; 384/1; 414/1; 461/1; C; Complex: The proenzyme forms a complex with C4a and is activated by cleavage
                                                                                                                                                                                                                                                                                                               classical-complement-pathway C3/C5 convertase (EC 3.4.21.43) C2 component pr N;Alternate names: C3 convertase; C5 convertase; complement C2 C;Speciae; Mus musculus (house mouse) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000 C;Accession: A38876; B36593; I54429 R;Ishkawa, N; Nonaka, M; Wetsel, R.A.; Colten, H.R. submitted to GenBank, January 1991 A;Reference number: A38875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 KEIRHTIILLTDGK--SNMGDSPKKAVTRIRELLSIEQNRDDYLDIXAIGVGKLDVDWKE 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERSQ-----DVTEVITSLDSASYKDHENATGANTYEVLIRVYSMMQTQMDRLGMETSAW 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGFDLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLR--MSFIVFSTRGTTLMKLTE 97
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A;Molecule type: mRNA
A;Residues: 660-677,'R',679,681-723,'G',725 <RES>
A;Cross.references: GB:M16271; NID:g199289; PIDN:AAA39562.1; PID:g199290
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Matches 74; Conserv
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A; Residues: 1-760 <ISH>
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1151 NVYPCYRL 1158
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A, Residues: 1551-1570;1593-1599;1639-1667 <GOR2>

G, Superfamily: collagen alpha 1(XIV) chain; fibronectin type III repeat homology; von Wi

G, Keywords: alternative splicing; colled coll; extracellular matrix; glycoprotein; trime

E; 40-204/Domain: von Willebrand factor type A repeat homology <WWAI>

F; 326-317/Domain: fibronectin type III repeat homology <FWNA>

F; 326-409/Domain: fibronectin type III repeat homology <FRNA>

F; 326-409/Domain: fibronectin type III repeat homology <FRNA>

F; 507-591/Domain: fibronectin type III repeat homology <FRNA>

F; 507-591/Domain: fibronectin type III repeat homology <FRNA>

F; 508-591/Domain: fibronectin type III repeat homology <FRNA>

F; 508-591/Domain: fibronectin type III repeat homology <FRNA>

F; 806-893/Domain: fibronectin type III repeat homology <FRNA>

F; 806-893/Domain: fibronectin type III repeat homology <FRNA>

F; 924-1089/Domain: non-collagenous NG4 #status predicted <NG4>

F; 1111-1353/Domain: non-collagenous NC2 #status predicted <NG2>
R;Gerecke, D.R.; FOley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin
J. Biol. Chem. 268, 12177-12184, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Status: preliminary
A Molecule type: mRNA
A Molecule type: mloblet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne, B Molecule type: mloblet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne, Mayne, M. Biochem. 201, 333-338, 1991
A Molecule type: mloblet type:
                                                                                     A, Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' region
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                                                                                                                                                                                                                                                                                                                         A Molecule type: mRNA; protein
A; Residues: 1-174 <GER>
A; Experimental source: embryo skin
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365)
R; Apte, S.3.
B; Apte, S.3.
A; Reference number: S30085
A; Reference number: S30085
A; Recession: S30085
A; Molecule type: mRNA
A; Residues: 1472-1660 <APT>
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R;Trueb, J.; Trueb, B.
Eur. J. Blochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443
A;Accession: S22916
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                                                                                                                                                                                           A; Reference number: A45974; MUID: 93280195
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A; Residues: 1472-1659 <GOR1>
A; Accession: S20833
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A; Accession: 5,64,0
A; Accession: 5,64,0
A; Molecule type: mRNA
A; Residues: 1.1888 G-TRU>
A; Cross-references: EmBL:X70793; NID:9288872; PIDN:CAA50064.1; PID:9288873
A; Cross-references: EmBL:X70793; NID:9388668
Bur. J. Blochem. 212, 483-490, 1993
Bur. J. Blochem. 212, 483-490, 1993
A; Title: Complete primary structure of chicken collagen XIV.
A; Reference number: S31211
A; Accession: S31211
A; Residues: 1.416.1460-1811,1843-1888 G-WAE>
A; Residues: 1.416.1460-1811,1843-1888 G-WAE>
A; Residues: 1.416.1460-1811,1843-1888 G-WAE>
A; Residues: Collagen alpha 1(XIV) chain; fibronectin type III repeat homology; Von C; Superfamily: collagen alpha 1(XIV) chain; long form #status predicted G-S1G>
C; Superfamily: collagen alpha 1(XIV) chain, long form #status predicted G-S1G>
F; 1.29-D/Domain: signal sequence #status predicted G-S1G>
F; 29-110/Domain: fibronectin type III repeat homology G-RN3D>
F; 29-110/Domain: fibronectin type III repeat homology G-RN3D>
F; 352-30/Domain: fibronectin type III repeat homology G-RN3D>
F; 322-100-Momain: fibronectin type III repeat homology G-R
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C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C;Accession: S42373
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98 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE 155
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Best Local Similarity 25.0%; Pred. No. 0.055;
Matches 62; Conservative 44; Mismatches 116; Indels
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hypothetical protein T20G5.3 - Caenorhabditis elegans
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submitted to the EMBL Data Library, March 1994
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C;Species: Gallus gallus (chicken)
C;Accession: 53121
C;Accession: 53121
Eur. J. Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Refleace number: 531211; MUID:9318668
A;Accession: 53122
A;Residues: 1000
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-1857 C*MAE;
A;Residues: 1-1857 C*MAE;
A;Ross-references: EMBL:X70792; NID:9288874; PIDN:CAA50063.1; PID:9288875
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
A;Note: the nucleotide sequence specific collage coll; extracellular matrix; glycoprotein; translatios:
C;Geneticos:
A;Gene: Coll4A1
C;Superfamily; collagen alpha 1(XIV) chain; fibronectin type III repeat homology <FN3A>
F;29-1857/Produatin: fibronectin type III repeat homology <FN3A>
F;350/Domain: fibronectin type III repeat homology <FN3A>
F;36-310/Domain: fibronectin type III repeat homology <FN3E>
F;31-10/Domain: fibronectin type III repeat homology <FN3E>
F;32-14/Domain: fibronectin type III repeat homology <FN3E>
F;32-1009/Domain: f
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                                                                                                                                                                                                                                                                               GNGFRHARNVDRV--LCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMK--AALQVS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII
                                      FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR
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25.0%; Pred. No. 0.054;
.tive 44; Mismatches 116; Indels 20
                                                                                                 531 VGDPTSQHGKEFLVEDVII 549
                                                                                                                                                                                                                                                                                                                                                                                                                            299 MND-----GLSFISSSVII 312
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1267 NVYPCYRL 1274
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                                                                             183
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NyAlternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; he NyContains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragmen C5 Specias: Homo sapiens (man) C5 Date: 19-Feb-1984 #sequence_revision 05-Aug-1994 #text_change 08-Dec-2000 C; Accession: S34075; A44622; A00934; A19188; A19947; B19947; B25971; S14339; A44628; Sxwellat, J.E.; Jahn, I.; de la Salle, H.; Hauptmann, G. Abbitted to the EMBL Data Library, March 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cype XII collagen alpha-1 chain - eastern newt (fragment)
Cypecies: Notophthalmus viridescens, Triturus viridescens (eastern newt)
Cypecies: Notophthalmus viridescens, Triturus viridescens (eastern newt)
Cypecies: Notophthalmus viridescens, Triturus viridescens (eastern newt)
Cypecession: 151027
R:Wei, Y: Yang, E.V.; Klatt, K.P.; Tassava, R.A.
Dev. Biol. 168, 503-513, 1995
A;Title: Monoclonal antibody MT2 identifies the urodele alpha 1 chain of type XII
A;Reference number: 151027; MUID:95246925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: 131027
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: mRNA
A;Residues: 1-929 <WEI>
A;Residues: 1-929 <WEI>
A;Residues: 1-929 <WEI>
E;Residues: 1-929 <WEI
A;Cross-references: EMBL:019494; NID:g632647; PIDN:AAA80217.1; PID:g632648
C;Superfamily: collagen alpha 1(XII) chaln; fibronectin type III repeat homology;
E;155-236/Domain: fibronectin type III repeat homology <3FR>
F;631-795/Domain: von Willebrand factor type A repeat homology <VWA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQI 102
                                                                                                                                                                                                                                                                                               315 GLVQYSSSVROEFPLGRFHTKKDIKAAVRNM-----SYMEKGTMTGAALKYLIDNSF 366
                                                                                                                                                                                                                                                       134 ENROGYRTAS -- VITALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARI 191
81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     693 KKSLMDAVANLPYKGGNTNTGSALKFILENNF---RPGVGMREKARKIAILLTDGKSQDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 LKKSCIEILAA----EPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKP
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                                                                                                                              82 FIV----FSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY----Y
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ICAGQGGRREDGGPACYGGFDLYFILDKSGSVL-HHWNEIYYFVEQLAHKF-ISPQLRMS
                                                                                                                                                                                                                                                                                                                                                                                                                          423 ASEPVAEHYFYTAD-FKTINQIGKKLQKKICVE---EDP---CACESLVKFQAKVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.8%; Score 118; DB 2; Length 929; Best Local Similarity 21.2%; Pred. No. 0.2; Matches 57; Conservative 51; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement factor B precursor [validated] - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               862 ---OEVYVRGTQTTTVLVGLKPETEYYVN 887
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A; Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
C; Complex: homotrimer
C; Superfamily: unassigned EGF-related proteins; EGF homology; von Willebrand factor type
C; Superfamily: unassigned EGF-related proteins EGF homology; von Willebrand factor type
C; Keywords: glycoprotein; homotrimer
F; 1-22/Domain: signal sequence #status predicted <SIG>
F; 23-496/Product: cartilage matrix protein #status predicted <MAT>
F; 39-206/Domain: von Willebrand factor type A repeat homology <VWA1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Speciës: Homo sapiens (man)
C;Speciës: Homo sapiens (man)
C;Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 21-Jul-2000
C;Accession: A37979; B37979
R;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Sh. B.Jol. Chem. 265, 19624-19631, 1990
A;Title: Structure and chromosomal location of the human gene encoding cartilage matrix A;Reference number: A37979; MUID:91060568
                                                                                                                                                                                       A;Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1. C;Superfamily: von Willebrand factor type A repeat homology; EGF homology; fibronectin if $512-679/Domain: von Willebrand factor type A repeat homology <VWAl> F:754-793/Domain: fibronectin type II repeat homology <2F1> F:754-793/Domain: EGF homology <EGF>
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A;Residues: 157-290,'L',292-496 <JE2>
A;Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483 CYGGFVDVSSNANLPPGRVCTVQTTCPKQKTDLVFLIDGSGSIGSYVFKNEVLRFVREFV 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 HKFI--SPQLRMSFIVFSTRGTTLMKLTE--DREQIRQGLEELQKVLPG----GDTYMH- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 --EGFERASEQIYYENRQGYR----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             649 TFAIGVTDHVLASELESIAGSPNRWFYV-DKFKDLDTRLRSMIQK-----AACPS 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :99
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                                                                                                                                                                                                                                                                                                                                                                                                                   7.4%; Score 128; DB 2; Length 3051; 27.1%; Pred. No. 0.15; ive 31; Mismatches 75; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;227-262/Domain: EGF homology <EGF>
F;273-437/Domain: von Willebrand factor type A repeat homology
F;76:344/Binding site: carbohydrate (Asn) (covalent) #status pr
F;221-238,234-247,249-262/Disulfide bonds: #status predicted
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                                                                  A;Molecule type: DNA
A;Residues: 1-3051 <SMI>
A;Crost-references: EMBL:Z30423; NID:g458479; PID:g458485
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.0%; Score 120.5; DB 2;
25.3%; Pred. No. 0.055;
tive 37; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GDB:127280; OMIM:115437
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hes 64; Conservative
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A; Residues: 1-496 <JEN>
A;Cross-references: GB:J05667
A;Accession: B37979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 CYGGF----
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                                 A; Accession: S42373
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Matches
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A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-764 cRES>
A; Cross-references: GB:S67310; NID:g452937; PIDN:AAD13989.1; PID:g4261689
A; Cross-references: GB:S67310; NID:g452937; PIDN:AAD13989.1; PID:g4261689
A; Title: Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic C
A; Reference number: 157824; MUID:94067177
A; Reference number: 157824
A; Reference number: 157824
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-31, 'Q' 33-764 <RE2>
A; Cross-references: GB:L15702; NID:g291921; PIDN:AAA16820.1; PID:g291922
C; Comment: 292-Cys has a free sulfhydryl.
C; Genetics:
A; Cross-references: GDB:119726; OMIM:138470
C; Genetics: A; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3; A; Introns: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3; A; Note: the list of introns may be incompleted
A; Note: gnee is located in the major histocomplete
A; Note: gnee is located in the major histocompatibility complex, class III region
C; Complex: complement factor B initially forms an inactive complex with complement factor C3b forming active C3/C5 convertase; Ba is released
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Superfamily: complement alternate pathway

C; Superfamily: complement C2; complement factor H repeat homology; trypsin homology;
C; Superfamily: complement C2; complement alternate pathway; duplication; glycoprotein; hyd
C; Superfamily: signal sequence #status predicted <SIG>
F; 12-57Domain: signal sequence #status experimental <MAT>
F; 26-754/Product: complement factor B #status experimental <MAT>
F; 26-754/Product: complement factor B fragment #status experimental <BAF>
F; 103-158/Domain: complement factor H repeat homology <FH12>
F; 156-218/Domain: complement factor H repeat homology <FH2>
F; 165-218/Domain: complement factor H repeat homology <FH3>
F; 268-458/Domain: von Willebrand factor H repeat homology <FH3>
F; 268-458/Domain: trypsin homology #status atypical <TRX>
F; 482-722/Domain: trypsin homology #status atypical <TRX>
F; 37-6,62-98,103-145,131-128,165-205,191-218,470-596,511-527,599-615,656-682,695-725
F; 37-6,62-98,103-145, 131-188,165-205,191-218,470-596,511-527,599-615,656-682,695-725
F; 259-260/Cleavage site: Arg-Lys (complement factor D) #status experimental
F; 226,576,699/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: Bb is a serine proteinase; C3/C5 convertase cleaves complement C3 alph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---QGY-RTASVIIALTDG-----ELHEDLFFYSE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : :|::|
243 EGVDAEDGHGPGEQQKRKIVLDPSGSMNIYLVLDGSDSIGASNFTGAKKCLVNLIEKVAS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 KFISPQLRMSFIVFSTRGTTLMKLTE----DREQIRQGLEEL----QKVLPGGDTYMHEG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 QGGRREDG-GPA-----CYGGFDLYFILDKSGSV-----LHHWNEIYYFVEQLAH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REANRSRDLGAIVYCVG--VKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
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356 -KKALQAVYSAMSWPDDVPPEGWNRTRHVIILMTDGLHNMGGDPITVIDEIRDLLYIGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63; Mismatches 109;
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19.6%; Pred. No. 0.37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----QSLSLC------GMVWEHRKGTD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.6%
Best Local Similarity 19.6%
Matches 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163
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                                                                                                                                                                                                                                                                   A.Status: preliminary
A.Status: mRNA
A.Molecule type: mRNA
A.Residues: 16-225, F', 227-259 <MOR>
R.Schwaeble, W.: Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Busche
R.Schwaeble, W.: Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Busche
R.Schwaeble, W.: Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Busche
R.Schwaeble, W.: Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Busche
A.Title: Human complement factor B: functional properties of a recombinant zymogen of th
A.Reference number: 154409; MUID:94041399
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A; Title: Internal homologies of the Ba fragment from human complement component factor A; Reference number: A44628; MUID:84158524
                                                                                       A.Cross-references: EMBL:X72875; NID:g297568; PIDN:CAA51389.1; PID:g297569 R; Woods, D.E.; Markham, A.F.; Ricker, A.T.; Goldberger, G.; Colten, H.R. Proc. Natl. Acad. Sci. U.S.A. 79, 5661-5665, 1982 A; Title: Isolation of cDNA clones for the human complement protein factor B, a class A; Reference number: A44622; MUID:83039428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 270-329 <NIE>
                            A; Accession: S34075
A; Molecule type: mRNA
A; Residues: 1-764 <MEJ>
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C; Function:
A; Description: structural component of extracellular polymer associated with anchorin C; Superfamily: unassigned collagens; animal Kunitz-type proteinase inhibitor homology C; Keywords: collad coll; extracellular matrix; glycoprotein; hydroxylysine; hydroxypr F; 1-16/Domain: signal sequence #status predicted <SIG> F; 17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT> F; 17-253/Domain: animoterminal nonhelical #status predicted <MAT> F; 17-253/Domain: unimoterminal nonhelical #status predicted <MAT> F; 21-31-316/Domain: thoronectin type III repeat homology <FN1> F; 32-413/Domain: fibronectin type III repeat homology <FN2> F; 508-593/Domain: fibronectin type III repeat homology <FN4> F; 508-593/Domain: fibronectin type III repeat homology <FN5> F; 568-593/Domain: fibronectin type III repeat homology <FN5> F; 568-593/Domain: fibronectin type III repeat homology <FN3> F; 568-593/Domain: fibronectin type III repeat homology <FN3> F; 568-593/Domain: fibronectin type III repeat homology <FN3> F; 568-593/Domain: fibronectin type III repeat homology <FN9> F; 568-593/Domain: fibronectin fi
Complex: type VII collagen is probably a homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1254-2783/Region: interrupted helical
F;1334-1336/Region: cell attachment (R-G-D) motif
F;2088-2010/Region: cell attachment (R-G-D) motif
F;2553-2555/Region: cell attachment (R-G-D) motif
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Job time: 260 sec
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Matches 52; Conserv
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A;Note: defects in this gene can result in dominant and recessive dystrophic epidermolys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: translated from GB/EMBL/DDBJ.
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: FFR', 372-517, 'DV', 520-540, 'W', 542-1255 <RES>
A;Cross-references: GB:S51236; NID:3262308; PIDN:AAB24637.1; PID:g262309
B;Seltzer, J.L.; Elsen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson, R.E.
A;Title: Chem. 254, 3822-3826, 1989
A;Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagena
A;Reference number: A30296; MUID:89139437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 'EFR', 340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', 524-528, 'C',
A; Residues: 'EFR', 340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', 524-528, 'C',
A; Cross-references: DDBJ:D11152; DDBJ:D13694; NID:9453698; PIDN:BAA02853.1; PID:9453699
A; Experimental source: Reratinocyte
A; Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
R; Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mat
B; Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mat
A; Title: Human type VII collagen: CDNA cloning and chromosomal mapping of the gene.
A; Reference number: S16316; MUID:91334380
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A; Residues: 815-892, E', 884-1439 <PAR>
A; Cross-references: GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96439.1; PID:g180915
A; Experimental source: keratinocyte
R; Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.; Cook, M.E.; Wright, J.;
J. Invest. Dermatol. 99, 691-696, 1992
A; Title: Noncollagenous (NOI) domain of collagen VII resembles multidomain adhesion prot
A; Reference number: 156328; MUID:93107742
                                                                                                                                                                                                  C;Date: 04-Nov-1994 Fsequence_revision 04-Nov-1994 #text_change 20-Sep-1999
C;Date: 04-Nov-1994 Fsequence_revision 04-Nov-1994 #text_change 20-Sep-1999
C;Accession: ASAG49; PH0R44; SIG316; 156328; A30236; I84686
R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Ultto, J.
J. Biol. Chem. 269, 20256-20262, 1994
A;Title: Cloning of human type VII collagen. Complete primary sequence of the alphal(VII A;Reference number: A54849; MUID:94327588
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A;Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous A; Reference number: 148103; MUID:93271985
A; Rccession: 184686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 'A', 1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;
A; Note: two reported peptides cannot be reliably located
R; Greenspan, D.S.
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 2395-2871, 'S., 2873-2944 <RE2>
A;Residues: 2395-2871, 'S., 2873-2944 <RE2>
A;Cross-references: GB:L06862; NID:9388713; PIDN:AAA89196.1; PID:9388714
B;Christiano, A.M.; Rynaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. US.A. 91, 3540-3553, 1994
A;Tille: Dominant dystrophic epidermolysis bullosa: identification of a Gly
A;Reference number: A55255; MUID:94224777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; cross-references: GB:L02870; NID:g987124; PIDN:AAA75438.1; PID:g987125 R; Tanaka, T.; Takahashi, K.; Furukawa, F.; Inamura, S. Biothem. Biotheys. Res. Commun. 183, 958-963, 1992 A; Itle: Molecular cloning and characterization of type VII collagen cDNA. A; Reference number: PHO844; MUID:92231902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: not compared with conceptual translation
                                             collagen alpha 1(VII) chain precursor - human
N.Alternate names: procollagen alpha 1(VII) chain
C.Species: Homo sapiens (man)
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A;Cross-references: GDB:128750; OMIM:120120
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A; Residues: 1-2944 <CHR>
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F;2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology GBIP-
F;387,786.1109/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;2167,2176,2185,2188,2664,2667,2673/Modified site: 4-hydroxyproline (Pro) #status ex
F;2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental
F;2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental
F;2635,2631/Binding site: carbohydrate (Lys) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 DLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIH 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF---ISPQ-LRMSFIVFSTRGTT---LMKL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2944;
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                                                                                                                                                                                                                                                                                                              6.5%; Score 111.5; DB 2; 24.1%; Pred. No. 3.3; tive 42; Mismatches 85;
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Human 1mmune/haema

Murine TANGO 197.

Mouse alpha-d subu Mouse beta 2 integ Mouse alpha d #1. Mouse alpha d poly Mouse alpha d prote Mouse alpha-d subu Mouse beta 2 integ Mouse beta 1 integ Mouse beta 1 integ Mouse alpha d #2. Mouse alpha d poly Mouse alpha d prote Mouse alpha d protein Rat alpha d protein Rat alpha d protein Rat alpha-d subuni Human beta 2 integri Human beta 2 integri Human beta 2 integri Human beta 2 integri

OM protein

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Sequence:

Searched:

Database

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TANGO: 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; crohn's disease; chronic myelogenous leukemia; cancer; liver disease; Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune disease; systemic lupus erythematosus; transgenic animal; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prognosis; prophylatic; therapeutic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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AAW72837
AAW72824
AAW72825
AAB18448
AAB18460
AAB18459
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AAW23061
                                     AAB01428
AAM84307
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AAW65101
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AAR78169
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                                                             AAR78167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB01422 standard; Protein; 333 AA
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  99WO-US31025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
 Human TANGO 197.
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A human TANGO 216
A human TANGO 216
Human novel extrac
A murine TANGO 216
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2: \SIDS1/gcgdata/hold geneseq/geneseqp_-embl/AA1981_DAT:*

3: \SIDS1/gcgdata/hold geneseq/geneseqp_-embl/AA1981_DAT:*

3: \SIDS1/gcgdata/hold geneseq/geneseqp_-embl/AA1981_DAT:*

5: \SIDS1/gcgdata/hold geneseq/geneseqp_-embl/AA1981_DAT:*

5: \SIDS1/gcgdata/hold geneseq/geneseqp_-embl/AA1981_DAT:*

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112: \SIDS1/gcgdata/hold geneseq/geneseqp_-embl/AA1991_DAT:*

113: \SIDS1/gcgdata/hold geneseq/geneseqp_-embl/AA1991_DAT:*

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1115: \SIDS1/gcgdata/hold geneseq/geneseqp_-embl/AA1991_DAT:*

1116: \SIDS1/gcgdata/hold geneseq/geneseqp_-embl/AA1991_DAT:*

1117: \SIDS1/gcgdata/hold geneseq/geneseqp_-embl/AA1991_DAT:*

1118: \SIDS1/gcgda
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Human protein sequ
A human TANGO 216
                                                                                                (without alignments)
310.481 Million cell updates/sec
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Human gene 4 encod
Human gene 4 encod
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                                                                                    9, 2002, 10:32:13 ; Search time 119.13 Seconds
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1 MATAERRALGIGFQWLSLAT.....TTHCSLHKIASGPTTAACME
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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AAE01439
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AAM38976
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AAB18457
AAU19662
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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797.5
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WPI; 2000-465743/40.

Result 8

Human alpha-d deri Rat alpha-d #1. R Human alpha-d. Ho Human Beta-integri

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Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, pociniasis, inflammatory bowel diseases, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodykin's chronic myelogenous leukemia, cancer, liver disease, Hodykin's disease, osteoarthritis, Lyme's disease, cacheria and autoimmune diseases e.g. myasthemia gravis, autoimmune diabetes and systemic diseases e.g. myasthemia gravis, autoimmune diabetes and systemic claps erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in parmacogenomics and for monitoring clinical trials. TANGO plarmacogenomics are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a continuous disorder or disorder or having a continuous disorder or disorder or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
                            Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1728; DB 21; Length 333; 100.0%; Pred. No. 5e-177; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:94.
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                                                                                                                                                       Claim 8; Fig 4; 209pp; English.
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Best Local Similarity
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N-PSDB; AAA47455
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AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted correcting genes, and AAE01436-AAE01513 represent the protein genes, and AAE01436-AAE01513 represent the protein genes, and AAE01436-AAE01513 represent the protein genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing, the genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing, and the protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of amount of the new protein. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the mutations disorders, cancer, tumours, foetal and developmental corrections for treatment of an protein and disorders, diseases of the immune system, altergules, neurological disorders, (e.g., rheumatoid arthritis), inflammation, altergules, neurological disorders, (e.g., rheumatoid as sthma, cardiovascular disorders, angiogenic disorders, kidney disorders, cardiovascular disorders, angiogenic disorders, kidney disorders, cardiovascular disorders, angiogenic disorders, kidney disorders, endocrine disorders, and infections. The proteins can also be used to aid wound contain and epithelial cell proliferation, to prevent skin aging cell contains and epithelial cell proliferation, to prevent skin aging cell contains and pathelial cell proliferation, to prevent skin aging partners, and in chemotaxis, and can be used of contains and entry and in chemotaxis, and can be used to contain the contains and in chemotaxis, and can be used to contain the contains and in chemotaxis, and can be used to contain the contains and in chemotaxis, and can be used to contain the contains and can be used to contain the contains and can be used 
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Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunoassays (ELISA). The present sequence represents a human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives
cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; chromosome 19.
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                                                                                                                                                                                                                                              1..27
/label= Signal_peptide
28..403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-2000; 2000WO-US30045.
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30-JUN-2000; 2000US-0215133.
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N-PSDB; AAD05303.
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95.4%; Score 1649; DB 22; 100.0%; Pred. No. 2.1e-168; iive 0; Mismatches 0;

Conservative

Query Match Best Local Similarity Matches 318; Conserv

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Birse CE,

Moore PA,

Komatsoulis GA,

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(HUMA-) HUMAN GENOME SCI INC.
05-NOV-1999; 99US-0163581.
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                                                                                                                                                                                                                                                                                              Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; Schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; prepared disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy;
                                        EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                  HEGFERASEQIYYENROGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                                    VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
                                                                                                                                                                                                                                                                                 Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein"
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                                                                                                                                                                                                                                                                                                                                                                                    binding partner identification; chromosome 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                    'label= Signal_peptide
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/note= "Encoded by
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/note= "Encoded
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AAD03309-AAD03379 represent cDNAS corresponding to 2.8 numan secreted AAD03309-AAD03379. AAD03379 represent the protein steps end conditions are useful for preventing.

AAE01514-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing.

The genes and their secreted proteins are useful for preventing, the reating or amedical conditions can be diagnosed by determining the mew protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the can include developing products for the diagnosis or treatment of and include developing products for the diagnosis or treatment of anormalities, haematopoletic disorders, diseases of the immune system, anormalities, haematopoletic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., alzheimer's disease, branchestinal disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, prepancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound can be used by their of primary tissues, to regenerate tissues, to identify their cognate ligands or binding pattners, and in chemotrasis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in diagnostic immunosasays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human cereted protein of the invention.
                                                                                                New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives .
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                                                                                                                                                                                                                                                                                                                                 AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elyyfveqlahkfispqlrmsfivfstrgttlmkltedreqirqgleelqkvlpggdtym
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Pred. No. 7.3e-168;
0; Mismatches 1;
                                                                                                                                                                                                                                                           Claim 11; Page 505-506; 562pp; English.
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Best Local Similarity 99.7%;
Matches 317; Conservative 0
2001-308778/32
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                                  N-PSDB; AAD05334
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the SGO uncleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                            HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                                                                                                                                                                                                                          EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                                                                                                                     Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                       1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
                                                                                           KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
Length 297;
                                      Indels
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Otsuki
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    Score 1392; DB 22;
Pred. No. 5.9e-141;
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A, Nagai K,
                                        2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                       241 VRGNGFRHARNVDRVLCSFKINDSVTLNE 269
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Sugiyama T, Wakamatsu
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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        80.6%;
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            Query Match
Best Local Similarity
Matches 267; Conserv
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the encoded polypeptides (AAM38642-AAM42213) with nootropic,
the encoded polypeptides (AAM38642-AAM42213) with nootropic,
to find the therapy. A composition containing a polypeptide or polynucleotide
containing a polypeptide or polynucleotide
cof the invention may be used to treat diseases of the peripheral nervous
cof the invention may be used to treat diseases of the peripheral nervous
cof the invention may be used to treat diseases of the peripheral nervous
cof localized neuropaths and central nervous system diseases, such as
cof lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
cutilisation of the activity, chemotectic/chemokinetic activity, haemostatic
cof cutilisation of the activity, cancer diagnosis and therapy, drug screening,
and thrombolytic activity, arthritis and inflammation, leukaemias and
consequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral scleroslis; SNy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ren F, War
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Zhou P, Goodrich R, Drmanac RT;
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                                                                                                                                                             AAM38976 standard; Protein; 297 AA
                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 2121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653191.
19-CCT-2000; 2000US-0653191.
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                                              301 dglsfisssviitthcs 318
                                                                                                                                                                                                                                            (first entry)
                            DGLSFISSSVIITTHCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-442253/47.
N-PSDB; AAI58132.
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Homo sapiens

leukaemia.

22-OCT-2001

AAM38976;

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AAM38976 RESULT

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26-JUL-2001.

Wang J, W Zhao QA,

Tang YT,

Sequence

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                                                  the 5'-end sequence's'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cons. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length AAH13628 and AAH13633 to AAH13622 represent human cDNA sequences; AAH03166 to AAH13628 and AAB95893 represent human amino acid sequences; and AAH13632 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain hernlation; latrogenic disease; inflammation; meningitis; Alzhelmer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF 259
                                                                                                                                                                                                                                                                                                                                                                                                                               80 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                  Score 966; DB 22;
Pred. No. 2.5e-95;
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                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A human TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB18456 standard; Protein; 488 AA.
                                                                                                                                                                                                                                                                                                                                                  55.9%;
98.9%;
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                                                                                                                                                                                                                                                         the present invention.
                                                                                                                                                                                                                                                                                                                                                                                          Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||||||:
181 kindsvtlsk 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 KINDSVTLNE 269
                                                                                                                                                                                                                                                                                           218 AA;
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                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                    Query Match
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AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO cescribes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO cellular proliferation, modulate cellular proliferation, modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate the proliferation of disorders, such as cancer, and lematopoietic associated diseases and disorders, such as cancer, and hematopoietic associated diseases and disorders, treat bone marrow, blood and hematopoietic associated diseases and disorders, spleen associated standard disorders, spleen associated as standard disorders, spleen associated as standard disorders, preat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral ocdema, hydrocephalus, brain herniations, latrogenic disease, inflammations, hydrocephalus and encephalitis, and treat hepatic disorders.

Correlal and viral meningitis, alsociated solesses, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

Correlation of bone and cartilage cells and correbral cancers, corrested to correct the present sequence does not appear in the specification; it was corrected as a sequence does not appear in the present sequence does not appear in the page of the correct 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 YYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRGCLEELQKVLPGGDTYMHE 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
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                                                                                          Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.4%; Score 801.5; DB 2
51.3%; Pred. No. 4.2e-77;
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                                                                                                                                                                                                 Disclosure; Page -; 175pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 LSFISSSVIITTHCS 318
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                                                                                                                                                 e.g. for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | || |:|:| | || 301 ksvisgslivtatecs
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                     2000-579269/54.
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                                             N-PSDB; AAA75158
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Best Local
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DB 21; Length 488; Indels

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MILL-) MILLENNIUM PHARM INC
                                                                                                                        01-MAR-2000; 2000WO-US05226.
                                                                                                                                                               262, 266 and 267 usetul a
e.g. for treating cancer
15-JAN-2001 (first entry)
                                                                                                                                           Barnes TM, Holtzman
                                                                                                                                                 2000-579269/54
                                                                                                                                                     N-PSDB; AAA75149
                                                                                                            WO200052022-A1
                                                                                                                               01-MAR-1999;
                                               Homo sapiens
                                                                                                                  08-SEP-2000
                                                        Peptide
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cellular proliferation; cellular differentiation; cellular adhesion; cellular proliferation; cellular differentiation; cellular decellular differentiation; cancer; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectrasis; pulmonary congestion; intestinal disorder; spleen associated disease; renal disorder; ischemic heart disease; hydrocephalus; cardiovascular disorder; ischemic heart disease; hydrocephalus; Alzaheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
disorder. They may also be used to treat disorders associated with the ovaries, cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic
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                                                                                                                                                                                                                                                                                                                                                             TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
                                                                                                                                                                                                                              Score 800.5; DB 21;
Pred. No. 5.4e-77;
                                                                                                                                                                                                                                46.3%; Scor.
51.3%; Pred. No. 5...
... 56; Mismatches
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                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                  488 AA;
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Matches 162;
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                                                                                                                                           disorders
                                                                                                                                                                                       Sequence
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                                                                                                             TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; whematopoietic associated disease, atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; highen respectively alsease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human and murine secreted proteins designated TANGO 216, 261, 266 and 267 useful as modulating agents of cellular processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44..213
/note= "von Willebrand factor A domain"
                                                                                Amino acid sequence of human TANGO 216 polypeptide.
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318..341
"...to= "transnmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sharp JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Fraser CC;

(first entry)

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cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                                                       TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
                                        A human TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2000; 2000WO-US05226.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barnes TM, Holtzman DA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA75159
                                                                                                                                                                                                                                                                                                                                                                                    WO200052022-A1.
                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1999;
15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-2000,
describes TANGO 266, TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 261 polypeptides can be used to endulate recillular adhesion. Modulate cellular adhesion. The proteins can be used to medulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, andulate cellular adhesion, modulate cell adhesion in proliferation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoletic associated diseases and disorders, atelectasis, and hematopoletic associated diseases and disorders, spleen associated diseases, modulate renal disorders, intestinal disorders, spleen associated diseases, modulate trenal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral ocedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bydrocephalus, brain herniations, latrogenic disease, inflammations, better and certificed disease, cerebral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxoplasmosis, Parkinson's disease, multiple Sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders. note: the present sequence does not appear in the specification; it was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 ISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYY 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 wlfpglwllvlsgpgggllraqegpscrrafdlyfvldksgsvannwieiynfvgqlaerf 73
                                                                                     Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
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Pred. No. 8.9e-77;
5; Mismatches 87; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           created using information provided.
                                                                                                                                                                               Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
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52.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 159; Conservative
                                                                                                                                for treating cancer
                  2000-579269/54.
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                                        N-PSDB; AAA75157
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Fraser CC;

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describes TANGO 266, TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 260 callular describes to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to creat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular adhesion, modulate cellular and cellular and cellular and cellular appear in proliferation, modulate cellular interactions, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as isonemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to creat disorders associated with the ovaries, and cerebral ocedma, hydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders. note: the present sequence does not appear in the specification; it was
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50.9%; Pred. No. 1.1e-76;
ive 57; Mismatches 95
Disclosure; Page -; 175pp; English.
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14-SEP-2000; 2000US-0233063.
14-SEP-2000; 2000US-0233064.
14-SEP-2000; 2000US-0233064.
14-SEP-2000; 2000US-0233065.
21-SEP-2000; 2000US-0234997.
25-SEP-2000; 2000US-0234997.
25-SEP-2000; 2000US-0234997.
27-SEP-2000; 2000US-0234998.
27-SEP-2000; 2000US-023498.
29-SEP-2000; 2000US-023636.
29-CT-2000; 2000US-0236369.
02-0CT-2000; 2000US-0236370.
02-0CT-2000; 2000US-0237039.
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02-0CT-2000; 2000US-0237037.

02-0CT-2000; 2000US-0237038.

02-0CT-2000; 2000US-0239393.

13-0CT-2000; 2000US-0239935.

13-0CT-2000; 2000US-0239935.

13-0CT-2000; 2000US-0249937.

20-0CT-2000; 2000US-0241785.

20-0CT-2000; 2000US-0241786.

20-0CT-2000; 2000US-0241786.

20-0CT-2000; 2000US-0241897.

20-0CT-2000; 2000US-0241897.

20-0CT-2000; 2000US-0241809.

20-0CT-2000; 2000US-0241809.
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2000US-0246478.
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2000US-0246524.
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                                    2000US-0225447.
2000US-0225755.
2000US-0225759.
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2000US-0226681.
2000US-0226868.
2000US-0226868.
2000US-0226868.
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2000US-0229343.
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2000US-0229509
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06-SEP-2000)
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08-SEP-2000)
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14-SEP-2000)
14-SEP-2000)
14-SEP-2000)
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                 14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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01-SEP-2000;
01-SEP-2000;
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22-AUG-2000;
                                                                                                                                                                          01-SEP-2000;
01-SEP-2000;
Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial, ophthalmic; cytostatic; antialzhehmers; immunedautoimmune disease; HIV infection; annemia; human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; accers; hyperproliferative disorder; breast neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological diseases; Alzheimer's disease; parkinson's disease; cardiovascular disorder; cardiac arrest; tachycardia; angina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive.
           242
                                                                                                            GFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD
                                                                                                   183 FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR
                                                                                                                                               243 GNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDG
                                                                                                                                                                                                                                                                                                                                        Human novel extracellular matrix protein, Seq ID No 312.
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2000US-020515.
2000US-020467.
2000US-0215135.
2000US-0215135.
2000US-021647.
2000US-0217487.
2000US-0217496.
2000US-0217496.
2000US-020963.
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2000US-0224519.
2000US-0225213.
2000US-0225214.
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2000US-0180628.
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2000US-0186530.
2000US-0189874.
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44-FBB-2000, 2
24-ARR-2000, 2
16-MAR-2000, 2
11-MAR-2000, 2
17-MAR-2000, 2
17-MAR-2000, 2
19-MAY-2000, 2
30-JUN-2000, 2
30-JUN-2000, 2
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07-JUL-2000; 2
11-JUL-2000; 2
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14-AUG-2000;
14-AUG-2000;
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The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPS). The novel human secreted extracellular matrix proteins (SPS). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPS. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPS by binding with the cells own genes and preventing their expression. The polynucleotides may be used as DNA probes in diagnostic assays. The SPS may also be used as antigens to produce antibodies and to identify modulators used as antigens to produce antibodies and to identify modulators antagonists and antagonists of the SPS. The anti-(SP) antibodies and antagonists and also be used to down regulate expression and activity of SPS and as diagnostic agents for detecting the presence of SPS in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM;
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                                                   2000US-0246528
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2000US-0246610
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2000US-0251988
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                                  2000US-0246527
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08-NOV-2000;
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06-DEC-2000;
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Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation,
                                                                                                                                                                                                                                                                                                                                                                                       194 SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 ISPQLRMSFIVFSTRGTTLMKLTEDREQIRQCLEELQKVLPGGDTYMHEGFERASEQIYY 133
                                                                                                                                                                                                                                                                                                                  134 ENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD 193
                                                                                                                                            Gaps
                                                                                                                                                                           WLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKF 73
                                                                                                                                                                                                                                                                 RVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIIT
                                                                                                                                                                                                                                                                                                                                                                                                         ||: |||| |||||:|||:||| :|| || || 348 skeqvfpvkggfqalkginsilaqssroygeefqivlsgrgfmlgsrng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder
                                                                                                                                          ë,
                                                                                                        DB 22; Length 587;
                                                                                                                                         91; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser CC;
                                                                                                      45.5%; Score 785.5; DB
51.8%; Pred. No. 3e-75;
                                                                                                      Query Match
Best Local Similarity 51.8%; Pred. No. 3e-75
Matches 158; Conservative 53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A murine TANGO 216 polypeptide clone.
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AAB18458-60 represent murine TANGO 216 proteins. The specification also cerescribes TANGO 266, TANGO 267, and TANGO 267. The TANGO CC collular differentiation and/or modulate cellular proliferation, modulate cellular adhesion. The cellular inferentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Wilebrand factor-associated clisorder, regulate extracellular matrix structuring, cellular adhesion, andulate cell adhesion in proliferative disorders, such as cancer, compulate the proliferation, differentiation, and/or function of cells can be used to treat any von Wilebrand disorders, such as cancer, condulate the proliferation, differentiation, and/or function of cells can hematopoietic associated diseases and disorders, treat bone marrow, blood coll mematopoietic associated diseases and disorders, spleen associated diseases modulate the proliferation, differentiation, differentiation, and/or function of bone and cartilage cells and to freat bone and/or cartilage associated diseases, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to freat bone and/or cartilage associated diseases or disorder. They may also be used to cartilage associated with the ovaries, and cerebral cerebral meningitis, Alzheimer's of sease, inflammations, brain meningitis, Alzheimer's Disease, cerebral context, in the specification, it was context the present sequence does not appear in the specification; it was context diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 VVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSM 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 NEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MATAERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHW 59
Novel human and murine secreted proteins designated TANGO 216, 261, 266, 266 and 267 useful as modulating agents of cellular processes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 MHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 VKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          created using information provided.
                                                                                    Disclosure; Page -; 175pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.78;
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                        262, 266 and 267 useful as e.g. for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 487 AA;
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3;

Gaps

4;

59

297

Amino acid sequence of a murine TANGO 216 polypeptide.

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The present sequence represents a murine TANGO 216 polypeptide. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular continuous modulate cellular adhesion, modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or matrix structuring, cellular interactions, modulate extracellular matrix structuring, disorders, such as cancer, modulate extracellular matrix structuring, and/or function of cells that appear in the bone marrow, and leukocytes, cand/or function of cells that appear in the bone marrow, and leukocytes, cand/or function of cells that appear in the bone marrow, and leukocytes, cand/or function of cells that appear in the bone marrow, and leukocytes, cand/or function of cells that appear in the bone marrow, and leukocytes, creat bone marrow, blood and hematopoietic associated diseases and disorders, spleen associated diseases, modulate renal disorders, treat chronic bronchitis, bronchial asthma and bronchiectasis, intestinal chronic bronchitis, bronchial asthma and bronchiectasis, intestinal cardiovascular disorders such as isochemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated with the disorder.
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             cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectrasis; pulmonary congestion; cedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spheen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; harin herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser CC;
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                       "extracellular domain"
                                                                                                                                                                                                                                                                                                                  /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                 "mature protein"
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                                                                                                                                                                                                                                                                         Location/Qualifiers
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/note= "e
34..487
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N-PSDB; AAA75150.
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                                                                                                                                                                                                                                                                                                   Peptide
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e.g. for treating cancer
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cellular proliferation; cellular differentiation; cellular adhesion;
von Willebrand factor associated disorder; cell trafficking; cancer;
hematopoietic associated disease; atelectasis; pulmonary congestion;
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
intestinal disorder; spleen associated disease; renal disorder;
cardiovascular disorder; ischemic heart disease; hydrocephalus;
brain herniation; iatrogenic disease; inflammation; meningitis;
Alzheimer's Disease; cerebral toxoplasmosis; parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                        60 NEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTY 119
                                                                                                                                     MHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVG 179
                                                                                                                                                                             VKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQV 239
                                                                                                                                                                                                                     VVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSM 299
                                                                                                                                                                                                                                                                         238 vltgravtsishdgsvlctftanstytksekpvsiqpssilcpapvlnkdgetlevsisy 297
                                                             Gaps
                                                                                1 MATAERRALGIGFQWLSLATLVLICAGOGG-RREDGGPACYGGFDLYFILDKSGSVLHHW 59
                                                                                            Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                             4
                                      Length 487;
                                     Score 771; DB 21; Length 4
Pred. No. 8.1e-74;
3; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser CC;
                                                                                                                                                                                                                                                                                                                                                                                                                                  A murine TANGO 216 polypeptide clone.
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                                                           53;
                                      44.6%;
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| ndgksavsrsltitatect 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2000; 2000WO-US05226.
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                                                            Conservative
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                                                 Similarity
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        487
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                                                            Matches 158;
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        Sequence
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describes TANGO 266, TANGO 216 proteins. The specification also describes TANGO 266, TANGO 262, and TANGO 267. The TANGO 260 cellular be used to modulate cellular proliferation, modulate cellular adhesion, modulate cellular adhesion. The proteins can be used to track any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, modulate cell trafficking and/or migration, modulate cellular interactions, modulate the proliferation in proliferative disorders, such as cancer, that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, understron or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated as such as isohemic heart disease, modulate trenal disorders, treat cardiovascular disorders such as isohemic heart disease, modulate the proliferation, differentiation, and or function of bone and cartilage cells and to treat bone and/or modular contine as the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimmer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

note: the present sequence does not appear in the specification; it was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 NEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTY 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MATAERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A murine TANGO 216 polypeptide clone.
Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              created using information provided.
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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, and TANGO 267. The TANGO 267 the TANGO 267. The TANGO 267 the TANGO 267. The TANGO 267 the TANGO 267 the tangent of tangent of
            hematopoletic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human and murine secreted proteins designated TANGO 216, 261, 265, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
cell trafficking; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 487;
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49.2%; Pred. No. 1.7e-73;
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       Willebrand factor-associated disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2000; 2000WO-US05226.
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157; Conservative
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contract diseases, rheumatorid arthritis, psoriasis, inflammatory versus-host diseases, rheumatorid arthritis, psoriasis, inflammatory versus-host diseases, rheumatorid arthritis, psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chowel disease, septic shock, ulcerative colitis, crohn's disease, chowel disease, osteoarthritis, Lyme's disease, cachexia and autoimmune diseases, osteoarthritis, Lyme's disease, cachexia and systemic diseases e.g. myasthemia gravis, autoimmune diabetes and systemic diseases e.g. myasthemia gravis, autoimmune diabetes and systemic ransgenic animals and the TANGO polypeptides themselves. Partial cransgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in TANGO-128, 140, 197, for diagnostic assays, prognostic assays, forensic biology, for diagnostic assays, prognostic assays, prognostic assays, conspections are suitable for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a methods for treating a subject at risk of a disorder associated with aberrant TANGO expression. A wide range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; crohn's disease; chronic myelogenous leukemia; cancer; liver disease; hodgkin's disease; sosteoarthritis; Lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus errythematosus; transgenic animal; diagnosis; prophylatic; therapeutic; mouse.
                                                                                                                                 240 VVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSM 299
                                                                                                                                                        Nucleic acids encoding TANGO polypeptides are useful as modulating
                                                      180 VKDFNETQLARIADSKDHVFPVNDGFQALOGIIHSILKKSCIEILAAEPSTICAGESFQV
                                                                             AAB01428 standard; Protein; 381 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC.
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 of cellular disorders can be treated.
                                381 AA;
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247 RHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFI 306 QQ ò

307 SSSVIITTTHCS 318 ||||||||||||||||||| 124 SSSVIITTTHCS 318 ò

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Search completed: August 9, 2002, 10:32:14 Job time: 133 sec

(USPTO) NNAJB 39A9 SIHT

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 9, 2002, 10:35:55; Search time 98.32 Seconds (without alignments) 1005.580 Million cell updates/sec Run on:

US-09-970-076-6 3025 1 MATAERRALGIGFQWLSLAT......QAPPPNRAPPPSRPPRPSV 564 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

528882 seqs, 175299045 residues Searched:

528882 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/paa/USO6\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/paa/USO3\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/paa/USO3\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/paa/USO3\_NEW\_COMB.pep:\*

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7: /cgn2\_6/ptodata/2/paa/USO3\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 187, App	232,	1823,		301,	-	18	2, 1	24	20,	Sequence 26, Appl	22,	14,	16,	10,		2639		10	8			Sequence 99, Appl		Sequence 26246, A	Sequence 9405, Ap
SUMMARIES	ID	PCT-US02-08253-187	PCT-US02-08253-232	US-60-389-987-1823.	PCT-US02-08253-194	PCT-US02-08253-301	US-10-038-307-4	US-10-038-307-18	US-10-038-307-2	US-10-038-307-24	US-10-038-307-20	US-10-038-307-26	US-10-038-307-22	US-10-038-307-14	US-10-038-307-16	US-10-038-307-10	US-10-038-307-12	US-10-104-047-2639	US-10-038-307-6	US-60-373-595-10	US-10-038-307-8	US-10-125-540-312	US-09-629-469A-11706	US-10-047-542-99	US-09-935-625-9406	US-09-935-625-26246	US-09-935-625-9405
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æ	Query Match	100.0	100.0	100.0	95.9	95.9	66.7	54.9	54.5	54.5	54.5	54.1	54.0	53.9	53.9	53.5	49.2	46.8	46.7	46.7	46.2	39.9	31.9	29.9	7.0	7.0	7.0
	Score	3025	3025	3025	2901	2901	2017	1991	1649	1649	1649	1636	1634.5	1629	1629	1619	1488	1416.5	1411.5	1411.5	1396.5	1206.5	996	903	211	211	211
	Result No.	1	7	m	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26

	sequence 20244, A Sequence 9383, Ap Sequence 17852, A	Sequence 9382, Ap Sequence 17851, A Sequence 9381, Ap		5343, 8099,	Sequence 25320, A Sequence 899, App	Sequence 5342, Ap Sequence 8098, Ap	Sequence 25319, A Sequence 898, App	5341,
US-09-935-625-26245 US-09-935-625-9404	US-U9-935-625-26244 US-09-935-625-9383 US-09-935-625-17852	US-09-935-625-9382 US-09-935-625-17851 US-09-935-625-9381	US-09-935-625-17850 US-09-935-625-900	US-09-935-625-5343 US-09-935-625-8099	US-09-935-625-25320 US-09-935-625-899	US-09-935-625-5342 US-09-935-625-8098	US-09-935-625-25319 US-09-935-625-898	US-09-935-625-5341
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ESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKM
                                                   PEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTGR
                                                                                            CINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPPSAPTPPIPSPSTL
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SGQUENCE 232. AAPDLICATION FC/TUSO208253
GGENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: Carson-Walter, Eleanor
APPLICANT: Vogelated, Bert
APPLICANT: Vogelated, Bert
APPLICANT: Vogelated, Bert
APPLICANT: Windler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REPERBENCE: 1107.00179
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FRASLSEQ for Windows Version 4.0
SEQ ID NO 232
LENGTH: 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                        PPPPQAPPNRAPPPSRPPRPSV 564
                                                                                                                                                                                   ; ORGANISM: Homo sapiens
PCT-US02-08253-232
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                             PEQEYEFPEPRILININMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTGR 480
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Sequence 1823, Application US/60389987
Sequence 1823, Application US/60389987
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Boin D.
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary W.
APPLICANT: Steven W.
APPLICANT: Glenn, Gary W.
APPLICANT: Taylor W.
APPLICANT: Glenn, Gary W.
APPLICANT: Taylor W.
APPLICANT: Glenn, Gary W.
APPLICANT: Glenn, Grenn, Grenn
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100.0%; Pred. No. 3e-176;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 564; Conservative
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; ORGANISM: Homo sapiens
US-60-389-987-1823
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GLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKMPEQEYEFP 428
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SVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPAEESEEDDDD
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GENERAL INFORMATION:

APPLICANT: Carson-Walter, Eleanor

APPLICANT: Carson-Walter, Eleanor

APPLICANT: St. Croix, Brad

APPLICANT: Vogelstein, Bert

APPLICANT: Worler, Kenneth

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REFERENCE: 1107.00179

CURRENT APPLICATION NUMBER: PCT/USO2/08253

CURRENT APPLICATION NUMBER: 60/282,850

PRIOR PELING DATE: 2001-04-11

PRIOR PELING DATE: 2001-04-11

PRIOR PELING DATE: 2001-04-11

PRIOR PELING DATE: 2001-08-01

WUMBER OF SED ID NOS: 359

SOFTWARE: FastSEQ for Windows Version 4.0
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96.8%; Pred. No. 1e-168;
1ve 7; Mismatches 1
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538; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Mouse
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PCT-US02-08253-301
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Best Local Si
Matches 538;
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                                                                                            LAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQCLEELQKVLPGGDTYMHEGFERAS 128
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ESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKM 420
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                          PEQEYEFPEPRILININMRRPSSPRKWYSPIKGKLDALWYLLRKGYDRVSVMRPQPGDTGR
                                       CINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPPSAPTPPIPSPPSTL
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                                                                                                                                                                                                                                                   APPLICANT: Carson-Walter, Eleanor
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Kincler, Reneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
NUMBER OF SEQ. ID NOS: 359
SOFTWARE: FRASESQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2901; DB 1;
Pred. No. 1e-168;
7; Mismatches 11;
                                                                                                                                                                                                                              Sequence 194, Application PC/TUS0208253 GENERAL INFORMATION:
                                                                                                                                 PPPPQAPPNRAPPPSRPPRPSV 564
                                                                                                                                                Query Match 95.9%;
Best Local Similarity 96.8%;
Matches 538; Conservative
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PCT-US02-08253-194
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Query Match
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Matches 318;
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LENGTH: 333
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                                              LENGTH: 551
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(9S-10-038-307-18

(9S-10-038-307-18

SEQUENCE 18, APPLICATION

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

APPLICANT: Judith J. HEALEY

APPLICANT: TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Budith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REPERENCE: 7863-253-999
CURRENT ELLING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 381
TYPE: PRT
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Pred. No. 3.7e-115;
3; Mismatches 4;
                                                                                                                     Sequence 4, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTIMAN
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98.1%;
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Best Local Similarity
Matches 371; Conserv
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US-10-038-307-4
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                                                                                                                                                                                                                                                                                                                 61 BIXYEVBOLAHKEISPOLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
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; Sequence 2, Application US/10038307
; Sequence 2, Application US/10038307
; GENERAL INFORMATION:
    APPLICANT: Theresa L. O'KEFF
    APPLICANT: Theresa L. O'KEFF
; APPLICANT: Theresa L. O'KEFF
; APPLICANT: Theresa D. O'KAYNAK
; APPLICANT: Theresa D. O'KAYNAK
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
; CURRENT APPLICATION NUMBER: US/10/038,307
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 7.5e-93;
                                                                                                                                                                             54.9%; Score 1661; DB 6;
100.0%; Pred. No. 2.5e-93;
Live 0; Mismatches 0;
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NUMBER OF SEQ ID NOS: 26
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
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Best Local Similarity 100.
Matches 320; Conservative
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US-10-038-307-2
                                                                                                     TYPE: PRT ORGANISM: Homo sapiens US-10-038-307-18
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APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILLE REPERBLOE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 20
ILENGTH: 564
TYPE: PAT
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEFFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FRASESEQ for Windows Version 4.0
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100.0%; Pred. No. 4.6e-92;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                           54.5%; Score 1649; DB 6; 100.0%; Pred. No. 1.4e-92;
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Matches 318; Conservative
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US-10-038-307-20
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US-10-038-307-26
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Matches 316; Conserv
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TYPE: PRT
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                                                                                     HEGFERASEQIYYENROGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV
                                                                                                                                                                  KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
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100.0%; Pred. No. 7.8e-93;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/10038307; GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEFFE
APPLICANT: Judith J. HEALEY
ITLE OF INVENTION: Tango 197 and Tango 216 Com
FILE REFERENCE: 7853-223-999
CURRENT APPLICATION NUMBER: US/10/038,307;
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LLORGTH: 345
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Best Local Similarity 100.
Matches 318; Conservative
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US-10-038-307-24
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US-10-038-307-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.9%; Score 1629; DB 6; 98.8%; Pred. No. 2.2e-91; tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Thereas L. O'KEEFE
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Com
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
SOFTWARE: PASLSEQ for Windows Version 4.0
Sequence 14, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Com
TITLE OF INVENTION: Tango 197 and Tango 216 COM
TITLE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 543
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98.8%;
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Best Local Similarity 98.8
Matches 317; Conservative
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Best Local Similarity 98.8
Matches 317; Conservative
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US-10-038-307-16
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US-10-038-307-14
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US-10-038-307-16
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                                                                                       HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                             KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
              EIYYEVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEBEE
APPLICANT: Theresa L. O'KEBEE
APPLICANT: Theresa U. O'KEBEE
TITLE OF INVENTION: Tango 197 and Tango 216 Com
FILE REFERENCE: 7853-553-99
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE FASTSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 342
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ORGANISM: Homo sapiens
US-10-038-307-22
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Matches 318; Conserv
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US-10-038-307-22
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US-10-038-307-14
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Length 543;
              Indels
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Score 1629; DB Pred. No. 2.2e-90; Mismatches
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Compositions and

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Sequence 10, Application US/10038307

GENERAL INFORMATION:
APPLICANT: James B. ROTHMAN
APPLICANT: Theresa L. O'REEFE
APPLICANT: Engin OZRAYNAK
TITLE OF INVENTION: Tango 197
TITLE OF INVENTION: Tango 197
CURRENT APPLICANT: 2020-06-28
CURRENT APPLICANT: US/10/038,307
CURRENT FILING DATE: 2020-06-28
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 10
SEQ ID NO 10
SEQ ID NO 10
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                                                      61 EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                     HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
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Pred. No. 8.8e-91;
0; Mismatches 3;
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Best Local Similarity 98.4<sup>1</sup>
Matches 316; Conservative
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Search completed: August 9, 2002, 10:35:57 Job time: 355 sec us-09-970-076-6.rapn

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 9, 2002, 10:44:30; Search time 507.33 Seconds Run on:

(without alignments)
391.298 Million cell updates/sec

3025 1 MATAERRALGIGFÜWLSLAT......QAPPPNRAPPFSRPPRPSV 564 9-920-026-60-sn Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

3502263 segs, 351980561 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2\_6/ptodata/2/paa/US101\_COMB.pep:\*/cgn2\_6/ptodata/2/paa/US60\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Sequence 187, App	Sequence 232, App	Sequence 6, Appli	Sequence 194, App	Sequence 301, App	Sequence 57, Appl	Sequence 57, Appl
SUMMARIES			ID		US-09-918-715-187	US-09-918-715-232	9-910-016-60-sn	US-09-918-715-194	US-09-918-715-301	PCT-US99-31025-57	US-09-471-179-57
			DB	1	23	23	23	23	23	_	18
			Match Length DB ID	1 1 1 1 1	564	564	564	562	262	381	381
	æ	Query	Match		100.0	100.0	100.0	95.9	95.9	66.7	66.7
			Score		3025	3025	3025	2901	2901	2017	2017
		Result	NO.		٦	7	e	4	Ŋ	9	7

Sequence 24, Appl Sequence 2, Appl Sequence 61, Appl Sequence 621, Appl Sequence 621, Appl Sequence 620, Appl Sequence 600, Appl Sequence 9, Appl Sequence 9, Appl Sequence 9, Appl Sequence 12, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 30, Appl Sequence 51, Appl Sequence 107, Appl Sequ	, , , , , , , , , , , , , , , , , , ,
	6 US-60-324-050 6 US-60-324-050 6 US-60-324-246
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## ALIGNMENTS

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APPLICANT: Brad St. Croix
APPLICANT: Brad St. Croix
APPLICANT: Brad St. Croix
APPLICANT: Brat Vogelstein
APPLICANT: Renneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 187
LENGTH: 564
                       Sequence 187, Application US/09918715 GENERAL INFORMATION:
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US-09-918-715-187
US-09-918-715-187
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Gaps ö Length 564; Indels Ouery Match 100.0%; Score 3025; DB 23; Best Local Similarity 100.0%; Pred. No. 1.4e-192; Matches 564; Conservative 0; Mismatches 0;

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; Pred. No. 1.4e-192;
0; Mismatches 0; I)
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GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Brad St. Croix
APPLICANT: Brad St. Croix
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATITIC OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATITIC OF INVENTION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR PILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR PLING DATE: 2000-08-11
PRIOR PLING DATE: 2000-08-11
PRIOR PLING DATE: 2000-08-11
NUMBER OF SEG ID NOS: 358
SOFTWARE: FRESEE FOR WINDOWS VERSION 3.0
SEQ ID NO 232
                                                                                                                                                                                                                                                                                                                                                                                       541 PPPPQAPPPNRAPPPSRPPRPSV 564
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Best Local Similarity 100.0%;
Matches 564; Conservative 0;
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US-09-918-715-232
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US-09-918-715-232
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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180
                                                                     ESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKM
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                                                                                                            KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
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100.0%; Score 3025; DB 23;
Best Local Similarity 100.0%; Pred. No. 1.4e-192;
Matches 564; Conservative 0; Mismatches 0;
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APPLICANT: Young, John A.T.
APPLICANT: Coller, Rebert J.
APPLICANT: Coller, Robert J.
APPLICANT: Mogridge, Jeremy S.
APPLICANT: Mogridge, Jeremy S.
FILLE REFERENCE: 960296.9776.
CURRENT APPLICATION NUMBER: US/09/970,076
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 2001-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              564
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                                                                                              ARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISS
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                                          ARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bert Vogelstein
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REPERENCE: 1107.00134
CURRENT FILIOT.00134
CURRENT FILIOG DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
SPRIOR FILING DATE: 2000-04-11
SPRIOR FILING DATE: 2000-04-11
SPRIOR FILING DATE: 2000-04-11
SEQ ID NO 301
LENGTH: 562
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llarity 96.8%; Pred. No. 2.5e-184;
Conservative 7; Mismatches 11;
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Best Local Similarity
Matches 538; Conserv
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; ORGANISM: Mouse
US-09-918-715-301
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                                                                                                                      CINFTRVKNNOPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPPSAPTPPIPSPPSTL
                HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV
                               KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
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GENERAL INFORMATION:
APPLICANT: Beat Vogelstein
APPLICANT: Beat Vogelstein
TITLE OF INFORMATION: ENDOTHELIAL CELL EXPRESSION PAT':
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SEOTTWARE: FESTSEQ FOI WINDOWS VERSION 3.0
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Pred. No. 2.5e-184;
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96.8%;
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Matches 538; Conservative
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US-09-918-715-194
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LENGTH: 562
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                                                 VKNNQPAKYPLNNAYHTSSPPAPIYTPPPPAPHCPPPPSAPTPPIPSPPGTLPPPQA 546
FPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTGRCINFTR 303
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Sequence 57, Application US/09471179
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REPERBENCE: 7853-173
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
NUMBER: CONTROL OF THE PROTEIN OF THE PROT
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 57
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0.8-09-196-753-24

Sequence 24, Application US/09796753

; GENERAL INFORMATION:
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98.1%;
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Best Local Similarity 98.1
Matches 371; Conservative
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                                                             ARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRH
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Pred. No. 1e-125;
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98.1%;
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ses 371; Conserv
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CRGANISM: Mouse
PCT-US99-31025-57
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    FPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPOPGDTGRCINFTR
                                                                                                                                                                                        VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN
                                                                             DDGLPKKKWPTVDASYYGGRCVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKMPEQEYE
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Best Local Similarity 100.0%; Pred. No. 1.5e-117;
Matches 364; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Collier, Robert J.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor FILE REFERENCE: 960296.97745
CURRENT APPLICATION NUMBER: US/09/970,076
CURRENT FILING DATE: 2001-10-03
PRIOR PRICIATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEO ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09970076 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            547 PPPNRAPPPSRPPRPSV 564
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ORGANISM: Homo sapiens
US-09-970-076-2
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PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR PLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1999-02-26
PRIOR PLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-05-14
PRIOR PILING DATE: 1999-06-18
PRIOR PILING DATE: 1999-06-19
PRIOR PILING DATE: 1999-06-30
PRIOR PAPLICATION NUMBER: 09/345,464
PRIOR PILING DATE: 1999-07-30
PRIOR PAPLICATION NUMBER: 09/471,179
PRIOR PILING DATE: 1999-09-20
PRIOR PILING DATE: 1999-12-29
PRIOR PILING DATE: 1999-12-29
PRIOR PILING DATE: 1999-12-29
PRIOR PILING DATE: 1999-12-29
PRIOR PAPLICATION NUMBER: 09/474,072
PRIOR PILING DATE: 1999-12-29
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-06-19
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
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Best Local Similarity 98.1%;
Matches 371; Conservative
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Best Local Similarity
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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                                                                                                                                                                                                               181 KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
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                                                                                                                                                                   Indels 11;
                                                                                                                                   DB 1; Length 403;
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62.6%; Score 1893.5; DB 2
Best Local Similarity 94.8%; Pred. No. 1.9e-117;
Matches 367; Conservative 2; Mismatches 7;
                                                                                                                                     Score 1893.5; DB 1
Pred. No. 1.9e-117;
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Sequence 621, Application US/09833245;
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/226, 931
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER: OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 621
LENGTH: 403
                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 ESEVSDHSRMA------VGGQG 376
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                                                                                                                                            62.6%;
94.8%;
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NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver.
SEQ ID NO 621
LENGTH: 403
                                                                            ), ORGANISM: Homo sapiens
PCT-US01-11988-621
                                                                                                                                                             Similarity
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Matches 367;
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                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 403;
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                                                                                                                                   TITLE OF INVENTION: 28 Human Secreted Proteins FILE REFERENCE: PS708PCT CURRENT APPLICATION NUMBER: PCT/USO0/30045 CURRENT FILING DATE: 2000-11-01 PRIOR APPLICATION NUMBER: 60/215,133 PRIOR FILING DATE: 1999-11-05 PRIOR FILING DATE: 2000-06-30 NUMBER: 60/215,133 PRIOR FILING DATE: 2000-06-30 NUMBER: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 621, Application PC/TUS0111988
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: PCT/US01/11988
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
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                                                                                           Sequence 94, Application PC/TUS0030045
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc
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Best Local Similarity 94.8
Matches 367; Conservative
                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
PCT-US00-30045-94
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PCT-US01-11988-621
                    361 ESEE 364
                                                                                 PCT-US00-30045-94
                                                                                                                                                                                                                                                                                                       SEQ ID NO 94
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LOCATION: (368)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
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llarity 98.6%; Pred. No. 3.7e-116;
Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                               Sequence 620, Application PC/TUS0111988
GEMERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: PCT/US01/11988
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR PELLON NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 620
LENGTH: 403
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OTHER INFORMATION:
NAME/KEY: SITE
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OTHER INFORMATION:
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OTHER INFORMATION:
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. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-USO0-30045-125
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                               DGLSFISSSVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPAE
                                                                          HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV
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Pred. No. 3.7e-116;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: 28 Human Sciences, Inc.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PS708PCT:
CURRENT APPLICATION NUMBER: PCT/US00/30045
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR APPLICATION NUMBER: 60/215,133
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 2000-06-30
SOFTWARE: PATENTING DATE: 2000-06-30
SOFTWARE: PATENTING DATE: 2000-06-30
SOFTWARE: PATENTING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 125, Application PC/TUS0030045 GENERAL INFORMATION:
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Best Local Similarity 98.6%;
Matches 361; Conservative (
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FEATURE:
MAME/KEY: SITE
LOCATION: (175)
OTHER INFORMATION: Xaa ec
NAME/KEY: STE
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OTHER INFORMATION: Xaa ec
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LOCATION: (331)
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PCT-US00-30045-125
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Job time: 869 sec
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prognosis; prophylatic; therapeutic; mouse
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| SIDS1/gcddata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS1/gcddata/hold-geneseqy-embl/AA1981.DAT:*
| SIDS1/gcddata/hold-geneseqy-embl/AA1983.DAT:*
| SIDS1/gcddata/hold-geneseqy-embl/AA1985.DAT:*
| SIDS1/gcddata/hold-geneseqy-embl/AA1986.DAT:*
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| SIDS1/gcddata/hold-geneseqy-geneseqp-embl/AA1990.DAT:*
| SIDS1/gcddata/hold-geneseqy-geneseqp-embl/AA1990.DAT:*
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                                                                                                                                                                                                                                                                                                                     1 MATAERRALGIGFOWLSLAT......OAPPPNRAPPPSRPPRRSV 564
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Compugen Ltd.
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  GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maximum Match 100%
Listing first 45 summaries
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AAB01422
AAB18456
AAB18447
AAB18455
AAB18455
AAB18458
AAB18460
                                                                                                         protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0, Gapext 0.5
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seq length: 200000000
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1874
1874
1412.5
1409.5
1397.5
1396.5
                                                                                                                                                                                                                                                                                            Perfect score:
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Maximum DB
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WPI; 2000-465743/40

Result No.

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Mammalian Ena (Men
Cotton fiber-speci
Sugar beet chitina
Human WASP protein
Amino acid sequenc
Novel human diagno
Drosophila melanog
Drosophila melanog
                                                                                   Human polypeptide
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Novel human diagno
Arabidopsis thalia
Human WAVEZ protei
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Carrot extensin.
Novel human diagno
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Mouse neural Mena+
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Murine WASP protei
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Human polypeptide
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Human polypeptide
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                                                          Human polypeptide
                                                                                                                                                                                                                                                                                             Mammalian enabled
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                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                               AAG46150
ABG27250
AAG49660
AAB73400
                                                                                                                                                                                                                        AAG67333
ABG14000
ABB70063
                                                                                                                                                                                                                                                     ABB58220
AAW37151
AAW37152
AAW37153
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AAG46152
AAG46151
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ABG21919
                                                                                                                                                                                                      AAR28150
AAM52315
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                            AAB92985
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                   AAU19662
                                                                                                                                                                                                                                                                                                                                                                                                    AAB01428 standard; Protein; 381 AA
                                                                                                                                                                                    AAW37
 (first entry)
1393.5
1392
1206.5
966
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Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory bowel diseases, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cacheria and autoimmune diseases e.g. myasthemia gravis, autoimmune diabetes and systemic disease, osteoarthritis, Lyme's disease, osteoarthritis, Lyme's disease, cacheria and systemic ransgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in the TANGO parmacogenomics and for monitoring clinical trials. TANGO pharmacogenomics and for monitoring clinical trials. TANGO copypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a continual and the continual and the continual and the continual and contin
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abnormality; developmental abnormality; haematopoietic disorder;
                   Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 RHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFI 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%; Score 2017; DB 21;
98.1%; Pred: No. 1.9e-151;
tive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of cellular disorders can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE01439 standard; Protein; 403 AA.
                                                                                                                                  Claim 8; Fig 27; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPPNRAPPPSRPPRPSV 564
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Best Local Similarity 98.1
Matches 371; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381 AA;
N-PSDB; AAA47479
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foetal
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AAE01439
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486

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AMD05300-AMD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE0136-AAE01513 represent the proteins they encode. CC AAE01514-AAE01544 represent human secreted protein fragments or variants. CAE01514-AAE01544 represent human secreted protein fragments or variants. CE AAE01514-AAE01544 represent human secreted protein or or variants. CC The genes and their secreted proteins are useful for preventing, therefore the protein or gene therapy. Pathological conditions can be diagnosed by determining the therapy. Pathological conditions can be diagnosed by determining the experience of amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the proliferative disorders, cancer, rumours, foetal and developmental conflict disorders, diseases of the immune system, abnormalities, haematopoietic disorders, disease, disease, allergies, neurological disorders, rehumatoid arthritis), inflammation, attended disorders, schizophrenia, asthma, conflicted disorders, schizophrenia, asthma, conflicted disorders, pregnancy-related disorders, end infections. The proteins can also be used to aid wound disorders, pregnancy-related disorders, and can be used conflict or apporting partners, and in chemotraxis, and can be used conflict or a protein of the invention conflictioned above, and allergating symptoms associated with the disorders mentioned above, and indiagnostic immunosasays e.g., radioimmunosasay or enzyme linked in immunosubent assay (ELISA). The present sequence represents a human immunosorbent assay (ELISA). The present sequence represents a human immunosorbent assay (ELISA). The present sequence represents an human immunosorbent assay (ELISA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy, neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder: schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; pregnancy-related disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; chromosome 19.
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                                                                                                                                                                                                                                                                                                                                                                          "Mature human secreted protein"
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                                                                                                                                                                                                                                                                                                                                   'label= Signal_peptide
                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-2000; 2000WO-US30045.
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30-JUN-2000; 2000US-0215133.
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                                                                                                                                                                                                                                                     Homo sapiens.
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Ruben SM,
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                                                                                  EIXYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                                                            HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                                               KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
                                                                                                                                                                                     VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAFILKEVGMKAALQVSMN 300
                    Gaps
                                    1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; proliferative disorder; cancer; tumour;
Length 403;
                                                                                                                                                                                                                                                                                                                                                                                   Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:125.
Score 1893.5; DB 22; Length
Pred. No. 1.3e-141;
2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Mature human secreted protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label= Signal_peptide
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/note= "Encoded by
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62.6%;
94.8%;
                                                                                                                                                                                                                                                                                                                                                                (first entry)
Query Match 62.6
Best Local Similarity 94.8
Matches 367; Conservative
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The genes and their secreted proteins are useful for preventing.

The genes and their secreted proteins are useful for preventing.

The genes and their secreted proteins are useful for preventing.

The genes and their secreted protein or gene

therapy. Pathological conditions can be diagnosed by determining the

amount of the new protein in a sample or by determining the presence of

mutations in the new genes. Specific uses are described for each of the

28 genes, based on the tissues in which they are most highly expressed,

and include developing products for the diagnosis or treatment of

proliferative disorders, cancer, tumours, foetal and developmental

abnormalities, haematopoietic disorders, diseases of the immune system,

AIDS, autoimmune diseases (e.g., rheumatid arthritis), inflammation,

allerytes, neurological disorders, (e.g., Alzheimer's disease,

Parkinson's disease), cognitive disorders, schizophrenia, asthma,

allerytes, neurological disorders, eraciopercens, atheroscalers,

cardiovascular disorders, pregnancy-related disorders, endocrine

disorders, and infections. The proteins can also be used to ald wound

the aling and epithelial cell proliferation, to prevent skin aging due to

sunburn, to maintain organs before transplantation, for supporting cell

culture of primary tissues, to regenerate tissues, to identify their

cognate ligands or binding partners, and in chemotaxis, and can be used

as a food additive or preservative to modify storages mentioned above, and

in disorder; supporting or prevent existin in the disorders mentioned above, and

alsorders and in the disorders and in the provent existin in the disorders and in the disorders mentioned as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in in disorder in the disorders mention the disorders and in the disorders and in the disor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode. AAE01514-AAE01544 represent human secreted protein fragments or variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecules encoding 2\theta human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birse CE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 505-506; 562pp; English.
/note= "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                               01-NOV-2000; 2000WO-US30045.
                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000; 2000US-0215133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Komatsoulis GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 361; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-308778/32.
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disorder associated with aberrant TANGO expression. A wide range of cellular disorders can be treated.
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                                                                                                              Matches 318; Conservative
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                                                                                    Query Match
Best Local Similarity
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                                                333 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB18456;
                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory bowel diseases, septic shock, ulcerative colitis, Crohn's disease, chronic myelogencus leukemia, cancer, liver disease, Hodgkin's chronic myelogencus leukemia, cancer, liver disease, Hodgkin's chronic myelogencus leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachexia and autoimmune clasease e.g. myasthemia gravis, autoimmune diabetes and systemic lugus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO phyreptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                               TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; crohn's disease; chronic myelogenous leukemia; cancer; liver disease; chronic myelogenous leukemia; cancer; liver cachexia; autoimmune disease; myasthemia gravis; autoimmune disease; systemic lupus erythematosus; transgenic animal; diagnosis; prophylatic; therapeutic; human.
                                                                                                                  VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN
                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Fig 4; 209pp; English.
                                                                                                                                                                                                                                                                     AAB01422 standard; Protein; 333
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N-PSDB; AAA47455.
                                                                                                                                                                                                                                                                                                                                                 Human TANGO 197
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TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular adhesion; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; when atopicatic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammathon; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 VRGNGFRHARNVDRVLCSFKINDSVILNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
                                                                                                                                                                                                                                                                                                                                                                             181 KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
                                                                                                                                                                                                                                                                                                                                                                                                       EIYYEVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                                                                                                                                                              121 HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
                                                                                                                      1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
                                                  ö
Length 333;
                                                  Indels
  54.5%; Score 1649; DB 21;
100.0%; Pred. No. 2.2e-122;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sharp JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A human TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB18456 standard; Protein; 488 AA.
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AAB18447 standard; Protein; 488 AA

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RESULT AAB18447

(first entry)

15-JAN-2001 AAB18447;

AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 261, TANGO 261, TANGO 262, and TANGO 267. The TANGO 260 polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular adhesion, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or cedema, emphysema, chronic bronchitis, bronchial asthma and bronchiactasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders note: the present sequence does not appear in the specification; it was created using information provided. Novel human and murine secreted proteins designated TANGO 216, 261, 266, 266 and 267 useful as modulating agents of cellular processes, Disclosure; Page -; 175pp; English. for treating cancer e.g. 

488 AA; Sequence

4; 63 YYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHE 122 GFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD 182 FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 242 GNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDG 302 LSFISSSVIITTTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPAEES 362 QEYEFPEPRNLNNNMRRPSSPR-----KWYSPIKGKLDALWVLLRKGYDRVSVMRPQ 474 Gaps 4 AERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEI 62 Length 488; Score 1412.5; DB 21; Length Pred. No. 2e-103; 77; Mismatches 123; Indels 46.78; Conservative PGDTGRCINFTRV 487 Similarity Query Match Best Local Simi Matches 274; 123 183 361 63 181 243 241 303 363 423 121 q g q 원 g õ g ò à ò g ò ð g ò à

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cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectrasis; puminonary conqestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; hallon, meningitis; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a human TANGO 216 polypeptide. The specification also describes TANGO 266, TANGO 261, TANGO 267. The TANGO Polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular dahesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cellular dahesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human and murine secreted proteins designated TANGO 216, 261, 265, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
                                                                                            FANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
                                                                                                                                                                                                                                                                                                                                                                                                                               "von Willebrand factor A domain"
                                                             Amino acid sequence of human TANGO 216 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser CC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "transnmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                  "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                  /note- "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                 "mature protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "cytoplasmic
                                                                                                                                                                                                                                                                                                      Jocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Fig 1A-C; 175pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                44..213
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                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                  Protein
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treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or ocedema, emphysema, chronic bronchlist, bronchlial asthma and bronchlectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or the disorder. They may also be used to treat disorders associated with the disorder. They may also be used to treat disorders associated with the disorder, inflammations, bacterial and viral meniations, latrogenic disease, inflammations, bacterial and viral meniations, latrogenic disease, inflammations, bacterial and viral meniations and treat hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 keeeeeplptkkwptvdasyyggrgvggikrmevrwgdkgsteegarlekaknavvkipe 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSFISSSVIITTTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPAEES 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 EEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKMPE 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 GFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                 YYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                    QEYEFPEPRNLNNNMRRPSSPR------KWYSPIKGKLDALWVLLRKGYDRVSVMRPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 GNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDG
                                                                                                                                                                                                                                                                                                                                                                  4 AERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEI
                                                                                                                                                                                                                                                                                                     DB 21; Length 488;
                                                                                                                                                                                                                                                                                                     ; Score 1411.5; DB 2]
; pred. No. 2.3e-103;
77; Mismatches 123;
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55.6%;
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Best Local Similarity 55.6%
Matches 274; Conservative
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AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 267. The TANGO 260 closures and the specification and control of the specification and control of the specification. The cellular differentiation and control of modulate cellular adhesion. The cellular differentiation and control of social trafficking and control of migration, modulate cellular differentiation, and land actor-associated and cell trafficking and control of second cellular interactions, and the proliferation of interaction of cells modulate the proliferation, and leukocytes, treat bone marrow, blood cell of that appear in the bone marrow, and leukocytes, treat bone marrow, blood cellular interaction of cellular interactions, interactional disorders, atelectasis, or or ocdema, emphysema, chronic bronchiticis, bronchiticitation, and forming disorders, such diseases, modulate the proliferation differentiation, as ischemic heart disease, modulate the proliferation differentiation, and cerebral ocdema, treat disorders associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to complain beniations, latrogenic disease, cerebral bacterial and viral meningitis, alzheimer's Disease, cerebral cartilage and encephalitis, and treat hepatic disorders.

Cy created using information provided.
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 ENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 ISPOLRMSFIVFSTRGTTLMKLIEDREQIRQGLEELOKVLPGGDTYMHEGFERASEQIYY 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
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                                                                                                                                                                                                                                                                                                                                                                                                                   JD,
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56.2%; Pre-
tive 77;
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Matches 271; Conserv
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15-JAN-2001 (first entry)
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D
                                                                                                                                                                                                                                                                                                                                                                                              TANGO 266; TANGO 216;; TANGO 261; TANGO 267;
cellular proliferation; cellular differentiation; cellular adhesion;
on Willebrand factor associated disorder; cell trafficking; cancer;
hematopoietic associated disease; atelectashs; pulmonary congestion;
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectashs;
intestinal disorder; spleen associated disease; renal disorder;
cardiovascular disorder; ischemic heart disease; hydrocephalus;
brain hernlation; iatrogenic disease; inflammation; meningitis;
Alzhelmer's Disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate
                                                                                                                     371
                                                                                                                                                    485
                                                                                              314 TTHCSDGSILAIALLILELLLALALLWWFWPLCCTVIIKEVPPPPAEESEEEDDDGLPKK 373
                                                                                                                                                                                                || |----rpprpkpthqppqtkwytpikgrldalwallrrqydrvslmrpqegdegrcinfs 483
          SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
                                                                                                           KWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEECAKLEKAKNARVKMPEQEYEFPEPRNL
                                                     RVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIIT
                                                                                                                                                                                      434 NNNMRRPSSPR-----KWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTGRCINFT
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                                                                                                                                                                                                                                                                                                                                                                            human TANGO 216 polypeptide clone.
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cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate the proliferation, differentiation, and/or function of cells modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysemm, chronic bronchills, bronchial sthma and bronchiectasis, intestinal disorders, spleen associated disease, modulate the proliferation, differentiation, as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder, They may also be used to treat disorders associated with the ovaries, and cerebral cedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

Created using information provided.
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55.4%; Pred. No. 4.1e-103;
1ive 78; Mismatches 123; Indels
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Best Local Similarity 55.49
Matches 273; Conservative
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MHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVG

60 NEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTY

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358 apmceeeedplpnkkwptvdasyyggrgvggikrmevrwgdkgsteegarlekaknavvm 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 VKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQV
                                                                                                                                                                                                                                                                                                                                                                 360 EESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVK
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                                                                         rango 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; latrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser CC;
                                   A murine TANGO 216 polypeptide clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2000; 2000WO-US05226.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holtzman DA,
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TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; won Willebrand factor-associated disorders; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; ocdema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; achemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                             Amino acid sequence of a murine TANGO 216 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                       "transnmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "extracellular domain"
                                                                                                                                                                                                                                                                                                             "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                 "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                            /noce= "cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                         "mature protein"
                                                                                                                                                                                                                                                                                   /note= "signal peptide"
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342..48
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Gaps

46.2%; Score 1397.5; DB 21; Length 487; 54.8%; Pred. No. 3e-102; tive 72; Mismatches 131; Indels 21;

Conservative

272;

Best Loca Matches

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Similarity

Query Match Local

487 AA;

1 MATAERRALGIGFQWLSLATLVLICAGOGG-RREDGGPACYGGFDLYFILDKSGSVLHHW

(first entry)

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4 20 MPEQEYEFPEPRNLNNNMRRPSSPR-----KWYSPIKGKLDALWVLLRKGYDRVSVM 471
ndgksavsrsltitatectngiaaivailvlllllgaalmwwfwplcckvvikdppppps 357
                                                               360 EESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDGLSFISSSVIITTTHCSDGSILAIALLILFLLIALALLHWWFWPLCCTVIIKEVPPPPA 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 VVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSM 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                             Fraser CC;
                                                                                                                                                                                                                                                                                             Sharp JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Fig 2A-C; 175pp; English.
                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC.
                                                                                                 01-MAR-2000; 2000WO-US05226.
                                                                                                                                                             99US-0122458.
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                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-579269/54.
N-PSDB; AAA75150.
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Matches 272;
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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO cestibles TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular adhesion. modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, cand hematopoietic associated diseases and disorders, spleen associated asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                         hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain hernlation; latrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                PANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267
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                                                                                                                                                                                                              AAB18460 standard; Protein; 487 AA.
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                                                               472 RPQPGDTGRCINFTRV 487
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rpqegdegrcinfsrv 484
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as ischemic heart disease, modulate the proliferation, differentiation and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral cedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalits, and treat hepatic disorders. In once: the present sequence does not appear in the specification; it was created using information provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDGLSFISSSVIITTHCSDGSILAIALLLFLLLALALLWWFWPLCCTVIIKEVPPPPA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 EESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVK 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420 MPEQEYEFPEPRNLNNNMRRPSSPR-----KWYSPIKGKLDALWVLLRKGYDRVSVM 471
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                                                                                                                                                                                                                                                                                                                                                                                                 MHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVG 179
                                                                                                                                                                                                                                                                            21; Gaps
                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MATAERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHW
                                                                                                                                                                                                                                                                                                                               Length 487;
                                                                                                                                                                                                                                          46.1%; Score 1395.5; DB 21; Lengt
54.8%; Pred. No. 4.3e-102;
.ive 72; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A murine TANGO 216 polypeptide clone.
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Matches 272;
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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 267, and TANGO 267. The TANGO 266 TANGO 266, TANGO 266, TANGO 267. The T
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                                                                                                                                                                                                                                                                                                                                                                                                              Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes. e.g. for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MATAERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHW
Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21; Length 487;
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54.6%; Pred. No. 6.2e-102;
iive 73; Mismatches 131;
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                                                                                                                                                                                                                                                                                                                               Fraser
                                                                                                                                                                                                                                                                                                                               Sharp JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                              99US-0122458.
                                                                                                                                                                                                     01-MAR-2000; 2000WO-US05226.
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                                                                                                                                                                                                                                                                                                                                 Holtzman DA,
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                                                                                                                    WO200052022-A1
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31-JAN-2000; 2000US-0179065.04-FEB-2000; 2000US-0180628.
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C.N.S disorders.
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                                                                                                                                                                                                                    specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang D;
                                                                                                                                                                                                                                                        peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehmer's; Parkinson's disease; Heamostetic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                         VVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSM
                                    NDGLSFISSSVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPA
                                                                                                                                                            360 EESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVK
                                                                                                                                                                                               358 apmeeeeedplpnkkwptvdasyyggrgyggikrmevrwgdkgsteegarlekaknavvm
                                                                                                                                                                                                                                   MPEQEYEFPEPRNLNNNMRRPSSPR-----KWYSPIKGKLDALWVLLRKGYDRVSVM
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Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; nootropic; immunosuppressant; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qian XB,
Yang Y,
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Xu C, Xue AJ,
R, Drmanac RT;
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Wehrman T, Xu
Goodrich R,
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2000US-052317.
2000US-0520312.
200US-053450.
200US-0653450.
200US-0653450.
200US-0633036.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
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19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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25-APR-2000;
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in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/hibhin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and thrombolytic activity, cancer diagnosis and thrombolytic activity.
                                                                                                                                                                                                                                                                                     ombolytic activity, cancer diagnosis and therapy, drug screening, for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted extracellular matrix protein; immunomodulatory;
Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; vascular;
cerebroprotective; thrombolytic; antimicrobial; ophthalmic; eytostatic;
antialzheimers; immune/autoimmune disease; HIV infection; anaemia;
human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
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Pred. No. 4.3e-102;
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Matches 267; Conservative
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0000us-0184664 0000us-0186350 0000us-018974 0000us-0199075 0000us-0293512 0000us-0209467 0000us-021513 0000us-021513 0000us-021513 0000us-021748 0000us-021748 0000us-021748	200008-022513. 200008-0225213. 200008-022526. 200008-022526. 200008-022526. 200008-0225270. 200008-022576. 200008-022575. 200008-022575. 200008-022575. 200008-022575. 200008-022576. 200008-022770. 200008-022784. 200008-022887. 200008-022887. 200008-022887. 200008-022887. 200008-022887. 200008-022887. 200008-022887. 200008-022887. 200008-022887. 200008-022887. 200008-022887.	20000S-02323 20000S-02323 20000S-02323 20000S-02324 20000S-02324 20000S-02330 20000S-02330 20000S-02330 20000S-02340 20000S-02340 20000S-02340 20000S-02340 20000S-02360
24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000; 18-MAY-2000; 07-JUN-2000; 07-JUN-2000; 07-JUL-2000; 07-JUL-2000; 11-JUL-2000; 11-JUL-2000; 11-JUL-2000; 26-JUL-2000;	14-AUG-2000; 13-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 16-AUG-2000; 17-AUG-2000; 18-AUG-2000; 18-AU	0.8 SEP - 2000 14 - SEP - 2000 15 - SEP - 2000 21 - SEP - 2000 21 - SEP - 2000 22 - SEP - 2000 25 - SEP - 2000 26 - SEP - 2000 27 - SEP - 2000 29 - SEP - 2000 20 - OCT - 2000 02 - OCT - 2000 02 - OCT - 2000 02 - OCT - 2000
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PR 02-CGT-2000; 2000BS-0239935.

PR 20-CGT-2000; 2000BS-0239935.

PR 20-CGT-2000; 2000BS-0239935.

PR 20-CGT-2000; 2000BS-0239935.

PR 20-CGT-2000; 2000BS-024126.

PR 20-CGT-2000; 2000BS-024126.

PR 20-CGT-2000; 2000BS-024136.

PR 20-CGT-2000; 2000BS-02446.

PR 20-CGT-2000

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EP1074617-A2
                                            07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
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                                                    The invention retailed witch call moretures acroading novel human secreted extracellular matrix proteins (SPS). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, dats, dogs, chickens or sheep. For example, disorders associated with decreased extracssion of SPS. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisens enlectules may be administered to treat diseases by gene therapy. The SPS may also be the cells own genes and preventing their expression. The polynucleotides may be administered to down regulate expression. The polynucleotides can also be used as DNA probes in diagnostic assays. The SPS may also be used as antigens to produce antibodies and to identify modulators used as antigens to produce antibodies and to identify modulators as also be used to down regulate expression and activity of SPS and as diagnostic agents for detecting the presence of SPS in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. cardiac Parkinsor's disease), neurological diseases (e.g. Alzheimer's disease, cartest, tachycardia and angina). Infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses tillude wound healing, maintenance of organs before transplantation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 TTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPAEESEEEDDDGLPKK 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 wlfpglwllvlsgpggllraqeqpscrrafdlyfvldksgsvanxwieiynfvqqlaerf 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 ISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENROGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 WLSLATLVLICAGGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKF 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 RVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to isolated nucleic acid molecules encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.9%; Score 1206.5; DB 22; Length 587; 56.2%; Pred. No. 5.1e-87; ive 67; Mismatches 111; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; SEQ ID No 312; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein sequence SEQ ID NO:11706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB92985 standard; Protein; 218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 56.29
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide comprises a 3'-end sequence, where the polynucleotide which comprises a 3'-end sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length AAH13613 to AAH13628 and AAH13633 to AAH13624 represent human anino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                  Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVNDGFOALOGIIHSILKKSCIEILAAEPSTICAGESFOVVVRGNGFRHARNVDRVLCSF
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                                                                                                                                                                                                                                                                  aito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                        Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID 11706; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 966; DB 22;
Pred. No. 1.5e-68;
                                                                                                                                                                                                                                                                                               Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                  Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                             sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                               99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.9%;
98.9%;
2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 31.9
Best Local Similarity 98.9
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the present invention.
                                                                                                                                                                                                                   (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218
                                                                                                        11-JAN-2000;
02-MAY-2000;
28-JUL-2000;
                                                                                                                                                             09-JUN-2000;
                                                  29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                               Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140
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Search completed: August 9, 2002, 10:32:13 Job time: 132 sec

us-09-970-076-6.rag

Fri Aug

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4.5
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2000
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- protein search, using sw model OM protein

Search time 61.73 Seconds •-August 9, 2002, 10:34:15 Run on:

(without alignments) 877.926 Million cell updates/sec

US-09-970-076-6 3025 1 MATAERRALGIGFQWLSLAT......QAPPPNRAPPPSRPPPRPSV Perfect score: Sequence: Title:

564

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 segs, 96089334 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		ď			SUMMARIES	
Result	Score	Query	Length	E	CL	Description
г	227		847		F96531	hypothetical prote
73	205.5		760		T06291	extensin homolog T
e	205		494		B96534	hypothetical prote
4	203		599		T10798	pherophorin-S - Vo
2	202		464		S22697	extensin - Volvox
9	201		1201		G86441	unknown protein [i
7	200.5	9	383		AE2295	hypothetical prote
ω	200.5	9.9	3124		A40020	collagen alpha 1(X
o	199.5	9.9	1392		T51947	probable transcrip
10	199	9.9	485	7	A33647	sulfated surface g
11	198	6.5	242		S54156	extensin-like prot
12	197.5	6.5	141		A34043	hypothetical proli
13	195.5	6.5	669		T05225	extensin homolog F
14	194	6.4	727	•	C84534	hypothetical prote
15	191.5	6.3	181	•	S14974	extensin class I (
16	191.5	6.3	306		A24354	precu
17	191.5		489	7	T11622	extensin class 1 p
18	191.5	6.3	708		D96711	hypothetical prote
19	191		322		825299	extensin precursor
20	189.5	6.3	388		S25298	extensin (clone To
21	189	6.2	368		C29356	hydroxyproline-ric
22	188.5	6.2	1206		S24407	formin isoform IV
23	188.5	6.2	1468		S11515	formin - mouse
24	186.5	6.2	163		A29356	hydroxyproline-ric
25	186	6.1	214		T10737	extensin-like cell
56	186	6.1	214		T09854	proline-rich cell
27	18	6.1	280		~	ike
28	185.5	6.1	439	7	S51939	chitinase (EC 3.2.
29	185.5	6.1	620	7	806733	hydroxyproline-ric

probable extensin	Wiskott-Aldrich sy	extensin-like prot	extensin class I (	extensin homolog H	extensin - almond	probable Pto kinas	extensin homolog F	extensin class I (	extensin CYC15 pre	extensin precursor	hypothetical prote	extensin class I (	hydroxyproline-ric	hypothetical prote	hypothetical prote
F84862	Appl9/	549915	S14970	T07623	S20790	F86387	T01456	S14981	T09964	T10863	E96636	S14972	A25494	D84672	T16342
~	7	7	N	~	a	N	~	~	7	~	N	a	7	7	7
212	205	1188	132	169	278	160	786	199	225	580	907	06	69	134	250
6.0 212		•													
	0.9	0.9	6.0		6.0	6.0	0.9	0.9	6.0	6.0		0.9	5.9	5.9	5.9

#### ALIGNMENTS

Н	
E	,

hypothetical protein F13F21.7 (imported) - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001
C; Accession: F96531
C; Authors: Hunter, J.L.; Mentlar, L.
Nature 408, 816-820, 2000
C; A.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia Rizzo, M.; Rooney, T.; Sakano, H.
S; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, W.; Wu, D.; Yu, G.; Fraser, C.H.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A66141; MUD:21016719
A; Residual type: DNA
A; Residual type: DNA
A; Residual type: DNA
A; Residual type: Lid A; CSTO>
A; Cross references: GB:AE005173; NID:g5430752; PIDN:AAD43152.1; GSPDB:GN00141

A; Map position: 1 Gene: F13F21.7

13; Gaps 88; Length 847; 60; Indels Ouery Match 7.5%; Score 227; DB 2; Best Local Similarity 31.5%; Pred. No. 3.7e-07; Matches 75; Conservative 15; Mismatches 60

355 PPPPAEES----EEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKL 410 ò

435 PQPPKHESPKPEEPENKHELPKQK-------ESPKPQPSKPEDSPKP 474 411 EKAKNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKW------YSPIKGKLDALWV 459 qq ò

475 EQPKPEESPKPEQP-QIPEP-----TKPVSPPNEAGGPTPDDPYDASPVK---a 460 LLRKGYDRVSVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAP 519 δ

520 HCPPPPP-SAPTPP---IPSPPSTLPPPPQAPPNRAPPP-----SRPPPRP 562 δ qq

557

qq

RESULT T06291

extensin homolog T9E8.80 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)

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Gaps

4;

Length 599; Indels

```
C;Species: Volvox carteri
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jul-2000
C;Datession: 322697; $21006
R;Ertl, H; Hallmann, A: Wenzl, S: Sumper, M.
EMED J. 11, 2055-2062, 1992
A;Title: A novel extensin that may organize extracellular matrix biogenesis in Volvox
A;Reference number: $22697; MuID:92289669
A;Accession: $22697;
  R;Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
EMBO J. 16, 25-34, 1997
EMBO J
                                                                                                                                                                                                        A;Cross-references: EMBL:V07752; NID:g1655698; PIDN:CAA69032.1; PID:g1655699
A;Cross-references: EMBL:V07752; NID:g1655699
A;Experimental source: strain HK 10; sub_species Nagariensis
A;Note: in contrast to the other pherophorins, pherophorin-S is targeted to the cell-c;Keywords: extracellular matrix; glycoprotein; pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----RVKM----PEQEYEFPEPRNLNNMRRPS 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 SPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAY 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 SP----SPVLTASPPLPKTSPPPPRVPPSPPPP-------VASPPPPPPP---RV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 LQGIIHSILKK----SCIEILAAEPST--ICAGESFQVVVRGNGFRHARNVDRVLCSFK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 INDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFI---SSSVIITTHC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       496 PLNNAXHTSSPPPAPIYTPPPPAPHCPPPPSAPTPPIPSPPSTLPPPPQAPPNRAPPP 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Mosidues: 1-464 <HAL>
A; Cross-references: EMBL:X65165; NID:g21991; PIDN:CAA46283.1; PID:g21992
C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 ADIVADSKNTVALVTAAAVVVQTTPSPPPPRVSTSPPPPARVSSSPPPATRSPPPRRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 SDGSILAIALLILFLLLALALWWFWPLCC-----TVIIKEVPPP-----PAEESEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PKKKWPTVDASYYGGRGVGGIKRMEVRW--GEKGSTEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---STKVNDLLTFVRNGGSLILVNGANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 202; DB 2; Length 464
; Pred. No. 7.6e-06;
46; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                            Score 203; DB 2; L
Pred. No. 9.1e-06;
1; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 ITEGLTSN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  extensin - Volvox carteri (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n
Similarity 23.0%;
                                                                                                                                                                                                                                                                                                                                                                                      6.7%;
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Best Local Similarity
Matches 38; Conserv
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Best Local Simi
Matches 100;
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C; Accession: T06291
R; Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuell R; Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuell R; Bevan, M.; Pohl, T.; Weizenece Database, April 1999
A; Accession: T06291
A; Molecule type: DNA
A; Residues: 1-760 CBEV>
A; Experimental source: Cultivar Columbia; BAC clone T9E8
A; Experimental source: cultivar Columbia; BAC clone T9E8
A; Map position: 4
A; Note: T9E8.80
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C;Genetics:
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C:Species: Volvox carteri
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
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Pred. No. 5.2e-06;
5; Mismatches 22; Indels
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Pred. No. 8.5e-06;
4; Mismatches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 53.5
Matches 38; Conservative
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PAPPKPQPS 111
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A;Molecule type: DNA
A;Residues: 1-494 <STO>
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Best Local S:
Matches 38,
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22;

Length 464;

407

364

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Gaps

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Collagen alpha I(XII) chain precursor - chicken
NiAlternate names: fibrochimerin
C; Species: Gallus gallus (chicken)
C; Species: Gallu
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Axaccession: S23814
Axaccession: S23814
Axaccession: S23814
Axaccession: S23814
Axaccession: S22811, x, ,2513-251
Axaccession: S26, x, ,2508-2511, x, ,2513-251
Axaccession: S26, x, ,2508-2511, x, ,2513-251
Axaccession: S26, x, ,2508-2511, x, ,2513-251
Axaccession: S26, x, ,2513-251, x, ,2513-251
Axaccession: S26, x, ,2513-251, x, ,2513-251, x, ,2513-251
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A; Residues: 2960-2976, Fr, 2978-3074, 'AG' <GOR3>
A; Residues: 2960-2976, Fr, 2978-3074, 'AG' <GOR3>
A; Cross-references: EMBL:M1/375; NID:9211649; PIDN:AAA48718.1; PID:9211650
A; Note: this sequence has been revised in reference A34485
B; Koch, M; Bernasconi, C; Chiquet, M.
Bur. J. Biochem. 207, 847-856, 1992
A; Title: A major oligomeric fibroblast proteoglycan identified as a novel large form
A; Reference number: S23814; MUID:92362621
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A; Residues: 2772-2793; 2846-2873 <GOR2>
A; Residues: 2772-2793; 2846-2873 <GOR2>
B; Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A; Title: Type XII collagen: distinct extracellular matrix component discovered A; Reference number: A28037; MUID:87317590
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A;Residues: 2456-2788,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g211285
A;Accession: B34485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274 PINSLVDIGEFLEQNG------QQLGNDGDINDIN-NNINNVQPDPPPPSDPPPDP
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A; Molecule type: protein
A; Residues: 2831-2832, T', 2834, R', 2836-2843; 3002-3014
B; Trueb, J; Trueb, B; Trueb, 
                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                           Score 200.5; DB 2 Pred. No. 7.4e-06;
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A; Experimental source: strain PCC 7120 C; Genetics:
A; Gene: all3916
                                                                                                                                                                                                                                                           6.6%;
                                                                                                                                                                                                                                                      Query Match 6.6
Best Local Similarity 40.5
Matches 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown protein [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C; Accession: G86441  
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Basen, N.F.; Hughes, B.; Huizar, L. Sonway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000  
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1.383 < KUR>
A; Residues: 1.383 < KUR>
A; Cross-references: GB:BA000019; PIDN:BAB75615.1; PID:g17133050; GSPDB:GN00179
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A; Cross-references: GB: AEO05172; NID: 911136725; PIDN: AAG31306.1; GSPDB: GN00141
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Pred. No. 3.1e-05;
1; Mismatches 53;
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26.2%; Pre-
tive 24;
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                                                                                                                                                                                                       553 -- PPP--SRPPPRP 562
                                                                                                                                                                                                                                                                ||| | ||| | 358 SPPPVVSPPPPP 371
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Best Local Similarity
Matches 62; Conserv
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                                                                                                                                                                                                                                                  PSSPRKWY-----SPIK--GKL--DALWVL--LRKGYDRV 468
                                                                                                                          376 PIVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKMPEQEYEFPEPRNLNN 435
HCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPAEESEEEDDDGLPKKKW 375
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                                                                                                                                                                                      2602 QITDRDYKPQVGV-----VLDPGSKVLSFFNKDTRGEVQTVTFD-----ND
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31.3%; Pred. No. 4.7e-05;
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ares 66; Conserv
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A;Map position:
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Best Local S:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.6%; Score 200.5; DB 1; Length 3124;
21.8%; Pred. No. 0.00012;
                                                                                  A;Status: preliminary
Modecule type: MRN-1257,'S',1259-1263,'E',1265-1280 <TRU>
R;Residues: 1-24 MRN-1257,'S',1259-1263,'E',1265-1280 <TRU>
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                                                 A; Accession: S28811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKHF--
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Best Local
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13;

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A; Reference number: A90159; MUID: 90147742
                                A, Accession: A34043
A, Molecule type: DNA
A, Residues: 1.141 < BAK>
A, Cross-references: GB:M32217
A, Accession: B34043
A, Molecule type: DNA
A; Residues: 59-136 < BAZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: M32217
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Local 35; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 4
A; Note: F17I5.160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: At2g15880
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 extensin-like protein - cowpea (fragment)

C;Species: Vigna unguiculata (cowpea)

C;Species: Vigna unguiculata (cowpea)

C;Date: (08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 11-Jan-2000

C;Accession: 554156

R;Arsenijevic-Maksimovic, I.; Broughton, W.J.; Krause, A.

Submitted to the EMBL Data Library, April 1995

A;Description: A class of root-hair specific extensins involved in rhizobium/legume inte

A;Reference number: 554155

A;Accession: 554156
                                                                                                                                            R.Ertl, H.; Mengele, R.; Wenzl, S.; Engel, J.; Sumper, M.
J. Cell Biol. 109, 3493-3501, 1989
A.Title: The extracellular matrix of Volvox carteri: molecular structure of the cellular A.Accession: A38647; MUID:90094551
A.Accession: A38647
A.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Status: G. MUID:901999; PIDN:CAA35953.1; PID:91405821
C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical proline-rich protein 1 - polychaete (Owenia fusiformis) (fragment)
C; Species: Owenia fusiformis
C; Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000
C; Accession: A34043; B34043
B34043; B34043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                        C;Species: Volvox carteri
C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C;Accession: A33647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 SPLPPSPQPTAS----SRPPSPPSPRP-----PSPPPPPP 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417 RVKMPEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 DIGRCINFTRVKNNQPAKYPLNNAYHISSPPPAP-----IYTPPPPAPHCPP----- 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPSA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               524 PPPSAPTPPIPS-----SRPPPRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-242 ARS>
A;Cross-references: EMBL:X86029; NID:9791147; PID:9791148
C;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 199; DB 2;
Pred. No. 1.3e-05;
    surface glycoprotein 185 - Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 PPPPSPPPPPPPPPPPPPSPSPSRKPPSPS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTPPIPSPPSTLPPPPQAPPNRAPPPSRPPRPS 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 42; Conserva
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C;Accession: T05225
E;Bevan, M.; Vitale, D.; Liguori, R.; Argiriou, A.; De Simone, V.; Hoheisel, J.; Mewe submitted to the Protein Sequence Database, July 1998
A;Reference number: 215404
A;Reference number: 215404
A;Recession: T05225
A;Molecule type: DNA
A;Residues: 1-699 <BEV>
A;Residues: 1-699 <BEV>
A;Cession: Columbia; BAC clone F1715
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein At2g15880 [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 02-Feb-2001 C;Accession: C84534
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujil, C.Y M.; Koo, H.; Moffett, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, eass, D.; Miteran, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Reference number: A84420; MUID:20083487
A;Residues: L-727 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473 PQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAP------HCPP 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        502 HTSSPPRAPIYTPPPRAPHCPPPPPSAPTPPIPSPPSTLPPPPQAPPNRAPPPSRPPPR 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 699;
   Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   524 PP----PSAPTPPIPSPPSTL--PPPP--QAPPPNRAPPP---SRPPPRP
                                                                       18;
         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
Score 197.5; DB 2
Pred. No. 3.2e-06;
2; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.5%; Score 195.5; DB 2
Best Local Similarity 42.7%; Pred. No. 3.5e-05;
Matches 47; Conservative 9; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                          extensin homolog F1715.160 - Arabidopsis thaliana
         6.5%;
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extensin class I (clone uG-18) - tomato (fragment)
extensin class I (clone uG-18) - tomato (fragment)
c;Species: Lycopersicon esculentum (tomato)
c;Species: Uycopersicon esculentum (tomato)
c;Species: Uy-1998 #sequence_revision 15-May-1998 #text_change 21-Jul-2000
c;Accession: S14974
c;Showalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.
Plant Mol. Biol. 16, 547-565, 1991
A;Itle: Tomato extensin and extensin-like cDNAs: structure and expression in response 1A;Reference number: S14970; MUID:91329690
A;Accession: S14974
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-181 <SHO>
A;Cross-references: EMBL:X55685; NID:q19229; PIDN:CAA39215.1; PID:q1345537
A;Cross-references: EMBL:X55685; NID:q19229; PIDN:CAA39215.1; PID:q1345537
C;Superfamily: hydroxyproline-rich glycoprotein
C;Reywords: cell wall; glycoprotein; hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8;
                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 PEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTGR 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 CINFTRVKNNQPAKYPLNNAYHTSSPPPAP-----IYTPPPPAPHCPP-----PPPS 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 PPYYYKSPPPPS-----PSPPPPYY-----30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35; Indels 73; Gaps
                                                                                                                                                                           473 PQPGD---TGRCINET--RVKNNQPAK---YPLNNAYHTS-----SPPPAPIYTPPPPA 518
                                                                                                                                                                                                    406 VHKPQPPKESPQPNDPXNQSPVKFRRSPPPPQQPHHHV-----------VHS 446
                                                                                        418 VKMPEQEYEFPEPRNLNNN-----MRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMR 472
                                                Gaps
                                                                                                                                                                                                                                                                 519 P-HCPPPPP---SAPTPPIPSPP----STLPPPP--QAPPPNRAPPP---SRPPP 560
                                                                                                                                                                                                                                                                                          48; Indels 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         528 APTPP-----IPSPPSTLPPPP----OAPPPNRAPPP----SRPPPRPS 563
6.4%; Score 194; DB 2; Length 727;
ilarity 33.3%; Pred. No. 4.6e-05;
Conservative 16; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 29.8%; Pred. No. 1.1e-05;
Matches 51; Conservative 12; Mismatches 35.
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                  Query Match
Best Local Similarity
Matches 59; Conserva
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091998 oryza sativ 095651 arabidopsis 095679 arabidopsis 043687 vigna ungui 094661 loryza sativ 095100 sus scrofa 095115 sus scrofa 095115 arabidopsis 095115 arabidopsis 09512 oryza sativ 094096 pneumocysti 09542 coxoplasma 096v14 pneumocysti 09542 toxoplasma 096v14 pneumocysti 095103 sus scrofa 090984 lycopersico 090981 lycopersico 090982 lycopersico 090982 lycopersico 090985 phaseolus v 094vw0 plutella xy 095pp6 chlamydomon 095m0 zea mays (m 055760 cicer ariet 033763 yossyplum b 043682 vigna ungui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Bradley K.A., Mogridge J., Mourez M., Collier R.J., Young J.A.T.;
Identification of the Cellular Receptor for Anthrax Toxin.";
Nature 414:0-0(2001).
EMBL, AF421380; AAL26496.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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O958m2 arabidopsis

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P93797 volvox cart

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries

    protein search, using sw model

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGIKRMEVRWGEKGSTEEGAKLEKAKNARVKMPEQEYEFPEPRNLNNNMRRPSSPR---- 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 EKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCSDGSILAIALL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGLSFISSSVIITTHCSDGSILAIALLILFLLALALAWWFWPLCCTVIIKEVPPPAE 360
                                                                                                                                                                                                                                                                 301 DGLSFISSSVIITTTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPPAE 360
                                                                                                                                       24. VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ31074 FIS, CLONE HSYRA2001476.
Homo sapiens (Human).
EMATYOLEM MetaZoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID=9606;
                                                                                                    241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
TISSUE.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.7%; Score 746.5; DB 11; Length 221; 59.9%; Pred. No. 1.6e-54; Live 30; Mismatches 44; Indels 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC003908; AAH03908.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 AA; 24505 MW; 31AB702E42E9CEB3 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL 24.5 KDA PROTEIN (FRAGMENT). Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                    1111
361 ESEE 364
                                                                                                                                                                                                                                                                                                                                                                                       361 ESEE 364
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237 FQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQ 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSV-IITTH 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 TYTVNETYTTSVKPVSVQLNSMLCPAPILNKAG------EWGLTVTOAGVKWHDLTH 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 GYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDH 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 VFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 LRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRO 137
Ninomiya K., Wagatsuma M., Kahda K., Kondo H., Yokoi T., Kodaira H., Ninomiya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Ostsuta N., Sato H., Hakamatsu A., Ishii S., Yamamoto J., Isono Y., Csuki T., Sato H., Mashatsu A., Tshii S., Yamamoto J., Isono Y., Kawai Hio Y., Satto K., Nishikawa T., Kiuchi H., Murakawa K., Yamashita H., Kamato K., Nakamira Y., Sekine M., Kiuchi H., Murakawa K., Yamashita H., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugao S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Sunnited (CCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO55636; BAB709761. "
SEQUENCE 245 AA; 26111 MW; BIAE6EBOAZEBEE06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                      Length 245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012475; AAH12475.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                           67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 AA; 10453 MW; 14F475F0B170E71A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:4705862) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 391.5; DB 4;
Pred. No. 2.6e-25;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                         19.0%; Score 574; DB 4;
49.2%; Pred. No. 5.1e-40;
vative 45; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=BREAST, AND MAMMARY ADENOCARCINOMA; Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 VSMNDGLSFISSSVIITTTHCSDGSILAIA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 49.2%
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Gaps

39;

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Q9XIB6 <sub>2</sub>

RESULT Q9XIB6

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thaliana chromosome 3. II. 4,251,695 bp covered by ninety Pl,
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2001 (TrEMBLrel. 19, Last annotation update)
EXTENSIN PROTEIN-LIKE.
Arabidopsis thaliana (Mouse-ear cress).
Ekkaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Agnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                428 PEPRNLNNNMRRPSSPR-------KWYSPIKGKLDALWVLLRKGYDRVSVMR 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 KEVPPPPAE-----ESEEEDDDGLPKKKWPTVDASYYGGRGVGIKRMEVRWGEKGST 404
          SEQUENCE.
SEQUENCE.
STRAIN-HK 10;
MEDLINE-21382906; PubMed-11489172;
MEDLINE-21382906; PubMed-11489172;
Hallmann A., Amon P., Godl K., Heltzer M., Sumper M.;
Transcriptional activation by the sexual pheromone and wounding:
new gene family from volvox encoding modular proteins with
(hydroxy)proline-rich and metalloproteinase homology domains.";
Plant J. 26:583-593(2001).
EMBL; AJ311549; CAC39318.1;
SEQUENCE 687 AA; 72017 MW; 6DD95714C350B3CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      522 PSPRPPPRPPRPSSPRPPPDPSPPPSPPSPPTSP--SPPDPAWANLPTSPDPPSPNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 PQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPSAPTPP
                                                                                                                                                                                                                                                                                                                                                                                                Length 687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tabata
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                                                                                                                                                                                                                                                                                                                                                                                                Score 213.5; DB 10; Length
Pred. No. 3.6e-09;
5; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato S., Nakamura Y., Asamizu E., Ti
to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNKNOWN_1.; E34E185E63BB47C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91;
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27.1%; Pred. No. 6.3e-09;
iive 27; Mismatches 91;
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"Structural analysis of Arabidopsis thal
"Structural analysis of Arabidopsis thal
Sequence features of the regions of 4,22
TAC and BAC clones.";
DNA Res. 7:217-221(2000).
EMBL; AP000735; BAB01698.1; -.
InterPro; IPR001226; Flavodoxin.
InterPro; IPR003892; LRR_out.
InterPro; IPR003882; Pistil_extensin.
InterPro; IPR002965; P_ITCh_extensin.
PRINTS; PR01213; PSTLEXTENSIN.
PRINTS; PR01218; PSTLEXTENSIN.
SMART; SM00370; LRR; SACTIVE STREET STREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      619 PPSPPPPSPPPSPPPN-PPPPSP 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533 IPSPPSTLPPPPQAPPNRAPPPSRPPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=COLUMBIA;
MEDLINE-20363099; PubMed-10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102822 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                    7.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 37.3
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaneko T., Kato T., S
Submitted (NOV-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       956 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Q9LJ64;
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                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435 PQPPKHESPKPEEPENKHELPKQK--------ESPKPQPSKPEDSPKP 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411 EKAKNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKW------YSPIKGKLDALWV 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 LLRKGYDRVSVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAP 519
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Sukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae; Volvox.
NCBI_TaxID=3068;
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Last annotation update)
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Pred. No. 3.5e-10;
                                                                                                                                                                      847 AA
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87
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61 VSMNDGLSFISSSVIITTT---QGSLHKIA
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, F13F21.7 PROTEIN.
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                                                                                                                                                                  PRELIMINARY;
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP. CD0749C6AF02BD74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492 PAKYPLNNAYHTSSPPPAPI----YTPPPPAPHCPPPPPSAPTPPIPSPPSTLPPPPQA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thallana chromosome 5. IV. Sequence features of the regions of 1,456,315 bp covered by nineteen bhysically assigned Pl and TAC clones.";

DNA Res. 5:41-54(1998).

EMBL; AB010070; BAB11454.1;
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Ender F., Hallmann A., Amon P., Sumper M.;
Response to the sexual pheromone and wounding in the green alga
Volvox: induction of an extracellular glycoprotein consisting almost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 120;
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); IPR002965; P_triA_cextensn.
)PR01217; PRICHEXTENSN.
3 1289 AA; 137558 MW; 898E55A2A618F5E0 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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23.9%; Pred. No. 1.4e-08;
tive 24; Mismatches 91;
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Pred. No. 2.7e-09;
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                                                                                                                                                                                  exclusively of hydroxyproline.",
J. Biol. Chem. 274:35023-35028(1999).
EMBL, AJ242540; CAB622801.;
InterPro: IPR003882; Pistil_extensin.
InterPro: IPR002965; P. rich_extensin.
PRINTS; PR01217; PRICHEXTENSIN.
PRINTS; PR01218; PSTLEXTENSIN.
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MEDLINE-98290546; PubMed-9628582;
                                                           MEDLINE=20044763; PubMed=10574980;
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409 HX
41547 MW;
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Best Local Similarity
Matches 74; Conserva
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nes 40; Conser
SEQUENCE FROM N.A.
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          EEGAKLEKAKNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKG 464
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Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae; Volvox.
NCBI_TaxiD=3068;
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MEDLINE-21382906; PubMed-11489172;
MEDLINE-21382906; PubMed-11489172;
MEDLINE-21382906; PubMed-11489172;
MEDLINE-21382906; PubMed-11489172;
"Transcriptional activation by the sexual pheromone and wounding:
"Transcriptional activation by the sexual pheromone and wounding:
"transcriptional activation by the sexual pheromone and wounding:
"how of the properties of the properti
                                                                                                                                                                                                                                                                                                         614 YDASPIKKRRPQPPSP----STEETKTTSPQSPPVHSPPPPPPPPPPPPPPPPHS
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae; Volvox.
NCBI_TaxID=3068;
                                                                                                                                                      EESPKPQPPKQETPK-PE---ESPKPQ-----PPKQEQPPKTEAPKMGSPPLESPVPNDP
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01-MAY-2000 (TIEMBLEEL. 13, Last sequence update)
01-JUN-2001 (TIEMBLEEL. 17, Last annotation update)
HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.0%; Score 213; DB 10; 51.9%; Pred. No. 8.1e-09; rative 5; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409 AA
                                                                                                                                                                                                                                                 YDR--VSVMRPQPGDTGRCINFTRVKNNQPAKYPLNN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1143 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q948Y6;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TREMBLREL. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             549 PNRAPPP----SRPPPRP 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             547 PPPNRAPPPSRPPRPS 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
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Gaps

Q9SBM1; Q9SBM1

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RESULT Q9SBM1

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RESULT Q9TOK5

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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           498 NNAYHTSSPPPAP---IYTPPPPAPHCPPPPPSAPTPPIPSPPSTLPPPPQAPPPNRAPP 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafil H., Araijo R., Huizar L., Rowley D., Buehler E., Dunn P., Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S., Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S., Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
ENBL: AC011807; AAC13059.1;
InterPro; IPR001561; LRR.
InterPro; IPR002965; P.rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUE-TESTIS; Hardy C.M., Holland M.K.; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U46069; AAA93320.1; MBROPS; M12.201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00019; LEURICHRPT.
PRINTS; PR01217; PRCHEXTENSN.
SMRRT; SM0370; LRR; 5.
SEQUENCE 494 AA; 54407 MW; BDC0011EEFD5C2E4 CRC64;
                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 205; DB 10;
55.1%; Pred. No. 1.1e-08;
tive 5; Mismatches 22;
                                                                                                                                                   494 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          919 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                        Created)
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                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001762; Disintegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                     PRELIMINARY;
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                                       554 PPSRPPPRPSV 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    555 PSRPPPRPS 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |: | |:||
103 PAPPKPQPS 111
                                                                                                                                                                                                                                              F14J22.4 PROTEIN.
F14J22.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         028659;
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                                                                                                                                                     O9FXA1
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                                                                                                             RESULT 12
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Q28659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFPEP-----RNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMR----PQPG 476
                                 815 PPPPFASVRRNSETLLPPPPPPPWKS-----LYASTFETHEACSTSSSPPPPPPP 866
                                                                                                             867 PPFSPLNTTKANDYILPPPPLPYTSIAPSPSVKILPLHGISSAPSPPVKTAPPPPPPPF 926
                                                                                                                                                                        NNAYHTSSPPPAPIYTPPPAPHCPPPPPS--APTPPIPSPPS-TLPPPPQAPPNRAPP 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503 TSSPPPA---PIYTPPPPAP-----HCPPPPPSAPTPPIPSPPSTLPPPQAPPNRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 205.5; DB 10; Length 760;
Pred. No. 1.9e-08;
4; Mismatches 20; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pohl T., Weizenegger T., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 348-747 FROM N.A.
Robben J., Grymonprez B., Volckaert G, Mewes H.W., Lemcke K.,
Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO49608; CAB40769.1; -.
EMBL; ALO4508; CAB4076.1; -.
Interpro; IPR001611; LRR.
Interpro; IPR003892; LRR_out.
Interpro; IPR003892; Pistil_extensin.
Interpro; IPR003892; Pistil_extensin.
Pfam; PF00560; LRR; 5.
R Interpro; IPR0030862; P_rich_extensin.
PRINTS; PR01217; PRICHEXTENSIN.
PRINTS; PR01217; PRICHEXTENSIN.
R PRINTS; PR012118; PSTLEXTENSIN.
SWART; SW00370; LRR; 4.
SEQUENCE 760 AA; 82245 MW; 20CDEIC8EGCEECFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W. Mayer K.F.X., Schueller C.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                       477 DTGRCINFTRVKN--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.8%;
                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19, EXTENSIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T9E8.80 OR AT4G13340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                          555 PSRPPPRPS 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                166 Sdddddddd 186
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Best Local S
                                                                                                                                                                                                                                                                                                                                                           Q9TOK5;
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Gaps

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22;

Length 494; Indels

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HTSSPPPAP----IYTPPPPAPHC--PPPPPSAPT----PPIPSPPSTLPPPPQAPPPN 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE003763; AAF56763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                  SEQUENCE FROM N.A.
                                                   Ephydroidea; Dru
NCBI_TaxID=7227
CG5514 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 ASP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Simil
Matches 70; (
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qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402 GSTEEGAKLEKAKNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLL 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        614 ----QHTVIQVAY-------EDDWCWSIDSNSGCSDYGDVQRNTYC 648
                                                                                                                                                                                                                                                                                                                                                                                                       178 VGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILA----AEPSTICA 233
                                                                                                                                                                                                                                                                                                                   FVEQLAHKF----ISPQLRMSFIVFSTRGTTLMKLIEDREQIRQGLEELQKVLPGGDTYM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .-----CDSGYAPPDCRNP 701
                                                                                                                                                                                                                                                                                             511 CSGKSASCPPDAYKQDGTPCDRVYRCLGGQCMNPDKQCSNIYGIPARSAP-----EECYV 565
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                         25 CAGQGGR-----REDGGPA-----CYGG------FDLYFILDKSGSVLHHWNEIYY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          462 RKGYDRVSVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHC
                                                                                                                                                                                                                                                                                                                                                              HEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAI---VYC
                                                                                                                                                                                                                                                                                                                                                                                                                            649 A-----SCVVYQAPNSDCQADEMCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 GESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPA----PILKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 GMKAALQVS-----MNDGLSFISSSVIITTTHCSDG----SILAIALLILFLLLALALLWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 FWPLCCIVIIKEVPPPAEESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LMNSKGDRFGNCGSPPALQSSYVPCADENIFCGKL-----ICTEVKLLPQILP-----
                                                                                                                                                                                                                                Length 919;
                                                                                                                                                                                                                                ; Score 204; DB 6; Length 919; Pred. No. 3.4e-08; 68; Mismatches 174; Indels
                                                                                                                                              PROSITE; PS50215; ADAM_MBPRO; 1.
PROSITE; PS50214; DISINTEGRIN_2; 1.
PROSITE; PS01186; EGF_2; UNKNOWN.1.
PROSITE; PS00430; TONE_DEPENDENT_REC_1; UNKNOWN_1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN.1.
SEQUENCE 919 AA; 100844 MW; 32654E431D7CEBAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      522 PP----PPPSAPTPPIPSPPSTLPPPPQAPPNRAPPPSRPPRP 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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             GPCR_Rhodpsn.
Pep_M12B_propep.
Reprolysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                    přam; PP00001; 7tm_1; 1.
přam; PP00000; disintegrin; 1.
přam; PP01562; Pep_M12B_propep; 1.
přam; PP01421; Reprolysin; 1.
ProDom; PD000664; Disintegrin; 1.
SWART; SMO0050; DISIN; 1.
                                                          IPR000130; Zn_MTpeptdse.
                                               TonB_boxC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 17,
                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 19.3%;
Matches 113; Conservative 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                         interpro; ipr002870;
Interpro; ipr001590;
Interpro; ipr000531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (
01-MAY-2000 (
01-JUN-2001 (
                                                           InterPro;
                                                                                                                                                                                                      SEQUENCE
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RC STRAIN-BERKELEY;

RA Adams W. C. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams H.D., Celniker S.E., Holt R.A., Eskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutron G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Barlan J.E., Agdayani A., An H.J., Andrews-Pfannkoch C.R., Baldwin D.,

RA Ballew R.M., Basu A., Barcandale J., Bayerktroglu L., Beasley E.M.,

Ballew R.M., Basu A., Bernsan B.P., Bhandari D., Bolshakov S.,

RA Berson K.Y., Benco P.V., Bernan B.P., Bhandari D., Bolshakov S.,

RA Borkva D., Borcham M.R., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Durbin K.J., Evangelista C. Davesport L.B., Davies P.,

ROSORO K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,

RA Gabriellan A.E., Gary N.S., Gelbart W., Classer K.,

RA Gotson K.J., Bavangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Gabriellan A.E., Gary N.S., Gelbart W., Classer K.,

RA Gotson K.J., Bavangelista C.C., Ferraz C., Ferriera S., Rieischmann W.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Alali M., Kalush F., Karpen G.H., Ke Z., Gubar W., Moshrefi A.,

RA Kalush F., Kadira C.D., Kraft C., Kraft C., Kraft C., Kraft C., Kraft C., McLeod M.P., McShrefi A.,

RA Missen P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Martis N.L., Wartei B., McIntosh T.C., McLeod M.P., McShrefi A.,

RA Reinert K., Remington K., Stapleton M., Stugski M.P., Smith H.,

RA Spier E., Sprading A.C., Stapleton M., Stugski M.P., Smith H.,

RA Sher E., Strading S., Pan S., Pollard J., Put V., Smith H.,

RA Sher E., Strading S., Pan S., Pollard J., Put V., Smith H.,

RA Sher E., Strading S.W., Woodaye T., Wuller E., Whang S., Zhu X., Smith H.,

RA Sher E., Strading S., Shon H., Shon S., Pollard S., Zhan K., Smith H.,

RA Sher E., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 TISTGLQILSIEDEIMSEVKANIDDANNASIESIAPEFVQVPAPPKVN----PPPPPPRP 363
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidee; Drosophila.
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InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 1151 AA; 125450 MW; AF8
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MEDLINE-97162277; PubMed-9009264;
Godl K., Hallmann A., Wenzl S., Sumper M.;
"Differential targetting of closely related ECM-glycoproteins: The pherophorin family from Volvox.";
EMBO J. 16:25-34(1997).
EMBL; Y07752; CAA69032.1; -.
                                                                                                                                                                                         Volvox carteri.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae; Volvox.
NCBL_TaxID=3067;
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
6.7%; Score 203; DB 10; Length 599
Best Local Similarity 55.9%; Pred. No. 2.2e-08;
Matches 38; Conservative 1; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
8BAA14D5A71F8082 CRC64;
                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PHEROPHORIN-S PRECURSOR.
                                                                                                                     599 AA.
                                                                                                                      PRT;
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CHAIN 18 599 PG
SEQUENCE 599 AA; 63436 MW;
                                                                                                                     PRELIMINARY;
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458 KVEPP--PPPAPA 468
                                  551 RAPPSRPPRPS 563 : || ||| ||:
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SEQUENCE FROM N.A.
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SIGNAL
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352 KEVPPP---PAEESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGA 408
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                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: John, Maliyakal E
APPLICANT: John, Maliyakal E
APPLICANT: Barton, Kenneth A
TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles and Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,327
FILING DATE:
CLASSIFICATION A35
PRIOR APPLICATION NUMBER: US/08/217,327
FILING BAPLICATION NUMBER: US 07/812,233
FILING APPLICATION NUMBER: US 07/812,233
FILING APPLICATION NUMBER: US 07/812,233
FILING APPLICATION NUMBER: US 07/812,233
FILING SAFET 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas 7,386
REGISTRATION NUMBER: 27,386
REGISTRATION NUMBER: 1122990831
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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ilarity 26.1%; Pred. No. 4.8e-09;
Conservative 18; Mismatches 56
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US-09-193-043-37
US-08-173-497-2
US-08-286-889-2
US-08-485-618-2
US-08-485-618-9
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US-08-485-618-9
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US-08-652-5
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US-08-482-293A-2
US-08-482-293A-2
US-08-482-293A-2
US-08-482-293A-9
US-08-943-363-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08217327
Patent No. 5474925
                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. Box 2113
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 608-251-9100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-217-327-6
Query Match
Best Local Similarity
Matches 59; Conserva
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Sequence 46,
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-217-327-4
520236-37
US-08-218-32-4
US-09-223-35-2
US-08-28-897-2
US-08-38-28-46
US-08-485-618-46
US-08-485-618-46
US-08-487-652-46
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US-08-943-353-45
US-08-943-353-53
US-08-943-353-53
US-08-899-595-3
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3-08-485-618-37
3-08-362-652-37
                                                                                                                                                                                                                                                        hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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3025
1 MATAERRALGIGFQWLSLAT.
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Match Length
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Gaps

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                                                                                             469 SVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPP-- 526
                                                                                                                409 KLEKAKNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Indels 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 186; DB 1; Length 214;
Pred. No. 8.7e-09;
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: John, Maliyakal E
APPLICANT: Barton, Kenneth A
TILLE OF INVENTION: Inmobilized Proteins in Cotton Fiber
NUMBER OF SEGUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                           527 ---SAPTPPIPSPPSTLPPPP----QAPPPNRAPPP---SRPPPR 561
                                                                                                                                                                             250 YKYKSPPPPMHSPP---PPTPVXKXKSPPPPMHSPPPPFK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,327
                                                              178 -KYKYKSPPPTPVXKYKSPPP-----PTPVKYKKSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
    144 КЅРРРКНЅРАРЕННҮКҮКЅРРРКНГРАРЕННУ--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/812,233
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  543 --- PPQAPPNRAPPPSRPPRP 562
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; Sequence 4, Application US/08217327
; Patent No. 5474925
                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Quarles and Brady
STREET: P.O. Box 2113
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-217-327-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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nes 39; Conserva
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Matches
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;Patent NO. 5202236
;Salah L.;McGandiss, RUSS;WEI, TENA;FILPULA, DAVID
;SUSAN L.;McCANDLISS, RUSS;WEI, TENA;FILPULA, DAVID
;;TILLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
Patent No. 520236; Pathy J.; ANDERSON, DAVID M.; STRAUSBERG, PAPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID TILLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
5.7%; Score 171.5; DB 6
Best Local Similarity 51.6%; Pred. No. 3.1e-07;
Matches 33; Conservative 4; Mismatches 16
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
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Patent No. 5985574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 559 PPRP 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     559 PPRP 562
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LENGTH: 334
5202236-3
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US-09-080-897-2
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Sequence 46, Application US/08286889

Patent No. 5470953

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Mich

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, 6300 Sear Tower

CITY: Chicago

STATE: Illinois

CONTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473 PQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAP--IYTPPPPAPHCPPPPP---- 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 1248;
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35.5%; Pred. No. 4.8e-06;
tive 3; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYZHA: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/323,735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/286,889
                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/080,897
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DCOKET NUMBER: UW97-001
TELECHMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 35.5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-323-735-2
      HILLSBOROUGH
                            CALIFORNIA
                                                                                                                                                                                                                                  FILING DATE
                                                                  94010
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US-08-286-889-46
    CITY: HII
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               616 TAISPPPLSGDATIPPPPPLPEGVGIPSPSSLPGGTAIPPPPPLPGSARIPPP--PPPL 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1248;
                                                                                                                                                                                                                       CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
COMPTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: STEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/080,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.5%; Score 167.5; DB 2;
35.5%; Pred. No. 4.8e-06;
tive 3; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
                                                                                                                                                                                         ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Morrow, Jan E.
APPLICANT: Welcsh, Piri L.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
                                                                                                     APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW97.
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09323735 Patent No. 6197932
APPLICANT: King, Mary-Claire
APPLICANT: Lynch, Eric D.
APPLICANT: Lee, Ming E.
APPLICANT: Worrow, Jan E.
APPLICANT: Welcsh, Piri L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: King, Mary-Claire
APPLICANT: Lynch, Eric D.
APPLICANT: Lee, Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 1248 amino acids
amino acid
GY: linear
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Best Local Similarity 35.55
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-09-080-897-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
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US-09-323-735-2
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TYPE: ami
TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 FTEFKSSLSPQSLVDAIVQLQ----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPOUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPAS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28.2%; Pred. No. 5.9e-06;
Matches 66; Conservative 42; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 46, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: D38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELEPHONE: 312-474-6300
TELEPHONE: 312-474-6448
TELEFX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: _ amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-889-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-485-618-46
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259 TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 FTEFKSSLSPQSLVDAIVQLQ----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 PACYG-GFDLYFILDKSGSV-LHHWNELYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-362-652-46
Sequence 46, Application US/08362652
Sequence 46, Application US/08362652
Sequence 46, Application US/08362652
Sequence 46, Application Sequence Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1155;
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COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.5%; Score 166; DB 1; 28.2%; Pred. No. 5.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Mismatches
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-485-618-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local_Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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CITY: Chicago
STATE: Illinois
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12;

12;

Gaps

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95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVF 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : | ||: | ||: | | :| | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                           Length 1155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STATE: Illinois STATE: Illinois Line States 21P: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.5%; Score 166; DB 2; Best Local Similarity 28.2%; Pred. No. 5.9e-06; Matches 66; Conservative 42; Mismatches 96
                                                  27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/482, 293A
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US-08-482-293A-46
Sequence 46, Application US/08482293A
; Patent No. 5831029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786F
TELECOMMUNICATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams Jr., Joseph A.
                                                                                                                                         TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                        US-08-605-672-46
                                                                                                                   TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 FTEFKSSLSPQSLVDAIVQLQ----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
GAPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray 6 Borun STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STATE: Illinois COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: COMPUTER: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/605,672
                                                                                                                                                                                                                                                                                                                                                                                              Score 166; DB 1;
Pred. No. 5.9e-06;
42; Mismatches 96
                                                                        27866/32391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
CLASSIFICATION: 530
RELOR APPLICATION UNMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION UNBER: US 08/265,889
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                   NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHRRACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28.2%;
Matches 66; Conservative 4;
    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein US-08-362-652-46
                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-08-605-672-46
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5.5%; Score 166; DB 4;
28.2%; Pred. No. 5.9e-06;
tive 42; Mismatches 96;
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illarity 28.2%; Pred. No. 5.9e-06;
Conservative 42; Mismatches 96
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US-09-193-043-66

Sequence 46, Application US/09193043

Sequence 46, Application US/09193043

SEQUENCE No. 6251395

SEPLICANT: Gallatin, Michael W.

APPLICANT: Gallatin, Michael W.

TITLE OF INVENTION: No. 6251395e1 Human 2

TITLE OF INVENTION: No. 6251395e1 Human 2

TITLE OF INVENTION: NO. 6251395e1 Human 2

CURRENT APPLICATION NUMBER: US/09/193.043

CURRENT FILING DATE: 1994-11-16

EARLIER FILING DATE: 1994-08-05

EARLIER FILING DATE: 1994-12-21

SADIMBER OF SEQ ID NOS: 114

SOUTHWARE: PATENTING DATE: 1997-10-03
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                     TELERX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.5%
Best Local Similarity 28.2%
Matches 66; Conservative
                                                                                                                                                                                                                                                  rrpE: amino acid; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-943-363-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Mus musculus
US-09-193-043-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 66; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1155
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US-09-193-043-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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Sequence 46, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION: W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/943,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.5%; Score 166; DB 2; Best Local Similarity 28.2%; Pred. No. 5.9e-06; Matches 66; Conservative 42; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                       27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: 111nois
COUNTRY: United States
ZIP: 66606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                   REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-630
TELEFAX: 312-474-648
                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-482-293A-46
                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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12; 95 LTEDR-----EQIRQGLEELOKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148 149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199 37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94 95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148 37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94 200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253 30; Length 1155; Length 1155; 96; Indels

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LIEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                   259 TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF 315
                  149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
CORRESPONDENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                       200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                    | : | ||: | | : | | : | | 316 KVGN-FVALRSIORQIQEK----IFAIEGTESRSSSSSFQHEMSQEGFSSALSMD 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.5%; Score 166; DB 1; Length 11: Best Local Similarity 28.2%; Pred. No. 5.9e-06; Matches 66; Conservative 42; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
TELECHONE: 312-474-6300
TELEFAX: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27866/32391
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                                                                                                                                                                                                                                                                                                    Sequence 53, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-362-652-53
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204 FTEFKSSLSPQSLVDAIVQLQ----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                   149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                    259 TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF 315
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
AITLE OF INVENTION: NO. 572853381 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 10.3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                     | : | || : | | : | | 316 | KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 30;
                                                                                                                                                       200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.5%; Score 166; DB 1;
28.2%; Pred. No. 5.9e-06;
tive 42; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
APPLICATION NUMBER: US 08/362,652
FILING DATE: 1-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 Sequence 53, Application US/08485618; Sequence 53, Application US/08485618; Patent No. 5728533; GENERAL INFORMATION: W Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 233 South Wacker
CITY: Chicago
STATE: Illinois
COUWIRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312-474-6300
312-474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253 | : | || : | || : | || : || || 316 KVGN-FVALKSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364 δy

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Search completed: August 9, 2002, 10:33:08 Job time: 187 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 9, 2002, 10:35:55; Run on:

Search time 98.32 Seconds (without alignments) 525.968 Million cell updates/sec

US-09-970-076-2\_COPY\_27\_321 1536 1 GOGGRREDGGPACYGGFDLY......GLSFISSSVIITTHCSDGS 295 Title: Perfect score:

Sequence:

Scoring table:

528882 segs, 175299045 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

528882 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptcdata/2/paa/US06\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptcdata/2/paa/US06\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptcdata/2/paa/US07\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptcdata/2/paa/US09\_NEW\_COMB.pep:\*

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7: /cgn2\_6/ptcdata/2/paa/US09\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptcdata/2/paa/US00\_NEW\_COMB.pep:\* ..........

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES		
Result No.	Score	Query Match	Juery Match Length DB	DB	U	Description	
1	1536	100.0	564	-	PCT-US02-08253-187 ( U	Sequence 187, App	
7	1536	100.0	564	Н	-US02-08253-2	Sequence	
m	1536	100.0	564	7	US-60-389-987-1823 NN	Sequence 1823,	
ಶ	1532	99.7	551	9	US-10-038-307-18)	Sequence	
ស	1520	0.66	333	φ	US-10-038-307-2 / M	Sequence 2,	
9	1520	99.0	345	9	US-10-038-307-24 F		
7	1520	99.0	564	φ	US-10-038-307-20	7	
80	1519	6.86	562	-	PCT-US02-08253-194	194,	
6	1519	6.86	562	-	PCT-US02-08253-301	301,	
10	1507	98.1	328	9	US-10-038-307-26	26, A	
11	1505.5	98.0	342	ø	US-10-038-307-22	22,	
12	1500	7.76	543	v	US-10-038-307-14	14,	
13	1500	7.76	543	9	US-10-038-307-16	16,	
14	1490	97.0	543	9	US-10-038-307-10	10,	
15	1479	96.3	534	9	US-10-038-307-12		
16	996	62.9	218	S	US-09-629-469A-11706	117(	
17	903	58.8	538	9	US-10-047-542-99		
18	790.5	51.5	488	9	US-10-104-047-2639		
19	790.5	51.5	488	9	US-10-038-307-6		
50	790.5	51.5	488	7	US-60-373-595-10	10	
21	777.5	50.6	587	9	US-10-125-540-312	312,	
22	770	50.1	487	9	US-10-038-307-8	8	
23	685	44.6	381	9	US-10-038-307-4	4	
24	145.5	9.5	1152	Ŋ	US-09-592-617A-43	43,	
25	138.5	9.0	1163	П	PCT-US02-10824-116	116,	
26	138.5	9.0	1163	7	US-60-369-452-33	Sequence 33, Appl	

1, A 257, 61,	e 63, Applee 61, Applee 63, Applee 22380, Percentage 63, Applee 62380, Percentage 63, Applee 63866, Applee 638666, Applee 638666, Applee 638666, Applee 6386666, Applee 6386666, Applee 6386666, Applee 63866666, Applee 63866666, Applee 6386666666, Applee 6386666666666666666666666666666666666		
Sequence Sequence Sequence	Sednence Sednence Sednence Sednence	Sequence Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence Sequence
US-09-805-354-1 PCT-US02-08253-257 PCT-US02-19669-61	PCT-USUZ-19699-63 US-10-177-293-61 US-10-177-293-63 US-10-155-881-22380 US-60-360-039-5866	US-10-155-881-33525 US-09-805-354-2 US-09-805-354-3 US-09-592-617A-59 US-10-150-821-4 US-60-389-987-1591	US-10-155-881-28757 PCT-US02-19669-27 US-10-177-293-27 US-10-009-557-7 US-09-904-920A-34
3331	16934	011147	014400
306	3063 3063 3063 646 3051	460 191 191 187 3594	7682 764 764 795 915
8888 6.2.5.6	∞ ∞ ∞ ∞ ∞ v. v. v. 4 €	88.2 7.7 6.7.7	4444
132.5 131 131	131 131 131 128.5 128	126 125.5 124.5 121.5 118.5	113.5 113.5 113.5 113.5
27 28 29	333 333 34	33 34 34 34 36 36 36 36 36 36 36 36 36 36 36 36 36	. 4 4 4 4 1 4 6 4 3

## ALIGNMENTS

RESULT

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US-60-389-987-1823
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                                                   Query Match
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207 ALQGIHSILKKSCIEILAAEPSTICAGESFOVVVRGNGFRHARNVDRVLCSFKINDSVT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 GOGGRREDGGPACYGGFDLYFILLDKSGSVLHHWNEIXYFVEQLAHKFISPQLRMSFIVFS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCSDGS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFURMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Tang, Bing
APPLICANT: Taylor, Bradford W.
APPLICANT: Glenn, Gary W.
APPLICANT: Glenn, Gary W.
APPLICANT: Warnorck, Dale E.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE REFERENCE: 660088 4652P2
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SEQ ID NO 1823
SEQ ID NO 1823
LENGTH: 564
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                                                                                    APPLICANT: Carson-Walter, Eleanor
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107,00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR PLILING DATE: 2001-04-11
PRIOR PLILING DATE: 2001-08-01
NUMBER OF SEO ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Score 1536; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.2e-136;
Matches 295; Conservative 0; Mismatches 0;
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                                                          Sequence 232, Application PC/TUS0208253 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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PCT-US02-08253-232
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RESULT 4
US-10-038-307-18
US-10-038-307-18
Sequence 18, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEFF
APPLICANT: There are a solid to the second of th
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100.0%; Pred. No. 2.7e-136;
ive 0; Mismatches 0;
Score 1536; DB 7;
Pred. No. 1.2e-136;
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Best Local Similarity 100.
Matches 294; Conservative
                                          Best Local Similarity 100.
Matches 295; Conservative
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US-10-038-307-18
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181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 240
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
27 GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
                                                                                                                                                    121 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
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100.0%; Pred. No. 3.8e-135;
ive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
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Best Local Similarity 100.0
Matches 292; Conservative
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ORGANISM: Homo sapiens
US-10-038-307-20
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US-10-038-307-20
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LENGTH: 564
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                                                                                                    APPLICANT: James B. ROTTMAN
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin Ozkaynak
APPLICANT: Judith J. HEALEX
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
SOFTWARE: FASTSEQ for Windows Version 4.0
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100.0%; Pred. No. 1.8e-135;
iive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.9e-135;
Matches 292; Conservative 0; Mismatches 0;
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                                                             Sequence 2, Application US/10038307 GENERAL INFORMATION:
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Matches 292; Conservative
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US-10-038-307-24
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TYPE: PRT
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10-038-307-2
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squence Journal Application PC/TUS0208253
squence JINPORMATION:
APPLICANT: Carson-Walter, Bleanor
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
PRIOR PELING DATE: 2001-08-01
SMIOR FILING DATE: 2001-08-01
SMIOR FILING DATE: 2001-08-01
SOFTWARE: FRSTSEQ for Windows Version 4.0
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: 9CT/US02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR RELIGATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
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4.7e-135;
ches 2;
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Pred. No. 4.7e-135;
2; Mismatches 2;
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98.6%;
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Best Local Similarity 98.6
Matches 291; Conservative
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PCT-US02-08253-194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 301
LENGTH: 562
                                                                                                                                                                                                                                                                                      Best Local Sim
Matches 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT
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                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                             25
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GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 60

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61 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120
                                           ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
               84
                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10038307

Sequence 2. Application US/10038307

GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'REFE
APPLICANT: Theresa L. O'REFE
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 GOGGRREDGGPACYGGFDLYFILDHSKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1507; DB 6;
Pred. No. 3e-134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.1%; scc. 100.0%; Pred. No. c. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEFFE
APPLICANT: Engin OZKAYNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Homo sapiens
US-10-038-307-26
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Matches 290; Conserv
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US-10-038-307-22
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121 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Theresa L. O'KEFF
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILLIG DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
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APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
  205 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ALTDGELHEDLEFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
                                                                                                       147 ALTDGELHEDLFFYS - - EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                                                                                181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                                                                                                                                                                                     265 LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSPKS 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCSDGS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDGS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 543;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.7%; Score 1500; DB 6;
llarity 98.6%; Pred. No. 2.8e-133;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 16, Application US/10038307; GENERAL INFORMATION: APPLICANT: James B. ROTTMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-038-307-10; Sequence 10, Application US/10038307; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 543
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 291; Conserv
                                                                                                                                                                                                                                                                                                                                                         US-10-038-307-16
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GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEFF
APPLICANT: Bigin OZKAYNAK
APPLICANT: Judith J. HEALEY
APPLICANT: Judith J. HEALEY
APPLICANT: Judith J. HEALEY
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION NUMBER: 202-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 VFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 LRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 GYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDH 171
                                                                                                                                                                                                                                                                                                                                                                                                    27 GQGGRREDGGPMDYKDDDDKACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQ 86
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                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 VFPVNDGFQALQGIIHSILKKSCIBILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLC
                         Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                            1 GQGGRREDGGP-----ACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQ
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                                                                                                                                                                                                                                                                                            Score 1505.5; DB 6;
Pred. No. 4.4e-134;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 of TITLE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                            Query Match 98.0%;
Best Local Similarity 97.0%;
Matches 292; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 98.6
11; Conservative
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US-10-038-307-22
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US-10-038-307-14
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Matches 291;
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                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLN 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 GITLAKLIEDREQIRQGLEELQKVLPGGDIYMHEGFERASEQIYYENRQGYRTASVIIAL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120
                                                                                                                                                                                                                                                                      1 GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 60
                                                                                                                                                                                                               27 GOGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIXYFVEQLAHKFISPQLRMSFIVFS 86
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEPERATE INTENDED BY SOUTHWAN APPLICANT: James B. NOTTMAN APPLICANT: Theresa L. O'KEEFE APPLICANT: Theresa L. O'KEEFE APPLICANT: Engin OzKANNAK TOTALE APPLICANT: Judith J. HEALEY TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods FILE REFERENCE: 7853-999 CURRENT APPLICATION NUMBER: US/10/038,307 CURRENT FILING DATE: 2002-06-28 NUMBER OF SEQ ID NOS: 26 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12.
                                                                                                                                                                                                                                                                                                                                                                                                                            5
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                                                                                                                                       Length 543;
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                                                                                                                                                                       3; Indels
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98.3%; Pred. No. 2.6e-131;
Live 0; Mismatches 3;
                                                                                                                                         Ouery Match
Best Local Similarity 98.3%; Pred. No. 2.5e-132;
Matches 290; Conservative 0; Mismatches 3;
               NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-10-308-307-12
Sequence 12, Application US/10038307
GENERAL INFORMATION:
2002-06-28
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US-10-038-307-12
                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-10-038-307-10
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Best Local Similarity
Matches 288; Conserv
   CURRENT FILING DATE:
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                                                                       Search time 507.33 Seconds
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204.668 Million cell updates/sec
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1536
1 GQGGRREDGGPACYGGFDLY......GLSFISSSVIITTHCSDGS 295
                                                                                                                                                                                                                                                                                                              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                            3502263 seqs, 351980561 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Sequence 2, Appli	Sequence 94, Appl	Sequence 621, App	Sequence 621, App	Sequence 187, App	Sequence 232, App	Sequence 6, Appli
SUMMARIES			ID	US-09-970-076-2	PCT-US00-30045-94	PCT-US01-11988-621	US-09-833-245-621	US-09-918-715-187	US-09-918-715-232	08-09-970-076-8
			8	23	-	-	22	23	23	23
		Ouery	Length	368	403	403	403	564	564	564
	ф	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0
			Score	1536	1536	1536	1536	1536	1536	1536
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11		999	403	7	US-09-833-245-620 PCT-US99-31025-9	Sequence 62 equence 9,
12	1520	0.66	333	2 2	US-09-223-546-9 US-09-471-179-9	7 6 90 7 6 90
15		999		577	US-09-599-596-9 US-09-796-753-12	- (7
16		98	562	0 0	US-09-970-076-8 US-09-918-715-194	13,
18		8 8 8 8 8 8	306	Ö	US-09-918-715-301 PCT-US99-31025-30	Sequence 30, App Sequence 30, Appl
20		 8 8 6 8	306	- =	US-09-471-179-30	Sequence 31, Appl Sequence 30, Appl
22		986	306	ä	US-09-471-179-51 PCT-US99-31025-132	Sequence 51, Appl Sequence 132, App
24.		93.	301	ıä,	US-09-471-179-132	Sequence 132, App
5 P 7 P		9 9 9 9	274	٦ =	PCT-US99-31025-50 US-09-471-179-50	Sequence 50, Appl Sequence 50, Appl
27		83.	297	۳;	US-09-488-725A-2121	Sequence 2121, Ap
29		58.	172	,	DCT-US99-31025-105	Sequence 10, Appl Sequence 105, App
30		58.	172	Ξ,	US-09-471-179-105	Sequence 105, App
32		51.	488	- <del>-</del> i	PCT-0500-0528-59 US-09-516-745-59	
33		51.	487	н,	PCT-US00-05226-107	Sequence 107, App
35		51.	484	<del>-</del>	US-U9-516-/45-10/ PCT-US00-05226-2	
36		51.	488	, , i	PCT-US00-05226-57	57
37		51.	488		US-09-516-745-2 US-09-516-745-57	- N
36		51.	488	7	US-09-756-753-52	Sequence 52, Appl
40		51.	4.88	ă č	US-60-318-891-10	, 20,
42		51.	488	× ~	US-60-318-903-20 US-60-322-468-6	, ,
43		51.	488	ñ	US-60-322-732-10	10,
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; Sequ	ence 2, RAL INFC	APPLICAT ORMATION:	100	660	9/00/560/50	
 ; APP	LICANT:	APPLICANT: Young, John A.T. APPLICANT: Bradley Kenneth	Tohn A.T.		ď	
 , APP	LICANT:	Collier	, Robe		<i>.</i>	
 ; APF	LICANT:	Mogridg	ie, Jer Anthr	Jeremy thrav T	· S. Tovin Recentor	
; FIL	E REFERE	ENCE: 960	1296.97	745		
CUR	RENT APE	PLICATION	NUMBER	B: 0	US/09/970,076	
PRI	OR APPLI	CATION N	IOMB	Ţ 09	7251,481	
, PRI	OR FILIN	NG DATE:	2000-1	2-05		
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Best Loc Matches	ia T	Similarity 100 95; Conservative	y lu ervativ	e c	0; Mismatches 0;	Indels 0; Gaps 0;
 ΛO	1 6066	GOGGRREDGGPACYGGFDLYFILDK	CYGGFE	LYFI	LDKSGSVLHHWNEIYYFVEOLAHKFISPQLRMSFIVF	KFISPQLRMSFIVFS 60
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RESULT 4
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                       APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Human Genome Sciences, Inc.
TITLE DEF INVENTION: 28 Human Secreted Proteins
FILE REPRENCE: PS708PCT
CURRENT APPLICATION NUMBER: PCT/US00/30045
CURRENT PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR APPLICATION NUMBER: 60/215,133
PRIOR FILING DATE: 1999-11-05
NUMBER FILING DATE: 2000-06-30
NUMBER FILING DATE: 2000-06-30
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: PCI/US01/11988
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PCT-0501-11988-621
FCT-0501-11988-621, Application PC/TUS0111988
; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 295; Conservative
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PCT-US00-30045-94
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100.0%; Pred. No. 7.4e-151;
iive 0; Mismatches 0;
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100.0%; Pred. No. 7.4e-151;
iive 0; Mismatches 0;
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Sequence 621, Application US/09833245

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546FCT
CURRENT APPLICATION NUMBER: US/09/833,245

CURRENT APPLICATION NUMBER: US/09/833,245

CURRENT FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-04-21

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 2267

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 621
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/229, 351
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 621
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PCT-US01-11988-621
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Best Local Similarity
Matches 295; Conserv
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APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR PILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR PRIOR DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/284,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-08-11
PRIOR PRIOR DATE: 2000-08-11
SPRIOR FILING DATE: 2000-08-11
SPRIOR FILING DATE: 2000-08-11
SPRIOR FILING DATE: 2000-08-11
SPRIOR APPLICATION NUMBER: 60/282,850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 232
LENGTH: 564
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APPLICANT: Young, Sheatley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Collier, Robert J.
APPLICANT: Collier, Sobert J.
TITLE OF INVENTION: Anthrax Toxin Receptor
FILE REFERENCE: 960296.97745
CURRENT APPLICATION NUMBER: US/09/970,076
CURRENT APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIN Ver. 2.1
SSOFTWARE: PatentIN Ver. 2.1
SENGTH: 564
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Best Local Similarity 100.
Matches 295; Conservative
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US-09-918-715-232
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GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Renneth Kinzler
TITLE OF INVENTON: BNOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107, 00134
CURRENT FILING DATE: 2001-08-01
PRIOR PAPLICATION NUMBER: 60/224,599
PRIOR PILING DATE: 2000-08-02
PRIOR PELING DATE: 2000-08-02
PRIOR PELING DATE: 2000-08-01
PRIOR PELING DATE: 2000-08-11
PRIOR PELING DATE: 2000-08-11
PRIOR PELING DATE: 2000-08-11
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100.0%; Pred. No. 1.2e-150;
ive 0; Mismatches 0; 1
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SOFTWARE: FastSEQ for Windows Version 3.0
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Sequence 232, Application US/09918715
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
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Matches 295; Conservative
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99.2%; Score 1524; DB 1;
llarity 99.3%; Pred. No. 1.3e-149;
Conservative 0; Mismatches 2;
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Sequence 620, Application PC/TUS0111988
Sequence 620, Application PC/TUS0111988
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Human Genome Sciences, Inc.
GURENT Human Genome Sciences, Inc.
FILE REFERENCE: PF546FCT
CURRENT APPLICATION NUMBER: PCT/US01/11988
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-14-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN NUMBER: 60/199, 384
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NAME/KEY: SITE
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CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-USOO-30045-125
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COCATION: (175)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
COCATION: (320)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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llarity 99.3%; Pred. No. 1.3e-149;
Conservative 0; Mismatches 2;
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PCT-US00-30045-125
Sequence 125, Application PC/TUS0030045
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
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LENGTH: 403
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LOCATION: (368) Leamino acids CT-US01-11988-620
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207 ALOGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 266
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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O'THER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (368)
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ORGANISH: Homo sapiens
ORGANISH: Homo sapiens
NAME/KEY: SITE
LOCATION: (175)
NAME/KEY: SITE
LOCATION: Xaa equals any of the naturally occurring 1
NAME/KEY: SITE
LOCATION: (220)
OTHER INFORMATION: Xaa equals any of the naturally occurring 1
NAME/KEY: SITE
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| GENERAL INFORMATION:
| APPLICANT MILLEUNLUM Pharmaceticals, Inc.
| ATTLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
| TITLE OF INVENTION: ENCODING THEM
| FILE REPRENCE: 7833-173-228
| CURRENT APPLICATION NUMBER: PCT/US99/31025
| CURRENT FILING DATE: 1999-12-23
| EARLIER PILING DATE: 1999-12-33
| EARLIER PILING DATE: 1998-12-36
| NUMBER OF SEO ID NOS: 135
| SOFTWARE: FastSEO for Windows Version 4.0
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Pred. No. 1.3e-149;
0; Mismatches 2;
   GENERAL INCURRALION:
GAPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546CPT
CURRENT APPLICATION NUMBER: 60/229, 358
CURRENT FILING DATE: 2000-04-12
PRIOR PAPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 620
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Best Local Similarity 99.3%;
Matches 293; Conservative (
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PCT-US99-31025-9
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GENERAL INFORMATION:
APPLICANT: HOLTZMAN, Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 09404/066001
CURRENT APPLICATION NUMBER: US/09/223,546
CURRENT FILING DATE: 1998-12-30
CURRENT FILING DATE: 1998-12-30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                           181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                                                                                                                                                                                                                                                                                                                1 GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
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100.0%; Pred. No. 2.6e-149;
iive 0; Mismatches 0;
                                                                               99.0%; Score 1520; DB 1; 1
100.0%; Pred. No. 2.6e-149;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100. Matches 292; Conservative
                                                                                     Query Match 99.0
Best Local Similarity 100.
Matches 292; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT; ORGANISM: Homo sapiens
US-09-223-546-9
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-31025-9
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US-09-796-753-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Application US/09599596

Sequence Application US/09599596

GENERAL INFORMATION:
Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM FILE REFERENCE: 09404/06601

CURRENT APPLICATION NUMBER: US/09/599,596

CURRENT PILING DATE: 2000-06-22

PRIOR FILING DATE: 1998-12-30

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Holtzman, Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 7853-173
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 02/223,546
PRIOR FILING DATE: 1998-12-30
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                                                                                                                                                                                                                                                                                                                                     Length 333;
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100.0%; Pred. No. 2.6e-149;
ive 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 2.6e-149;
Conservative 0; Mismatches 0;
                                                                                                                                                                                  NUMBER OF SEQ 1D NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
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100.08; Pre
                                  Sequence 9, Application US/09471179 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 292; Conservative
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US-09-471-179-9
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Matches 292; Conserv
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US-09-599-596-9
                        US-09-471-179-9
                                                                                                                                                                                                                        SEC ID NO 9
                                                                                                                                                                                                                                                       TYPE: PRT
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ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 240
                                                                                                      ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ 180
                                                                    61 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120
GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 86
                                                                                                                                                                                                                                    207 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFRINDSVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: McCarthy, Sean A. TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF FILE REFERENCE: 7853-227-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 103/99/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1999-02-26
PRIOR PRIOR APPLICATION NUMBER: 09/224,246
PRIOR PRILING DATE: 1999-02-26
PRIOR PRILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 2000-05-14
PRIOR PRILING DATE: 2000-05-14
PRIOR PRILING DATE: 2000-05-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09796753 GENERAL INFORMATION:
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                                                                                                                                                                                            Length 333;
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                                                                                                                                                                                         Query Match 99.0%; Score 1520; DB 21; Best Local Similarity 100.0%; Pred. No. 2.6e-149; Matches 292; Conservative 0; Mismatches 0;
| PRIOR FILING DATE: 2000-06-29
| PRIOR APPLICATION NUMBER: 09/606,317
| PRIOR FILING DATE: 2000-06-29
| PRIOR PLICATION NUMBER: 09/65,666
| PRIOR FILING DATE: 2000-09-20
| PRIOR FILING DATE: 2000-09-30
| PRIOR FILING DATE: 2000-09-30
| NUMBER OF SEQ ID NOS: 162
| SEQ ID NO 12
| LENGTH: 333
| TYPE: PRT
| ORGANISM: HOMO SAPIENS
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Search completed: August 9, 2002, 10:44:30 Job time: 868 sec

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              Sequence 2, Appll Sequence 99, Appl Sequence 2, Appll Sequence 99, Appl Sequence 99, Appl Sequence 99, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 43, Appl
                                                                                                                                                                                                                                                           Patent No. 5424399
                                                                                                                                                                                                                                                                         3, Appli
3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTY: United States
ZIP: 60666-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: ELOPPY 418h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                         Sequence 3,
                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLILCATION NUMBER: US/08/286,889
FILING DATE:
            US-08-485-618-2
US-08-485-618-9
US-08-485-618-99
US-08-605-672-2
US-08-605-672-99
US-08-605-672-99
US-08-482-293A-99
US-08-943-363-99
US-08-943-363-99
US-09-193-043-2
US-09-193-043-99
US-09-193-043-99
US-09-193-043-99
US-08-476-062A-43
                                                                                                                                                                                                                                                                        US-08-173-497-3
US-08-286-889-3
                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 23-DEC-1993
ATTORNEY-AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELECHONE: 312-474-6300
                                                                                                                                                                                                                                                           5424399-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 46, Application US/08286889
; Patent No. 5470953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELGEAX: 312-4/2 TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 46: SEQUENCE CHARACTERISTICS: "MGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.8
Best Local Similarity 28.2
Matches 66; Conservative
) MOLECULE TYPE: protein US-08-286-889-46
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 TOPOLOGY:
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US-08-286-889-46
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158.433 Million cell updates/sec
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Sequence 46,
Sequence 46,
Sequence 46,
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                                                                                                                  ; Search time 45.48 Seconds
                                                                                                                                                                                                       1536
1 GQCGRREDGCPACYGGFDLY......GLSFISSSVIITTHCSDGS
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcvuS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcvuS_COMB.pep:*
                                  Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-362-652-46
US-08-605-672-46
US-08-943-363-4-46
US-08-193-043-46
US-08-193-043-46
US-08-362-618-53
US-08-465-618-53
US-08-465-618-53
US-08-943-53
US-08-943-53
US-08-362-652-37
US-08-362-652-37
US-08-362-652-37
US-08-362-652-37
US-08-485-618-55
US-08-362-652-37
US-08-485-618-55
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US-08-943-363-55
US-09-193-043-55
US-08-173-497-2
                                                                                                                                                                                                                                                                                                                                            hits satisfying chosen parameters:
              GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                            231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                       us-09-970-076-2_COPY_27_32
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    protein search, using sw model

                                                                                                                  August 9, 2002, 10:33:03
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                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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1161
1161
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LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
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                                                                                                                                                                                                              69 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
                                                                                                  204 FTEFKSSLSPÖSLVDAIVÖLÖ----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                         TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 Integrin Alpha Subunit
144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT
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                                                                                                                                                                                                                                                                                               174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                                                                                                                                                                                                                    Length 1155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicay-
STATE: Illinois
COUNTY: United States
ZIP: 6060-6402
ZIP: 6060-6402
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IPM PC compatible
COMPUTER: PatentIR Release #1.0, Version #1.25
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APPLICATION NUMBER: US 08/173,497
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-MG-1994
ATTORNEY,AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMUNICATION INFORMATION:
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GENERAL INFORMATION:
GAPPLICANT: Gallatin, w. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 46, Application US/08362652
Patent No. 5766850
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INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
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Best Local Similarity
Matches 66; Conservi
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                                                                                                                                                          123 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                                                                                                                                                                                                                                         69 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
                              2 Integrin Alpha Subunit
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                                                                                                                                                                                                                                                                                                                                                         174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
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233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/485,618
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US-08-485-618-46
Sequence 46, Application US/08485618
Setent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human
TITLE OF SEGUENCES: 103
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APPLICATION NUMBER: US 08/173,497
RILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
FILING DATE: 1-DEC-1994
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 233 South Wacker Drive, 65
CITY: Chicago
STRATE: Illinois
COUNTY: United States
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUT
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TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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INFORMATION FOR SEQ ID NO: 46:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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Best Local 3
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123 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                69 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 68
                                                                                                                                                                                                                                                                    Sequence 46, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Callatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                             | : | | | : | | : | | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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IELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Cnlcsy
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
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Matches 66; Conservative
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US-08-482-293A-46
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                                                                      144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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                                              123 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 68
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                      174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                                                   | : | | : | | | : | | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.8%; Score 166; DB 2; 28.2%; Pred. No. 2.8e-09; tive 42; Mismatches 96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 2-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAMME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27866/32684
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APPLICATION NUMBER: US/08/605,672
                                                                                                                                                                                                                                                                       US-08-605-672-46
Sequence 46, Application US/08605672; Patent No. 5817515
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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Best Local Similarity 28.2%
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-605-672-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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10.8%;
28.2%;
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CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Mus musculus US-09-193-043-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                       RESULT 7
US-09-193-043-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 46
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TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                    11 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 68
                                                                                                                                                                                                                                                   APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                          174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VETSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 166; DB 2;
; Pred. No. 2.8e-09;
42; Mismatches 96;
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-MG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., JOSEPH A.
NAME: Williams Jr., JOSEPH A.
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                Sequence 46, Application US/08943363
Patent No. 5837478
                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
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28.2%;
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Best Local Similarity 28.29
Matches 66; Conservative
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3Y: linear
                                                                                                                                                                                                                      : Patent No. 5837478
: GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                STREET: 233 SC
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                     RESULT 6
US-08-943-363-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 TDGGKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
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APPLICANT: Callatin, W. Michael
APPLICANT: Callatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
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                                                                                174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                | : | || : | || : | | | : | | | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
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Pred. No. 2.8e-09;
2; Mismatches 96; Indels 3
                                                                                                                                                                                                                                                            Sequence 46, Application US/09193043
; Sequence 46, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION;
; APPLICANT: Gallatin, Michael N.
; APPLICANT: Gallatin, Michael N.
; TITLE OF INVENTION: NO. 6251355el Human 2
FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193,043
; CURRENT FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1993-12-21
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-08-05
; EARLIER FILING DATE: 1994-08-05
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ DI NOS: 114
; NUMBER OF SEQ DI NOS: 114
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69 LTEDR-----EQIROGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 53, Application US/08605672
Sequence 53, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 581751561 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
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                                                                          PatentIn Release #1.0, Version #1.25
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                                                                                                                                       FILING DATE:

CLASSIPICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 38,659

TELECOMUNICATION INFORMATION:

TELECHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                         27866/32391
                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
         : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEO ID NO: 53
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
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Best Local Similarity 28.2
Matches 66; Conservative
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                                 COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patenti
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            MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 68
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Sequence 53, Application US/08362652
Sequence 53, Application US/08362652
Sequence 53, Application US/08362652
Sequence 53, Application US/0836262
SEMENAL INFORMATION:
APPLICANT: Callatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTON: NO. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATSHALI, O'TOOLe, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
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COMPUTER: FLORDY disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/485,618 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27866/32797
                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          RAME: WILLIAMS Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/3*
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-6448
TELEX: 25-3856
INFORMATION FOR SEO ID NO: 53: SEOUBNE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-485-618-53
                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Gaps

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123 TDGELHEDLFFYSE--REANRSRDLGALVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
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Sequence 53, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
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; Pred. No. 2.9e-09;
42; Mismatches 96; Indels 3
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
                                    FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AGG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., JOSEPH A.
NAME: WILLIAMS JR., JOSEPH 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27866/32684
APPLICATION NUMBER: US/08/482,293A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 271
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.8%;
Best Local Similarity 28.2%;
Matches 66; Conservative 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
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COUNTRY: United States
ZIP: 60606-6402
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
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US-08-943-363-53
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Sequence 53, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 166; DB 2; Length 1161;
; Pred. No. 2.9e-09;
42; Mismatches 96; Indels 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60606-6402
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                           CURRENT APPLICATION DATE.

CURSENI PALLALION DATA.

FILING DATE:

CLASSIPICATION: 530

PRIOR APPLICATION: 530

PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 38,659

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.8%;
28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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Best Local Similarity 28.2%
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-605-672-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 233 St
CITY: Chicago
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US-08-482-293A-53
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TELEX: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : | | : | | : | | : | | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
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                                                                                                                                        30;
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10.4%; Score 159.5; DB 1; Length 1151;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
Matches 63; Conservative 41; Mismatches 93; Indels 29;
                                                                                            Length 1161;
                                                                                         10.8%; Score 166; DB 4; Length 116
28.2%; Pred. No. 2.9e-09;
tive 42; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/08/286,889
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38.6559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37, Application US/08286889 Patent No. 5470953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC COMPATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
                                                                                                                                           66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-889-37
; ORGANISM: Mus musculus US-09-193-043-53
                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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US-08-286-889-37
                                                                                            Query Match
                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 KVGN-FVALRSIORQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.8%; Score 166; DB 2; Length 1161; 28.2%; Pred. No. 2.9e-09; tive 42; Mismatches 96; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 6521395el Human 2
FILE REFERENCE: 27866/3504
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER PILING DATE: 1993-12-23
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-12-21
EARLIER PILING DATE: 1994-12-21
EARLIER PILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PALENTING DATE: 1997-10-03
                                                                                                        PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTONNEY,AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: 312-474-6300
                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-193-043-53
; Sequence 53, Application US/09193043
; Patent No. 6251395
                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 312-4,
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
"YPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-943-363-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Sequence 37, Application US/0848513

Sequence 37, Application US/0848513

Sequence 37, Application US/0848513

Sequence 37, Application US/0848513

Sequence 37, Application US/084851

Sequence 37, Application US/084851

Sequence 37, Application US/084851

Sequence 37, Application US/084851

Sequence 37, Application US/084154

Sequence 37, App
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                                                                                                                                                                                                                                                         72 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 130
                                                                                                                                                                                                                                                                                                                                                                                                   131 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 181
18 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE---- 71
                                                          29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 LRSIQRQLQEK----IFAIEGTQSRSSSSFQHEMSQEGFSSALTSD 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:

OURRENT ASSTSTEM:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,618

FILING DATE:

CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/485,618

FILING DATE:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 33-DEC-1993

PRIOR APPLICATION NUMBER: US 08/286,889

FILING DATE: S3-DEC-1994

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATE:

APPLICATION NUMBER: US 08/362,652

APPLICATION NUMBER: US 08/362,652

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

RESISTATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32797

TELLECOMMUNICATION INFORMATION:

TELLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.4%; Score 159.5; DB 1; larity 27.9%; Pred. No. 1.5e-08; Conservative 41; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-485-618-37
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Matches 63; Conserva
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US-08-485-618-37
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DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 130
                                                     131 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 181
                                                                                               DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
                                                                                                                             182 LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                            Search completed: August 9, 2002, 10:33:05 Job time: 184 sec
                                                 72
                           Db
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4.5
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2000
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OM protein - protein search, using sw model

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9, 2002, 10:34:12 ; Search time 61.73 Seconds (without alignments) 459.199 Million cell updates/sec

Perfect score:

US-09-970-076-2\_COPY\_27\_321 1536 1 GÜGGRREDGGPACYGGFDLY......GLSFISSSVIITTHCSDGS 295 Sequence:

**BLOSUM62** Scoring table:

283138 seqs, 96089334 residues Gapop 10.0 , Gapext 0.5 Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	cell surface glyco	surface	collagen alpha 1(X	leukocyte surface	antigen Em100 - Ei	la 1	immunodominant mic	classical-compleme	collagen alpha 1(X	collagen alpha 1(X	hypothetical prote	$\neg$	cartilage matrix p	complement factor	collagen alpha 1(V	complement factor	collagen alpha 2(V	cartilage matrix p	cartilage matrix p	hypothetical prote	complement factor	sporozoite surface	hypothetical prote		thrombospondin-rel	dnaK protein (heat	kinesin-like prote	collagen alpha 2(V	collagen alpha 2(V
·	TD.	RWHU1B	RWHU1C	A40020	800551	A48569 '	A45974	A45638	C2MS	S31212	S78476	842373	151027	A37979	ввни	A54849	BBMS	S21369	S66522	A33809	T28797	151579	A46283	T23087	S33578	S04531 .	B96958	T50240	S09646	CGHU2A
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	Length	1153	1163	3124	1153	724	1747	712	760	1857	1888	3051	929	496	764	2944	761	1029	200	493	267	747	574	460	597	559	869	817	917	1018
	March	9.5	9.3	9.3	9.5	9.0	8.9	8.8	8.5	8.5	8.5	8.3	7.7	7.4	7.4	7.3	7.2	7.1	7.1	7.0	6.9	6.8	6.5	6.5	6.5	6.4	6.4	6.4	6.4	6.4
į	score	145.5	143.5	143	141	139	137	134.5	131	130	130	128	118	113.5	113.5	111.5	110.5	109.5	108.5	107.5	105.5	104	100.5	100	99.2	66	66	66	66	66
Result	. So	7	7	æ	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	29

hypothetical prote	hypothetical prote	collagen alpha 3(V	dnaK protein NMB05	collagen alpha 3(V	hypothetical prote	integrin alpha-1 -	probable retroelem	transcription regu	inter-alpha-inhibi	integrin alpha-E c	integrin alpha-1 c	undulin 1 - human	hypothetical prote	probable chaperone	transposase (04) B
T04822	T46488	CGHU3A	н81185	A37797	T47637	A55348	F84811	AF1166	JC5953	A53213	A45226	A40970	E70121	B81917	B83736
~	~	-	~	_	7	~	7	7	7	7	7	7	7	7	7
537	741	3176	642	3137	949	272	689	334	932	1179	1151	843	340	642	292
	6.4	6.4	6.3	6.3	6.3	6.2	6.3	6.2	6.2	6.2	6.2	6.1	6.1	6.0	9.0
6.4				97 6.3				95.5 6.2							92 6.0

Our Surface glycoprotein CD11b precursor [validated] - human
NyAlternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein
eukocyte integrin alpha chain; neutrophil adherence receptor alpham chain
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 31-Dec-2000
C;Accession: A31108; A28915; A41600; A30892; A3218; A46526; A26091; I52567
R;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3,

A; Reference number: A31108; MUID:88315033

A; Accession: A31108
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Coss : 1-1153 < COR>
A; Cross references: GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A; Note: part of this sequence was confirmed by protein sequencing
A; Note: part of this sequence was confirmed by protein sequencing
B; Arnaout, M.A.; Gupta, S.K.; Plerce, M.W.; Tenen, D.G.
J. Cell Biol. 106, 2153-2158, 1988
A; Title: Anino acid sequence of the alpha subunit of human leukocyte adhesion recepto
A; Reference number: A28915; MUID:88257215
A; Rocession: A28915

A; Molecule type: mRNA
A; Residues: 1-499, 501-965, 'P', 967-1153 <ARN>
A; Residues: 1-499, 501-965, 'P', 967-1153 <ARN>
A; Residues: 1-499, 501-965, 'P', 967-1153 <ARN>
A; Rossidues: 1-499, 501-965, 'P', 967-1153 <ARN>
A; Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA
A; Note: the authors translated the codon TAC for residue 1129 as Thr
A; Note: part of this sequence, including the amino end of the mature protein, was con
R; Shalley, C.S.; Annaout, M.A.
B; Shalley, C.S.; Annaout, M.A. 88, 10525-10529, 1991
A; Title: The promoter of the CD11b gene directs myeloid-specific and developmentally
A; Reference number: A41600
A; Molecule type: DNA
A; Residues: 1-9 <SHE>
A; Cross-references: GB:M76724; NID:g180018; PIDN:AAA58410.1; PID:g553115
B; Annaout, M.A.; Remoid-O'Donnell, E.; Plerce, M.W.; Harris, P.; Tenen, D.G.
Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988
A; Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adh
A; Accession: A30892.

A; Wolecule type: mRNA A; Residues: 917-1042 <AR2> A; Residues: 917-1042 <AR2> A; Residues: 917-1042 <AR2> B; Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J. Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989 A; Title: cDNA sequence for the alpham subunit of the human neutrophil adherence recep A; Reference number: A32218; MUID:89098893 A; Accession: A32218

A;Molecule type: mRNA A;Residues: 9-1153 <HIC> A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

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cell surface glycoprotein CD11c precursor - human
N;Alternate names: leukocyte adhesion receptor p150,95 alpha chain
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Best Local Similarity 24.8
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-834 <CO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A35543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75
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A; cross-references: CBB1.20599; OMIN:120980
A; Aproposition: 16p11.2-16p11.2
A; Cross-references: CBB1.2
A; Note: promoter contains a GAFA motif and two Spl consensus binding sites
A; Note: promoter contains a GAFA motif and two Spl consensus binding sites
A; Note: promoter contains a GAFA motif and two Spl consensus binding sites
A; Note: promoter cells urface glycoprotein CD11b; von Willebrand factor type A repeat home
C; Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
C; Keywords: alternative splicing; calcium factor broad status predicted cEXT>
F; 11-1159, Product: cell surface glycoprotein CD11b status predicted
F; 1109-1134 Region: calcium/magnesium binding status predicted
F; 530-614 Region: calcium/magnesium binding status predicted
F; 530-614 Region: calcium/magnesium binding status predicted
F; 1109-1134 / Domain: thranemhrane status predicted < TTM>
F; 1115-1153 / Domain: thracellular status predicted < TTM>
F; 1135-1153 / Domain: thracellular status predicted < TTM>
F; 1155-1153 / Domain: thracellular status predicted < TTM>
F; 185-1153 / Domain: thracellular status predicted < TTM>
F; 185-1153 / Domain: thracellular status predicted < TTM>
F; 185-1153 / Domain: thracellular status predicted < TTM>
F; 185-1153 / Domain: thracellular status predicted < TTM>
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F; 185-1153 / Domain: thracellular status predicted < TTM>
F; 185-1153 / Domain: thracellular status predicted < TTM>
F; 185-1153 / Domain: thracellular status predicted < TTM>
F; 185-1153 / Domain: thracellular status predicted < TTM>
F; 185-1165 / 1951, 1951, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975, 1975
       A; Note: part of this sequence was confirmed by protein sequencing R; Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G. J. J. Immunol. 150, 480-490, 1993
J. Immunol. 150, 480-490, 1993
A; Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in during evolution.
A; Reference number: A46526; MUID:93123748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A. Cross-references: GB:W84477; NID:g180184; PIDN:AAA51960.1; PID:g553219
C;Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                mature
                                                                                                                                                                                            A, Reference number: A46526; MUID:93123748
A, Recession: A46526
A, Accession: A46526
A, Status: not compared with conceptual translation
A, Wolecule type: DNA
A, Status: not compared with conceptual translation
A, Wolecule type: DNA
A, Residues: 1-499, 501-1153 <FLE>
A, Residues: 1-499, 501-1153 <FLE>
A, Residues: 1-499, 501-1153 <FLE>
A, Residues: Interpreted from NGI backbone (NGBIP:121963)
A, Note: sequence extracted from NGI backbone (NGBIP:121963)
A, Note: sequence extracted from NGI backbone (NGBIP:121963)
A, Note: sequence extracted from NGI backbone (NGBIP:121963)
A, Reference number: A68-371, 1986
A; Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across (A, Reference number: A90664; MUID:87076671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKDFNETQLAR----IADS--KDHVFP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 DGEKFGDPLGYEDVIPEADRE---GVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQ 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
Blood 79, 865-870, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: translated from GB/EMBL/DDBJ;Molecule type: DNA;Residues: 1-9 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 17-31 <PIE>
A; Experimental source: granulocytes
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Matches 60; Conserv
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RESULT RWHU1C

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A; Cross-references: GDB:119758; OMIM:151510
A; Cross-references: GDB:119758; OMIM:151510
A; Cross-references: GDB:119758; OMIM:151510
A; Cross-references: GDB:11.2-16p11.2
A; Map position: 16p11.2-16p11.2
C; Superfamily: cell surface glycoprotein CDIlb; von Willebrand factor type A repeat h C; Superfamily: cell surface glycoprotein; glycoprotein; aignal sequence *status predicted <SIG>F; 1-197/Pomain: signal sequence *status predicted <SIG>F; 20-1163/Product: cell surface glycoprotein CDIIC *status predicted <MAT>F; 20-1107/Domain: extracellular *status predicted <EXT>F; 20-1107/Domain: von Willebrand factor type A repeat homology <VWA4>
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                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A36584
A; Accession: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Note: this revision to the sequence from reference A35543 includes the carboxyl end
A; Note: this revision to the sequence from reference A35543 includes the carboxyl end
A; Note: this revision to the sequence from reference A35543 includes the carboxyl end
A; Note: this revision of an integrin alpha subunit, the leukocyte p150,95 molecu
A; Reference number: A35543; MUID:90153906
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: A36584; A35543; S00864
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K.; Larson, R.S.; Springer,
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; pred. No. 0.0021;
43; Mismatches 89;
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                                                                                                                                                                                             R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A. J.; Boll. Chem. 265, 12750-12751, 1990
A;Reference number: A36584
A;Contents: erratum
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A; Cross-references: GB:M81695; EMBL:Y00093;
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R.Corbi, A.L.; Miller, L.J.; O'Connor, K.;
EMBO J. 6, 4023-4028, 1987.
A.Title: CDNA cloning and complete primary
A.Reference number; $00864; MUID:88166645
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leukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse
NyAlternate names: complement-3 receptor alpha chain
C'Species: Mus musculus (house mouse)
C'Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change 22-Oct-1999
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change 22-Oct-1999
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change 22-Oct-1999
C;Accession: R: Pytela, R.
EMBO J. 7, 1371-1378, 1988
A:Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the A:Reference number: $00551; MUID:88312584
A:Accession: $00551
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A; Residues: 1-1153 (PVT>
A; Residues: 1-1153 (PVT>
A; Cross-references: EMBL: X07640; NID: 952982; PIDN: CAA30479.1; PID: 952983
A; Orote: the authors translated the codon CAC for residue 569 as Gln
A; Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Rober
Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A; Title: A partial genomic DNA clone for the alpha subunit of the mouse complement re
A; Reference number: 159078; MUID: 86287312
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Wolecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 ILKKSCIEILAAEPSTICAGESPQVVVRGNGFRHARNV---DRVLCSFKINDSVTLNEKP 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         497 NRVKDIIQAINTFPYRGGSTNTGKAMTYVREKVFVTSK-GSRPNVPRVMILITDGK-SSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          611 LTQSVCLRI----
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A.Introns: 2845/3; 2887/3; 2889/3; 2922/1; 2885/1; 3008/1; 3065/1
C.Superfamily: collagen alpha 1(XII) chain; fibronectin type III repeat homology; von Wi C.(Seywords: alternative splicing; cell binding; colled coll; connective tissue; disulfid C.(Seywords: alternative splicing; cell binding; colled coll; connective tissue; disulfid F;1-23/Domain: signal sequence #status predicted <SIG> F;24-3134/Product; collagen alpha 1(XII) chain #status predicted <MAT> F;24-1189-3134/Product; collagen alpha 1(XII) chain short splice form #status predicted F;34-1189-3134/Product; collagen alpha 1(XII) chain short splice form #status predicted <IIIA> F;34-114/Domain: IIIA #status predicted <IIIA> F:34-114/Domain: fibronectin type III repeat homology <FN3B> F:332-444/Domain: fibronectin type III repeat homology <FN3B> F:332-44/Domain: fibronectin type III repeat homology <FN3B> F:332-45/Domain: fibronectin type III repeat homology <FN3B> F:321-805/Domain: fibronectin type III repeat homology <FN3B> F:321-805/Domain: fibronectin type III repeat homology <FN3B> F:305/Domain: fibronectin type III repeat homology <FN3B> FN3B> FN3B>
                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-3124 < YAM>
A; Rocason, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
B; Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
A; Title: Type XII collagen A large multidomain molecule with partial homology to type I A; Reference number: A34485; MUID:90062079
A; Accession: A34485
A; Molecule type: mRNA
A; Residues: 2456-2758, A, 2760-2802, F', 2804-2976, F', 2978-3124 < GOR>
A; Cross-references: EMBL:J05137; NID:9211284; PIDN:AAA48635.1; PID:9211285
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A.Molecule type: protein
B.Molecule type: protein
A.Molecule type: protein
A
     C;Accession: A40020; A34485; B34485; A28037; S22814; S22254; S28811
R;Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Obar J. Cell Biol. 115, 209-221, 1991
A;Title: The complete primary structure of type XII collagen shows a chimeric molecule whous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site. A;Reference number: A40020; MUID:92011862
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A; Residues: 2772-2792; 2846-2873 <GOR2>
A; Residues: 2772-2792; 2846-2873 <GOR2>
B: Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A; Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA
A; Reference number: A28037; MUID:87317590
A; Accession: A28037
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A.Residues: 2960-2976,'F',2978-3074,'AG' <GOR3>
A.Cross-references: EMBL:M7375; NID:g211649; PIDN:AAA48718.1; PID:g211650
A;Cross-references: EMBL:M7375; NID:g211649; PIDN:AAA48718.1; PID:g211650
A;Notch: this sequence has been revised in reference A34485
B;Koch, M.; Bernasconi, C.; Chiquet, M.
Eur. J. Blochem. 207, 847-856, 1992
A;Title: A major oligomeric fibroblast proteoglycan identified as a novel large form A;Reference number: S23814; MUID:92362621
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A;Residues: 2811-2832, Tr, 2834, 'R, 2836-2843;3002-3014 <DUB>

A;Residues: 2811-2832, Tr, 2834, 'R, 2836-2843;3002-3014 <DUB>

R;Trueb, J.; Trueb, B.

Biochim. Biophys. Acta 1171, 97-98, 1992

Biochim. Biophys. Acta 1171, 97-98, 1992

A;Title: The two splice variants of collagen XII share a common 5'A;Reference number: $28811; MUID:93042014

A;Accession: $28811
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A;Molecule type: mRNA
A;Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
A;Cross-references: EMBL:X67327
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A; Accession: 3-vor.
A; Receute type: mRNA
A; Residues: 1472-1660 (APT>
A; Residues: 1472-1660 (APT>
A; Residues: 1472-1660 (APT>
A; Residues: BMBL:X65122; NID:g62871; FIDN:CAA46238.1; PID:g938175
A; Cross-references: EMBL:X65122; NID:g62871; FIDN:CAA46238.1; PID:g938175
A; Trueb, J: Trueb, B.
Eur. J: Biochem. 207, 549-557, 1992
A; Reference number: $22916; MUID:92339443
A; Reference number: $22916; MUID:92339443
A; Residues: Preliminary
A; Molecule type: mRNA
A; Residues: 286-494, Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439 (-FRU)
A; Residues: 286-494, Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439
A; Residues: 286-494, Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439
A; Residues: 201, 333-338, 1991
A; Title: Cloning of a cDNA for a new member of the class of fibril-associated collage
A; Reference number: $17035; MUID:92037585
A; Molecule type: mRNA
A; Residues: 1472-1659
A; Resid
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A; Residues: 1-1747 <GER>
A; Residues: 1-1747 <GER>
A; Reperimental source: embryo skin
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365)
B; Apte, S:S
submitted to the EMBL Data Library, March 1992
A; Reference number: S30085
A; Accession: S30085
102 SDSRAQNADLLAAAAKKLPYAAGSTYTHLGLAKA-EEILFSFQKGGRDNAPKMILVMTDG 160
                                                                                                              161 A-----SSRRSQTLSAAEKLRNRGVIIVVLGVGTGVNSAECRSIAGCDTSDTVECPR
                                                                         126 ELHEDLFFYSERE----ANRSRDLGALVYCVGV-KDFNETQLARIA--DSKDHV-FP-
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                                                                                                                                                                                                                  175 -VNDGFQALQGIIHSILKKSCIEI----LAAEPSTI--CAGE 209
                                                                                                                                                                                                                                                           213 YLQSNWGGVSSQINGIIKAACKDLAKDAVCSEWSEYGPCEGE 254
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No. 0.012;
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A; Accession: A45974
A; Status: preliminary
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                                                                                                                                                           A Gene: Mac-1

S. Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat home

C. Superfamily: cell adhesion; glycoprotein; transmembrane protein

C. Superfamily: cell adhesion; glycoprotein; transmembrane protein

F. 1-16/Domain: signal sequence #status predicted <SIG>

F. 17-115/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental

F. 148-318/Domain: von Willebrand factor type A repeat homology <WMA2>

F. 1106-1129/Domain: transmembrane #status predicted <TWM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNETQLARIAD-----SKDHVFP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----REQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYE-NRQGYRTASVIIALT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 IHFTFNDFKRNPSPRSHVSPIKQLNGRTKTASGIRKVVRELFHKTNGARENAAKILVVIT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 DIVFLIDGSGSI----LMQYSDEFR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLYFILDKSGSVLHHWNEIYYFVEQLAHKFIS---PQLRMSFIVFSTRGTTLMKLTED-- 72
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                                                A;Residues: 11-44 <RES>
A;Cross-references: GB:M14293; NID:g198993; PIDN:AAA39484.1; PID:g554193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.2%; Score 141; DB 2; Length 1153; 24.2%; Pred. No. 0.0033;
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26.6%; Pred. No. 0.0026;
iive 40; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : <del>-:</del> - - - -
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Best Local Similarity 24.29
Matches 71; Conservative
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356 -SASITSN-----
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Best Local S:
Matches 59,
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23.2%; Pred. No. 0.012;
Live 56; Mismatches 115;
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C; Date: 22-Apr. 1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C; Accession: A45638
R; Tomley, F.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.
Mol. Blochem. Parasitol. 49, 277-288, 1991
A; Title: Sequence of the gene encoding an immunodominant microneme protein of Eimeria
A; Reference number: A45638; MUID:92131064
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A) Note: sequence ext.
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F; 288-296/Domain: vol
F; 288-296/Domain: tl
F; 309-371/Domain: tl
F; 372-432/Domain: tl
F; 494-556/Domain: tl
F; 560-610/Domain: tl
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A; Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146 C; Superfamily: von Willebrand factor type A repeat homology; EGF homology; fibronecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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                                                                                                                 A;Cross-references: EMEL:X70793; NID:9288872; PIDN:CAA50064.1; PID:9288873 R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B. Bur. J. Biochem. 212, 483-490, 1993 A;Title: Complete primary structure of chicken collagen XIV. A;Reference number: S31211; MUID:93185668
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Pred. No. 0.05;
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A; Residues: 1-416;1460-1811,1843-1888 <WAE>
A; Cross-references: EMBL:X70793
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A; Reference number: S78476
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Matches 62; Conserv
                                                                             A; Molecule type: mRNA
A; Residues: 1-1888 <TRU>
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A; Acteus: nucleic acid sequence not shown; translation not shown
A; Accession: 331212
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: mRNA
A; Residues: 1-1857 (MRE)
A; Cross-references: EMBL:X70792; NID:9288874; PIDN:CAA50063.1; PID:9288875
A; Gene: Coll4A1
C; Superfamily: collagen alpha 1(XIV) chain; fibronectin atrix: glycoprotein; trime C; Keywords: alternative splicing; coiled coil; extracellular matrix: glycoprotein; F:1-28 Domain: signal sequence #status predicted cSIGO
F; 29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted cMAT>
F; 29-110/Domain: fibronectin type III repeat homology cFN3A>
F; 34-433/Domain: fibronectin type III repeat homology cFN3A>
F; 34-644/Domain: fibronectin type III repeat homology cFN3F>
F; 321-1009/Domain: fibronectin type III repeat homology cFN3F>
F; 321-1009/Domain: fibronectin type III repeat homology cFN3A>
F; 322-1009/Domain: fibrone
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C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Aug-1999
C;Accession: 878476; S31211
Submitted to the EMBL Data Library, January 1993
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                                                                                                                                                                                                                                                                                                                            collagen alpha 1(XIV) chain precursor, short form - chicken c; Species: Gallus gallus (chicken) C; Species: Gallus gallus (chicken) C; Species: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Aug-1999
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R;Waelchli, C; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb,
Eur. J. Blochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668
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; Pred. No. 0.049;
44; Mismatches 116; Indels 2
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nilarity 25.0%;
Conservative 44
                                                                                                                     : | | : | || 531 VGDPTSQHGKEFLVEDVII 549
                                                                         ----GLSFISSSVII 286
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Best Local Similarity
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cartilage matrix protein precursor - human
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Best Local Similarity 26.09
Matches 59; Conservative
                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-496 <JEN>
A; Cross-references: GB:J05667
A; Accession: B37979
                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type XII collagen alpha-1 chain - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C;Accession: 151027
R;Wei, Y.; Yang, E.V.; Klatt, K.P.; Tassava, R.A.
Dev. Biol. 168, 503-513, 1995
A;Title: Monoclonal antibody MT2 identifies the urodele alpha 1 chain of type XII collages A;Reference number: 151027; MUID:95246925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wi
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C;Superfamily: collagen alpha 1(XII) chain; fibronectin type III repeat homology; von
F;155-236/Domain: fibronectin type III repeat homology <3RF>
F;631-795/Domain: von Willebrand factor type A repeat homology <VWA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||| CYGGFVDVSSNANLPPGRVCTVQTTCPKQKTDLVFLIDGSGSIGSYVFKNEVLRFVREFV 542
                                                                                                                                                                                                                                                                                                                                                                         96 --EGFERASEQIYYENRQGYR----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 148
                                                                                                                                                                                                                                                                                                                                                                                                                  602 VQEGF-----SERRGARPQQSDIARVAIILTDGRSQDNV----TGPADSARKLSIN 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 RQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGY----RTASVIIALTDGELHED 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVN-DGFQALQGIIHSI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 LKKSCIEILAA----EPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                 -----DLYFILDKSGSVLHH--WNEIYYFVEQLA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQI 76
                                                                                                                                                                                                                                                                                   45 HKFI--SPQLRMSFIVFSTRGTTLMKLTE--DREQIRQGLEELQKVLPG----GDTYMH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 203
  homology <VWA1>
<2F1>
                                                                                                                                                      :99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                          Length 3051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.7%; Score 118; DB 2; Length 929; Best Local Similarity 21.2%; Pred. No. 0.19; Matches 57; Conservative 51; Mismatches 135; Indels
                                                                                                                                                      Indels
                                                                                                                                                 75;
F;512-679/Domain: von Willebrand factor type A repeat F;754-793/Domain: fibronectin type II repeat homology F;1201-1244/Domain: EGF homology <EGF>
                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
Residues: 1-929 <WEI>
                                                                                                        Query Match 8.3%; Score 128; DB 5
Best Local Similarity 27.1%; Pred. No. 0.14;
Matches 64; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: |: :: |: 862 ---QEVYVRGTQTTTVLVGLKPETEYYVN 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 FSVEDTYLLCPAPILKEVGMKAALQVSMN 274
                                                                                                                                                                                               13 CYGGF----
                                                                                                                                                                                                                                       483
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RESULT A37979

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A Map position: 1935-1935
A; Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
C; Complex: homotrimer
C; Complex: homotrimer
C; Superfamily: unassigned EGF-related proteins; EGF homology; von Willebrand factor t C; Keywords: glycoprotein; homotrimer
F; 1-22/Domain: signal sequence #status predicted <SIG>
F; 1-22/Domain: signal sequence #status predicted <MAT>
F; 23-496/Product: cartilage matrix protein #status predicted <MAT>
F; 227-26/Domain: von Willebrand factor type A repeat homology <WMA1>
F; 227-262/Domain: whilebrand factor type A repeat homology <WMA2>
F; 273-437/Domain: whilebrand factor type A repeat homology <WMA2>
F; 274/Af/Bhinding site: carbohydrate (Asn) (covalent) #status predicted
F; 221-238, 234-247, 249-262/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Denoise the factor B precursor (validated) - human
NyAlternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; he N;Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; he N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragmen C;Species: Homo sapiens (man)
C;Date: 19-Feb-1984 #sequence_revision 05-Aug-1994 #text_change 08-Dec-2000
C;Accession: S34075, A44622; A00934; A19188; A19947; B19947; B25971; S14339; A44628; Submitted to the EMBL Data Library, March 1993
A;Reference number: S34075
A;Accession: S34075
A;Molecule type: MRNA
A;Residues: 1-764 <MED>
C;Species: Homo sapiens (man)
C;Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 21-Jul-2000
C;Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 21-Jul-2000
C;Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #.K.; Eddy Jr., R.L.; Byers, M.G.;
R;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.;
J. Biol. Chem. 265, 19624-19631, 1990
A;Title: Structure and chromosomal location of the human gene encoding cartilage matr A;Reference number: A37979; MUID:91060568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 157-290,'L',292-496 <JE2>
A;Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1; PI
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R;Woods, D.E.; Markham, A.F.; Ricker, A.T.; Goldberger, G.; Colten, H.R.
Proc. Natl. Acad. Sci. U.S.A. 79, 5661-5665, 1982
A;Title: Isolation of cDNA clones for the human complement protein factor B, a class A;Reference number: A44622; MUID:83039428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 --VIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADS--KDHVF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY----YENRQGYRTAS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 CYGG-----FDLYFILDKSGSVL-HHWNEIXYFVEQLAHKF-ISPQLRMSFIV---FSTR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:CRTM
A;Cross-references: GDB:127280; OMIM:115437
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A: pathway: complement alternate pathway

A: pathway: complement C2; complement factor H repeat homology; trypsin homology;

C; Superfamily: complement C2; complement alternate pathway; duplication; glycoprotein; hyd

C; Keywords: acute phase; complement alternate pathway; duplication; glycoprotein; hyd

F; 10-25-70-main: signal sequence #status experimental <AMT>

F; 20-259/Product: complement factor B #status experimental <AMT>

F; 30-259/Product: complement factor B #status experimental <AMT>

F; 30-259/Domain: complement factor H repeat homology <FH1>

F; 30-36/Domain: complement factor H repeat homology <FH2>

F; 65-218/Domain: complement factor H repeat homology <FH3>

F; 66-748/Product: G3/G5 convertase Bb fragment #status experimental <ABE>

F; 68-458/Domain: trypsin homology #status atypical <ATRY>

F; 482-752/Domain: trypsin homology #status atypical <ATRY>

F; 310-318, 103-145, 131-138, 165-205, 191-218, 478-596, 511-527, 599-615, 656-682, 695-725

F; 329-260/Cleavage site: carbohydrate (Asn) (covalent) #status experimental

F; 256, 576, 699/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                    A, Cross references: GDB:119726; OMIM:138470
A; Cross references: GDB:119726; OMIM:138470
A; Map position: 6p21.3-6p21.3
A; Map position: 6p21.3-6p21.3
A; Map position: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3; A; Mitrons: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 54.01; 59/3; 54.01; 59/3; 54.01; 65/3; 54.01; 65/3; 54.01; 65/3; 54.01; 65/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 652/3; 619/1; 619/1; 652/3; 619/1; 619/1; 619/1; 652/3; 619/1; 619/1; 619/1; 652/3; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1; 619/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: Bb is a serine proteinase; C3/C5 convertase cleaves complement C3 alph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 1(VII) chain precursor - human N;Alternate names: procollagen alpha 1(VII) chain (N;Alternate names: procollagen alpha 1(VII) chain (Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Species: Homo vor-1994 #sequence_revision 04-Nov-1994 #text_change 20-Sep-1999 (C;Accession: A54649; PR044; S16316; 156328; A30296; I84686 R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Ultto, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FERASEQIYYENR-----QGY-RTASVIIALTDG-------ELHEDLFFYSE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 REANRSRDLGAIVYCVG--VKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC 194
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-31, Q', 33-764 <RE2>
A;Gessereferences: GB:L15702; NID:g291921; PIDN:AAA16820.1; PID:g291922
C;Comment: 292-Cys has a free sulfhydryl.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -KKALQAVYSMMSWPDDVPPEGWNRTRHVIILMTDGLHNMGGDPITVIDEIRDLLYIGKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 113.5; DB 1;
Pred. No. 0.34;
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19.6%; Pred. No. 0.34;
tive 63; Mismatches
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Matches 66; Conserva'
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A;Molecule type: mRNA
A;Residues: 16-225, F', 227-259 <MOR>
A;Residues: 16-225, F', 227-259 <MOR>
A;Residues: 16-225, F', 215-259 <MOR>
A;Residues: 16-225, F', 21-259 <MOR>
A;Schwaeble, W:, Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Busche Immunobiology 188, 221-232, 1993
A;Title: Human complement factor B: functional properties of a recombinant zymogen of the A;Reference number: 154409; MUID:94041399
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     A;Accession: A44622
A;Aoleoule type: mRNA
A;Residues: 467-546;550-595;752-764 <WOO>
A;Cross-references: GB:J00185; GB:J00186
A;Nole: the authors translated the codon TAC at 519 as Thr; the nucleic acid translation
A;Nole: J.E.; Anderson, J.K.; Davison, E.A.; Woods, D.E.
J. Biol. Chem. 259, 3407-3412, 1984
A;Title: Complete primary structure for the zymogen of human complement factor B.
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A; Note: glycosylation sites were determined
A; Note: glycosylation sites were determined
B; Christle, D.L.; Gagnon, J.
Biochem. J. 209, 61-70, 1983
A; Title: Amino acid sequence of the Bb fragment from complement factor B. Sequence of the A; Christle: Amino acid sequence of the Bb fragment from complement factor B. Sequence of the A; Christle: Apoctants: the final paper in a series documenting the sequence, glycosylation site, an A; Accession: A19188
A; Molecule type: protein
A; Residues: 260-296, Tr. 298-764 < CHR>
B; Campbell, R.D.; Porter R.R.
B; Campbell, R.D.; Porter R.R.
A; Title: Molecular cloning and characterization of the gene coding for human complement
A; Reference number: A19947; MUID: 83273641
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A; Molecule type: brotein; mRNA
A; Residues: 26-764 <MOL>
A; Cross-references: GB: K01566
A; Note: nucleic acid translation differs from the sequence shown in having 300-Leu, 328-
A; Note: 736-Ser was also found
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A; Molecule type: mRNA
A; Residues: 1-764 CRES>
A; Residues: 1-764 CRES>
A; Cross-references: GB:S67310; NID:9452937; PIDN:AAD13989.1; PID:94261689
A; Cross-references: GB:S67310; NID:9452937; PIDN:AAD13989.1; PID:94261689
A; Cross-references: GB:S67310; NID:9452937; PIDN:AAD13989.1; PID:94261689
A; Cross-references: GB:S67310; NID:94967177
A; Rithe: Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic A; Reference number: 157824; MUID:94067177
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A; Residues: 270-329 <NIE>
A; Note: binding site for carbohydrate to lysine under artificial conditions
R; Morley, B.J.; Campbell, R.D.
EMBO J. 3, 153-157, 1984
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A; Residues: 339-509 <CAl>
A; Residues: 339-509 <CAl>
A; Cross-references: GB; J00126; NID: g187723; PIDN: AAA36226.1; PID: g553536
A; Cross-references: GB; J00126; NID: g187723; PIDN: AAA36226.1; PID: g553536
A; Title: Cell-specific expression of the human complement protein factor A; Reference number: A25971; MUID: 87102880
A; Reference number: A25971; MUID: 87102880
A; Residues: 1999 < WULD: A; Residues: 1-99 < WULD: A; Residues: A; A; Residues: A; A; Residues: A; A; Residues: A; R
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A;Status: translated from GB/EMBL/DDBJ
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A; Residues: 346-764 <CAM>
A; Cross-references: GB:J00125
A; Accession: B19947
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Search completed: August
Job time: 254 sec
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A; Residues: 815-892, 'E', 894-1439 <PAR>
A; Residues: 815-892, 'E', 894-1439 <PAR>
A; Cross-references: GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96439.1; PID:g180915
A; Experimental source: Keratinocyte
B; Gammon, W. R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.; Cook, M.E.; Wright, J.; J. Invest. Dermatol. 99, 691-696, 1992
A; Title: Noncollagenous (NCl) domain of collagen VII resembles multidomain adhesion prot A; Reference number: 156328; MUID:93107742
A; Reference number: 156328
A; Status: translated from GB/EMBL/DDBJ
A; Reference number: A54849; MUID:94327588
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A;Molecule type: mRNA
A;Molecule type: mID:g262309
B;Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson, R.E.
B;Delo. Chem. 264, 3822-3826, 1989
A;Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagena
A;Reference number: A30296; MUID:89139437
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Astrible: The carboxyl-terminal half of type VII collagen, including the non-collagenous Astrible: The carboxyl-terminal half of type VII collagen, including the non-collagenous Astrible: The carboxyl-terminal half of type VII collagen, including the non-collagenous Astrible: preliminary, translated from GB/EWBL/DDBJ
Astrible: Systems: preliminary, translated from GB/EWBL/DDBJ
Astrible: 2395-2871, 'S', 2873-2944 <RE2>
Astross-references: GB:L06662; NID:9388713; PIDN:AAA89196.1; PID:9388714
R;Christiano, A.M.; Ryynaenen, M.; Uitc, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
Astrible: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser subs
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A; Note: defects in this gene can result in dominant and recessive dystrophic epidermolys
A; Note: there are 118 introns
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A; Residues: 'EFR', 340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', 524-528,'C',
A; Residues: 'EFR', 340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', 524-528,'C',
A; Rasidues: 'EFR', 340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', 524-528,'C',
A; Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
A; Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
A; Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
A; Note: Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A; Title: Human type VII collagen: CDNA cloning and chromosomal mapping of the gene.
A; Reference number: S16316; MUID: 91334380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: structural component of extracellular polymer associated with anchoring in Superfamily: unassigned collagens; animal Kunitz-type proteinase inhibitor homology; is Reywords: colled coll; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprol. F:1-16,Domain: signal sequence #status predicted <SIG> F:17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;
A;Note: two reported peptides cannot be reliably located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A55255; MUID:94224777
A; Contents: annotation
C; Comment: Prolines and lysines at the third position of the tripeptide repeating unit ed and subsequently 0-glycosylated.
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:L02870; NID:9987124; PIDN:AAA75438.1; PID:9987125 R;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S. Blochem. B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: there are 118 introns
C;Complex: type VII collagen is probably a homotrimer
C;Function:
                                                                                                                                                                                                                                                                                                                   Status: not compared with conceptual translation
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A;Cross-references: GDB:128750; OMIM:120120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Residues: 1-2944 <CHR>
                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
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9, 2002, 10:34:15

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F;37-1253/Domain: amino-terminal nonhelical *status predicted <NC1>
F;36-201/Domain: von Willebrand factor type A repeat homology <WwAl>
F;331-318/Domain: fibronectin type III repeat homology <FN1>
F;337-413/Domain: fibronectin type III repeat homology <FN3>
F;414-502/Domain: fibronectin type III repeat homology <FN3>
F;588-53/Domain: fibronectin type III repeat homology <FN4>
F;588-77/Lomain: fibronectin type III repeat homology <FN6>
F;686-77/Lomain: fibronectin type III repeat homology <FN6>
F;686-77/Lomain: fibronectin type III repeat homology <FN8>
F;1052-1104/Lomain: call attachment (R-G-D) motif F;1189-1254/Tomain: call attachment (R-G-D) motif F;280-295/Lomain: animal Kunitz-type proteinase inhibitor homology <FR28/6-295/Lomain: animal kunitz-type proteina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIH 187
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24.1%; Pred. No. 2.9;
iive 42; Mismatches 85;
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Best Local Similarity 24.1%
Matches 52; Conservative
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Fri Aug 9 10:57:02 2002

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2. \SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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275.051 Million cell updates/sec
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1 GQGGRREDGGPACYGGFDLY......GLSFISSSVIITTHCSDGS 295
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human gene 4 encod	Human gene 4 encod	Human TANGO 197.	Human polypeptide	Human protein sequ	A human TANGO 216	Amino acid sequenc	A human TANGO 216	A human TANGO 216	Human novel extrac	Amino acid sequenc
	ΠD	AAE01439	AAE01469	AAB01422	AAM38976	AAB92985	AAB18456	AAB18447	AAB18455	AAB18457	AAU19662	AAB18448
	DB	22	22	21	22	22	21	21	21	21	22	21
a Duery	Length	403	403	333	297	218	488	488	488	488	587	487
% Query	Match	100.0	99.5	0.66	82.2	62.9	51.5	51.5	51.5	51.3	50.6	50.1
	Score	1536	1524	1520	1263	996	791.5	790.5	790.5	787.5	777.5	770
Result	No.	г	7	m	4	5	9	7	80	σ	10	11

A murine TANGO 216 A murine TANGO 216 A murine TANGO 216 Murine TANGO 197. Human immune/haema Mouse alpha-d subu Mouse alpha-d #1. Mouse alpha-d #1. Mouse alpha-d prote Mouse alpha-d #2. Mouse alpha-d prote Mouse alpha-d #2. Mouse alpha-d poly Mouse alpha-d poly Mouse alpha-d poly Mouse alpha-d poly Rat alpha-d prote Mouse alpha-d poly Rat alpha-d protein Rat alpha-d alloregrin Rat alpha-d alloregrin Rat alpha-d alloregrin Rat alpha-d subuni Rat alpha-d alloregrin Rat alpha-d concein Rat alpha-d compos Human beta-1 integrin Rat alpha-d compos Human beta-1 integrin	AAE01439 standard; Protein; 403 AA.  AAE01439.  17-JUL-2001 (first entry)  Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:94.  Human gene 4 encoded secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; infilammation; allergy; neurological disorder; Alzheimer's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psorlasis; sepsis; diabetes; atherosclerosis; sations and isorder; anglogenic disorder; ricepanacy-related disorder; prognancy-related disorder; infection; wound healing; vulnerary; endocrine disorder; infection; wound healing; vulnerary; endocrine disorder; infection; chromosome 19.  Homo sapiens.  Location/Qualifiers  FREY    Location/Qualifiers   Location   Location
AAB18458 AAB18460 AAB18459 AAB18459 AAAR78167 AAR78167 AAW520002 AAW65002 AAW72346 AAW65003346 AAW65003346 AAW65003346 AAW72836 AAW72836 AAW72836 AAW72836 AAW72836 AAW72836 AAW72836 AAW72834 AAW65001 AAW72834 AAW65001 AAW72834 AAW73345 AAW72834 AAW73345 AAW72834 AAW73345 AAW72834 AAW73345 AAW73345 AAW73345 AAW73345	d; Protein; 403 AA.  Ist entry)  oded secreted protein HWLFR02  protein; proliferative disord  ty; developmental abnormality  sorder; AIDS; autoimmune dise  lergy; neurological disorder;  sociognic ognitive disorder;  sociogner; sepsis; diabetes; an  isorder; pregnancy-related  er; infection; wound healing,  emotaxis; food additive; gene  identification; chromosome 19  Location/Qualifiers  127  /label= Signal_peptide  28403  /note= "Mature human secreted
484 484 21 488 21 81 81 81 81 81 81 81 81 81 81 81 81 81	entry)  de secreted  tein; proli developmen dev: ALDS; gy; neurolo is cognitive is cognitive is seps sorder; angio sorder; pre infection; infection infectin
	tandard; Prote  (first entr  4 encoded sec reted protein; commality; ency; no; allergy; no; chemotaxis the chemotaxis truer identification.  Location  1.27 /label=28.403 /note=1.
0.00	439 stand; 439; L-2001 ( gene 4 el ; secrete; i abnorma mmation; mnson's di mson's di
2 2 4 3 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3	A439 AAE01439 st. AAE01439; 17-JUL-2001 Human gene imflammatio serinflammatio skin disord cardiovascu qastrointes endocardiovascu cardiovascu cardiovascu homo sapien Key Peptide Protein WO200134626
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XX AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE0145-AAE01513 represent the proteins they encode. CC AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the emount of the new protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of amount of the new genes. Specific uses are described for each of the proliferative disorders; cancer, tumours foctal and developmental proliferative disorders; disorders, diseases of the immune system, allory autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allory autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allory accorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, schizophrenia asthma, complicated disorders, pregnancy-related disorders, and infections. The proteins can also be used to aid wound disorders, and infections. The proliferation, to prevent skin aging due to cannow a formary tissues, to regenerate tissues, to identify their culture of primary tissues, to regenerate tissues, to identify their contrure of primary tissues, to regenerate tissues, to identify their contrure of primary tissues, to regenerate tissues, to identify their conducts specific for a protein of the invention can be used in antidodes specific for a protein of the invention can be used in antidodes specific for a protein of the invention can be used in mannoscribent assay (ELISA). The present sequence represents a human control of the invention.
                                                                                                                                                                                                                                 New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRGTTLMKLTEDREQIRQGLEELGKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120
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100.0%; Pred. No. 5.3e-157
:ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                         Claim 11; Page 485-486; 562pp; English.
                                                                                                                                             Komatsoulis GA, Moore PA,
                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
01-NOV-2000; 2000WO-US30045.
                                        99US-0163581
2000US-0215133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295; Conservative
                                                                                                                                                                                        WPI; 2001-308778/32.
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                                                                                                                                                                                                           N-PSDB; AAD05303
                                               05-NOV-1999;
                                                                  30-JUN-2000;
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Best Local S
                                                                                                                                                    Ruben SM,
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Gaps

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AAD05300-AAD05379 represent CDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode. AAE01514-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
                                                                                                                                                                                  Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; inmune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; endocrine disorder; infection; wound healing; vulnerary; endocrine disorder; infection; additive; gene therapy;
267 lnekpfsvedtyllcpapilkevgmkaalqvsmndglsfisssviittthcsdgs 321
                                                                                                                                                           Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:125.
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                                                                                                                                                                                                                                                                                                                                    binding partner identification; chromosome 19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Unknown
/note= "Encoded by WGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by KTC"
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                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Unknown
/note= "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                              ¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Unknown
                                                                           AAE01469 standard; Protein; 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-2000; 2000WO-US30045.
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2000US-0215133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Komatsoulis GA,
                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 33
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30-JUN-2000;
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                                                                                                             AAE01469;
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                                                                   AAE01469
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99WO-US31025

23-DEC-1999;

06-JUL-2000.

WO200039284-A1

mutations in the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 28 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tummours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, allergies, neurological disorders (e.g., Theumatold arthritis), inflammation, allergies, neurological disorders, (e.g., Alzheimer's disease, Rarkinson's disease), cognitive disorders, schizophrenia, asthma, skinson's disease), cognitive disorders, schizophrenia, atheroscierosis, cardiovascular disorders, angiogenic disorders, and infections. The proteins can also be used to aid wound the protein and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell colluture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in remotaxis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in diagnostic immunosasays e.g., radioimmunosasay or enzyme linked imvance secreted protein of the invention. 

403 AA; Sequence

ö 181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 240 61 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120 121 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ 180 Gaps 241 LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCSDGS 295 ö Length 403; Indels Score 1524; DB 22; Pred. No. 1.1e-155; 0; Mismatches 2; 99.2%; Matches 293; Conservative Similarity Query Match Best Local 87 147 g a qq à g à ò ò g ö

AAB01422

AAB01422 standard; Protein; 333 AA 20-OCT-2000 (first entry) Human TANGO 197. AAB01422; 

TANGO, 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; Theumacioid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; Crohn's disease; chronic myelogenous leukemia; cancer; liver disease; chronic myelogenous leukemia; cancer; liver disease; doughth's disease; obstearthritis; lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus erythematosus; transgenic animal; diagnosis; prognosis; prophylatic; therapeutic; human.

Homo sapiens

Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, Theumatoid arthritis, postiasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chiseases e.g. myasthemia gravis, autolimmune disbetes and systemic diseases e.g. myasthemia gravis, autolimmune disbetes and systemic lupus erythematosus. The nucleic acids are also useful for producing lupus erythematosus. The nucleic acids are useful in TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, prognostic assays, prognostic assays, prognostic assays, prognostic assays, prognostic assays, complements and for monitoring clinical trials. TANGO colypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range 240 121 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ 180 206 61 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120 Gaps 1 GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 60 producing 181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT ö 241 LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCS 292 Length 333; Indels 0; 99.0%; Score 1520; DB 21; 100.0%; Pred. No. 2.1e-155; ive 0; Mismatches 0; of cellular disorders can be treated Claim 8; Fig 4; 209pp; English. (MILL-) MILLENNIUM PHARM INC 98US-0223546. Best Local Similarity 100. Matches 292; Conservative WPI; 2000-465743/40. 333 AA; N-PSDB; AAA47455. 30-DEC-1998; Holtzman DA; Sequence Query Match ò g QQ ò g ò 셤 δλ qq ò

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AAM38976 standard; Protein; 297 AA 22-OCT-2001 (first entry) AAM38976; RESULT AAM38976 XXXX

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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries
                                                                                                                                                                                                                                                                      Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                  Example 4; SEQ ID NO 2121; 10078pp; English.
      Human polypeptide SEQ ID NO 2121.
                                                                                                                                                                                                                                                                        Liu C, Asundi V, Ch
Wang Z, Wehrman T, X
Zhou P, Goodrich R,
                                                                                                                                                                            2000US-0552317.
2000US-0598042.
2000US-062312.
2000US-0653450.
2000US-065191.
2000US-069346.
                                                                                                                                                                   2000US-0488725
                                                                                                                                                26-DEC-2000; 2000WO-US34263
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N-PSDB; AAI58132.
                                                                                                                                                                                                                                                        (HYSE-) HYSEO INC.
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                                                                                                              WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification.
                                                                                            Homo sapiens.
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09-JUL-2000;
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                                                                                                                                 26-JUL-2001
                                                                                                                                                                                                                                                                                     J, YO
                                                                        leukaemia.
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                                                                                                                                                                                                                                                                                     Wang
                                                                                                                                                                                                                                                                                              Zhao
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Wang D;

Ren F, Wa

Qian XB, Yang Y,

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The invention relates to human nucleic acids (AALS7798-AAL61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinininin activity, chemotactic/chemokinetic activity, haemotactic/chemokinetic activity, haemotactic/chemokinetic activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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le-127;
0;
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2; Mismatches
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99.2%; Pred. No. le
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                                                                                                                                                                                                                                                                                                                                                                                                                                         297
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches 24
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The present invention describes primer sets for synthesising 5602

(cf. 1111-length cDNAs defined in the specification. Where a primer set

(cf. 1111-length cDNAs defined in the specification. Where a primer set

(comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of

(comprises) to the complementary strand of a polynucleotide which comprises one of

(complementary strand of a polynucleotide which comprises a 5'-end

(complementary strand of a polynucleotide which comprises a 5'-end

(complementary strand of a polynucleotide which comprises a 5'-end

(complementary strand of a polynucleotide which comprises a 5'-end

(complementary strand of a polynucleotide comprises a 5'-end

(complementary strand of a polynucleotide comprises a 6'-end

(complementary strand of a polynucleotide suddence, where the

(complementary strand of a polynucleotides and the complementary to a

(complementary strand of a polynucleotides and the complementary to a

(complementary strand of a polynucleotides and the specification. The primers as 1'-end sequence is selected from those defined in

(complementary strand) the primers are useful for synthesising polynucleotides,

(complementary full-length cDNAs. The primers are also useful for the

(complementary full-length cDNAs. The primers are also useful for the

(complementary strand any specialised methods. AAH03166 to AAH13638 and

(complementary specialised methods. AAH03166 to AAH13632

(complementary strand amino acid sequences; and AAH13632 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                        240
                                                                                       ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ 180
                   Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto J;
                                                                      181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
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Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; SEQ ID 11706; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                 Human protein sequence SEQ ID NO:11706.
                                                                                                                                                                                                                                                                              AAB92985 standard; Protein; 218 AA.
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Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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11-JAN-2000; 2
02-MAY-2000; 2
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                                                                                                                                                        241 LNE 243
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Homo sapiens
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AAB18447
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                                                                                                                                                                                                                                                                                                                                                                                             TANGO 266; TANGO 216;; TANGO 261; TANGO 267; TANGO 267; Cellular deferation; cellular adhesion; cellular adhesion; cellular adhesion; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disosas; atelectasis; pulmonary congestion; coedema; emphysema; chronic bronchitis; bronchial asthma; bronchied asteriar and lasorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain heartation; latrogenic disease; hydrocephalus; Alzhehmer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO
                                                                                                                                                 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 173
                                                                                                                                                            PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSF 233
                                                                                                                                                                                                      MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY 113
                                                                                    Gaps
                                                                                                                   Novel human and murine secreted proteins designated TANGO 216, 261 262, 266 and 267 useful as modulating agents of cellular processes.
                                                                                    ö
                                                             Length 218;
                                                                                   0; Indels
                                                              Score 966; DB 22;
Pred. No. 7.9e-96;
2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser
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                                                                                                                                                                                                                                                                                                                                                                          A human TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page -; 175pp; English.
                                                                                                                                                                                                                                                                                                             AAB18456 standard; Protein; 488 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC.
                                                              62.9%;
98.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2000; 2000WO-US05226
                                                                                                                                                                                                                                                                                                                                                        15-JAN-2001 (first entry)
                                                                                  Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holtzman DA,
            of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for treating cancer
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|kindsvtlsk 190
                                                                                                                                                                                                                                     KINDSVTLNE 243
                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                  AAB18456;
                                Sequence
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polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Wilebrand factor-associated disorder, requiate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, cand hematopoietic associated diseases and disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral coopenal toxy propressions of disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

Created using information provided.
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Best Local Similarity 53.23
Matches 157; Conservative
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08-SEP-2000
                                     Barnes TM,
                                                                                disorders
                                                                                   Sequence
  Peptide
       Protein
     Domain
          Domain
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TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; schemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; highen cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                      120 IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGF 179
                                                                                                                                      gpggllraqeqpscrrafdlyfvldksgsvannwieiynfvqqlaerfvspemrlsfivf 85
                                                                                                                                                                                          180 QALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSV
                                                                                                                                                                                                                                                                    240 TLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCSDG 294
                                                                                                                                                                                                                                                                                        A human TANGO 216 polypeptide clone.
                                                                                                                                                                                                                                                                                                                                                                                                             AAB18455 standard; Protein; 488 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-579269/54.
N-PSDB; AAA75157.
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AAB18455
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                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a human TANGO 216 polypeptide. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular random indulate cellular differation, modulate cellular differation, modulate cellular differation, modulate cellular andresion, and cell trafficking and/or migration, would cellular interactions, modulate cell adhesion in proliferation, modulate cellular interactions, modulate cell adhesion in proliferation, disorders, such as cancer, modulate the proliferation, differentiation of cells that appear in the bone marrow, and leukcoytes, cand/or function of cells that appear in the bone marrow, and leukcoytes, cellular interactions, plood and hematopoietic associated diseases and disorders, spleen associated diseases, modulate renal disorders, treat certoints, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the cardiovascular disorders such as ischemic heart disease, modulate the disorder. They may also be used to treat disorders associated diseases or collise, cerebral coedma, hydrocephalus, brain herniations, iatrogenic constrince, cerebral coedma, hydrocephalus, brain herniations, iatrogenic constrince, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, disperser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human and murine secreted proteins designated TANGO 216, 261, 266, 266 and 267 useful as modulating agents of cellular processes.
                                                                                                                                                                                                "von Willebrand factor A domain"
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Le= "transnmembrane domain"
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                                                                                                                        "extracellular domain"
                                                                                                                                                                                                                                      "transmembrane domain"
                                                                                                                                                                                                                                                                          /note= "cytoplasmic domain"
                                                                                                                                                              "mature protein"
                                                                                    /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sharp JD,
                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Fig 1A-C; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC.
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/note= "v
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342..48
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AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, modulate cellular interactions, modulate cell trafficking and/or migration, modulate cellular adhesion in proliferation disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood
Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of ceilular processes,
                                                                                                                                                                                                                                  Disclosure; Page -; 175pp; English.
                                                                                                                                  e.g. for treating cancer
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Length 488;

51.5%; Score 790.5; DB 21; Length 53.2%; Pred. No. 2.5e-76; ive 54; Mismatches 81; Indels

Best Local Similarity 53.2 Matches 157; Conservative

Query Match Best Local S

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1 GQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNBIYYFVEQLAHKFISPQLRMSFIVF 59

Fraser CC;

Sharp JD,

(MILL-) MILLENNIUM PHARM INC.

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cellular proliferation; cellular differentiation; cellular adhesion;
von Willebrand factor-associated disorder; cell trafficking; cancer;
hematopoietic associated disease; atelectasis; pulmonary congestion;
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
intestinal disorder; spleen associated disease; renal disorder;
cardiovascular disorder; ischemic heart disease; hydrocephalus;
brain herniation; latrogenic disease; hydrocephalus;
Alzhehmer's Disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
               pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, toxoplasmosis, parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

note: the present sequence does not appear in the specification; it was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVI 119
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSV
and hematopoietic associated diseases and disorders, atelectasis,
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                                                                                                                                                                                                                                                                                                                                             DB 21; Length 488;
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                                                                                                                                                                                                                                                                                                                                         51.5%; Score 790.5; DB 2.53.2%; Pred. No. 2.5e-76; tive 54; Mismatches 81.
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                                                                                                                                                                                                                                                  using information provided.
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AAB18455-57 represent human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO COLULAR DESCRIBERATION, modulate pollyleration, modulate pollyleration, modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, modulate cell adhesion in proliferation, modulate cellular interactions, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary conquesting congestion or oedema, emphysema, chronic bronchitatis, bronchial associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disorders, treat cardiovascular disorders such as ischemic heart disorders, treat cardiovascular disorders such as ischemic heart disorders, treat cardiovascular disorders associated diseases of disorder. They may also be used to treat disorders associated with the ovaries, and cerebral codema, cartilage associated diseases of disorder. They may also be used to treat disorders associated with the ovaries, and cerebral codema, concephalus, brain meniations, iatrogenic disease, inflammations, brain meniations, iatrogenic disease, inflammations, brain meniations, iatrogenic disease, inflammations, brain meniations, and treat hepatic disorders.

Coorplessmosis, Parkinson's disease, multiple sclerosis, brain ceres, interact hepatic disorders, once the present sequence does not appear in the specification; it was note: the present sequence does not appear in the parelication; it was note: the present sequence does not appear in the present sequen
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                                                                                                                                                                                 Novel human and murine secreted proteins designated TANGO 216, 261, 262, 265 and 267 useful as modulating agents of cellular processes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 TLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG 294
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                                                                 Fraser CC;
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                                                                   Sharp JD,
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                                                                                                                                                                                                                                                                                Disclosure; Page -; 175pp; English.
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                                                                   Holtzman DA,
                                                                                                                                                                                                                                      e.g. for treating cancer
                                                                                                                WPI; 2000-579269/54
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14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232401.
14-SEP-2000; 2000US-0233064.
15-SEP-2000; 2000US-0234998.
13-CCT-2000; 2000US-023696.
13-CCT-2000; 2000US-0239937.
13-CCT-2000; 2000US-0239937.
13-CCT-2000; 2000US-0239937.
13-CCT-2000; 2000US-0239937.
13-CCT-2000; 2000US-02341785.
13-CCT-2000; 2000US-0241785.
13-CCT-2000; 2000US-0241786.
13-CCT-2000; 2000US-0241787.
13-CCT-2000; 2000US-024677.
13-CCT-2000; 2000US-024677.
13-CCT-2000; 2000US-0246528.
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17 - NOV - 2000;
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       Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial, ophthalmic; cytostatic; antianzbelmers; immune/autoimmune disease; HIV infection; anaemia; human immunodeficiency vivus; rheumatoid arthritis; multiple sclerosis; accers; hyperproliferative disorder; breast neoplasm; melanoma; sezary syndrome; Gauchors's disease; neurological diseases; Alzheimer's disease; Parkinson's disease; cardiovascular disorder; cardiac arrest; tachycardia; angina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive.
                                    Human novel extracellular matrix protein, Seq ID No 312.
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2000US-0229344.
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2000US-0186350
                 06-DEC-2001 (first entry)
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44-FEBS-2000; 2
52-MAR-2000; 2
116-MAR-2000; 2
119-MAR-2000; 2
129-MAR-2000; 2
129-MAR-2000; 2
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                                                                                            The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPS). The novel human secreted extracellular matrix proteins (SPS). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPS. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPS by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPS may also be used antagonists) of the SPS. The anti-(SP) antibodies and antagonists may also be used to down regulate expression and activity of the Administry of antagonists may also be used to down regulate expression and activity of the Administry of antagonists and antagonists of the SPS in samples.
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Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation,
                                                                                                                                                                                                                                                                                Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
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Pred. No. 8.5e-75;
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2000US-0251479.
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Best Local Similarity
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hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain hernlation; latrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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                                                                                                                                                                                                                                                                                                                              cellular proliferation, cellular differentiation, cellular adhesion, von Willebrand factor-associated disorder, cell trafficking, cancer,
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                                                                                                                                                                                                                                                                                            266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267
                                                                                                                                                                                                                          Amino acid sequence of a murine TANGO 216 polypeptide.
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/note= "transnmembrane domain"
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AAB18448 standard; Protein; 487
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N-PSDB; AAA75150.
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           disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's brain cancers, hydrocephalus and encephalitis, and treat hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treat bone marrow, blood and hematopoietic associated diseases and
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                                                                                                                                                                                                                                                                                             50.1%; Score 770; DB 21; Length 487; 52.8%; Pred. No. 4.1e-74;
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Best Local Similarity 52.8%
Matches 150; Conservative
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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 267, and TANGO 267. The TANGO CC describes TANGO 266, TANGO 267, and TANGO 267. The TANGO CC cellular differentiation and/or modulate cellular adhesion. The cellular differentiation and/or modulate cellular adhesion. The disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular adhesion, condulate cell adhesion in proliferative disorders, such as cancer, and cell trafficking and/or migration, and/or function of cells cand hematopoietic associated diseases and disorders, atelectasis, bronchial pulmonary congestion or oedema, emphysema, chronic bronchial, bronchial conducts the pronchiectasis, intestinal disorders, spleen associated as teachers, spleen associated diseases, modulate the proliferation, differentiation, as ischemic heart disease, modulate the proliferation, differentiation, as ischemic heart diseases, modulate the proliferation, differentiation, cartilage associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, treat disorders associated with the ovaries, and cerebral conceptables parkinson's disease, multiple sclerosis, brain cancers, bydrocephalus and encephalitis, and treat hepatic disorders. It was conceined the present sequence does not appear in the specification; it was notes and mentation or appear in the specification; it was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 KKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVED 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.1%; Score 770; DB 21;
52.8%; Pred. No. 4.1e-74;
iive 52; Mismatches 80;
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                                   Fraser
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                                     Sharp JD,
                                                                                                                                                                                                    Disclosure; Page -; 175pp; English.
(MILL-) MILLENNIUM PHARM INC.
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Best Local Similarity 52.8
Matches 150; Conservative
                                                                                                                                                                       for treating cancer
                                     Holtzman DA,
                                                                           2000-579269/54.
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                                         Sarnes TM,
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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO clother beginning to bolypeptides can be used to modulate cellular proliferation, modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, addlate cellular interactions, modulate cell adhesion in proliferation, addlate cellular interactions, and hematopoietic associated diseases and disorders, atelectasis, that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or cedema, emphysema, chronic bronchitis, bronchial sthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate the proliferation, differentiation, as ischemic heart diseases, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases with the ovaries, and cerebral oceana, corporations, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxophylasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

CC hydrocephalus and encephalitis, and treat hepatic disorders.

note: the present sequence does not appear in the specification; it was created using information provided.
                                                             TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267; CACULUAR PROLÍFICATION: CELLULAR defiferation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; hematopoietic associated disease; atelectasis; pulmonary congestion; intestinal emphysema; chronic bronchita; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; Alzheimer's Disease; cerebral toxoplasmosis; parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser CC;
                      A murine TANGO 216 polypeptide clone
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Query Match 50.1%; Score 769; DB 21; Length 487; Best Local Similarity 52.8%; Pred. No. 5.3e-74; Matches 150; Conservative 52; Mismatches 80; Indels 2; Gaps 1;

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AAB18458-60 represent murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated adisorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular adhesion, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pronchial pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; hydrocephalus; Alzheiner's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
EDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHED 130
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                                              191 KKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVED
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asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or for function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, bydrocephalus, brain herniations, iatrogenic disease, inflammations, daterial and viral menigitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple scalerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

Order the present sequence does not appear in the specification; it was created using information provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; crohn's disease; chronic myelogenous leukemia, cancer; liver disease; Hodgkin's disease; osteoarthritis; Lyme's disease; cacheratis autoimnume disease; myasthemia gravis; autoimnume diabetes; systemic lupus erythematosus; transgenic animal; diagnosis; prophylatic; therapeutic; mouse.
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                                                                                                                                                                                                                                                                                                                                               2; Gaps
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ilarity 52.5%;
Conservative 53
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                                                                                                                                                                                                                          Sequence
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nucretic actus actudating cellular processes like asthma, graft versus-host diseases, rheumatord arthritis, psoriasis, inflammatory versus-host diseases, rheumatord arthritis, psoriasis, inflammatory versus-host diseases, rheumatord arthritis, psoriasis, inflammatory cornus-host disease, septic shock, ulcerative colitis, croin's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachexia and autoimmune disease, osteoarthritis, Lyme's disease, cachexia and autoimmune classes e.g. myasthemia gravis, autoimmune diabetes and systemic liseases e.g. myasthemia gravis, autoimmune diabetes and systemic cransgenic animals and the TANGO polypeptides themselves. Partial rangonic animals and the TANGO polypeptides themselves. Partial cransgenic animals and for diagnostic assays, prognostic assays, coparamacogenomics and for monitoring clinical trials. TANGO plypeptides are suitable for both prophylactic and therapeutic polypeptides are suitable for both prophylactic and therapeutic disorder associated with aberrant TANGO expression. A wide range of cellular disorders can be treated.
                                                 Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 QLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGF 220
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Pred. No. 4
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                                                                                                                                                 Claim 8; Fig 27; 209pp; English.
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Best Local Similarity 99.3%;
Matches 134; Conservative
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Job time: 130 sec
            WPI; 2000-465743/40.
N-PSDB; AAA47479.
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OM protein - protein search, using sw model

August 9, 2002, 10:30:02; Search time 98.32 Seconds (Without alignments) 656.123 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-970-076-2 1914 1 MATAERRALGIGFOWLSLAT......VIIKEVPPPPAEESEENKIK 368

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

528882 segs, 175299045 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptodata/2/paa/USO6\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/paa/USO6\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/paa/USO3\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/paa/USO9\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/paa/USO9\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/paa/USO9\_NEW\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/paa/USO9\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptodata/2/paa/USO9\_NEW\_COMB.pep:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 187, A		Sequence		Sequence 301,	18, A	'n	Sequence 24, Appl	20,	26,	Sequence 22, Appl	14,	П	10,	12,	Sequence 1170	Sequence 263	Sequence 6, Appli	10,	317	8, 2	4	99,	43,	Sequence 116,	33, A
SUMMARIES	ΩI	PCT-US02-08253-187	PCT-US02-08253-232	US-60-389-987-1823	PCT-US02-08253-194	PCT-US02-08253-301	US-10-038-307-18	US-10-038-307-2		US-10-038-307-20	US-10-038-307-26	US-10-038-307-22	US-10-038-307-14	US-10-038-307-16	US-10-038-307-10	US-10-038-307-12	US-09-629-469A-11706	US-10-104-047-2639	US-10-038-307-6	US-60-373-595-10	US-10-125-540-312	US-10-038-307-8	US-10-038-307-4	US-10-047-542-99	US-09-592-617A-43	PCT-US02-10824-116	US-60-369-452-33
	Query Match Length DB	564 1		564 7	562 1	562 1	551 6	333 6	345 6	564 6	328 6	342 6	543 6	543 6	543 6	534 6	218 5	488 6	488 6	488 7	587 6	487 6	381 6	538 6	1152 5	1163 1	1163 7
•	Query Match	99.0	0.66	99.0	93.7	93.7	86.8	86.2	86.2	86.2	85.5	85.4	85.1	85.1	84.6	77.7	50.5	50.3	50.0	50.0	49.0	48.9	47.5	47.2	7.6	7.2	7.2
	Score	1894	1894	1894	1793	1793	1991	1649	1649	1649	1636	1634.5	1629	1629	1619	1488	996	962.5	957.5	957.5	938.5	936.5	606	903	145.5	138.5	138.5
	Result No.	1	7	e	4	5	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56

Sequence 22380, A Sequence 31525, A Sequence 257, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 51, Appl Sequence 27, Appl Sequence 27	Sequence 7, Appli Sequence 34, Appl
US-10-155-881-22380 US-09-805-354-1 US-10-155-881-33525 PCT-US02-19669-61 PCT-US02-19669-61 US-01-177-293-63 US-01-177-293-63 US-09-805-354-2 US-09-805-354-2 US-09-805-354-3	US-10-009-557-7 US-09-904-920A-34
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APPLICANT: St. Croix, Bard
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Woncht
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/VS02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
SPRIOR FILING DATE: 2001-04-11
SPRIOR FILING DATE: 2001-08-01
SOFTWARE: PESTSEQ for Windows Version 4.0
SEC ID NO 232
LENGTH: 564
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GENERAL INFORMATION: APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
                                                                                                                                                   Sequence 232, Application PC/TUS0208253 GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Homo sapiens
PCT-US02-08253-232
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PCT-US02-08253-232
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APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Gibson, Gary M.
APPLICANT: Gibson, Danie E.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088 4.65P2
CURRENT APPLICATION NUMBER: US/60/389,987
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARR: FeatSEQ for Windows Version 4.0
SEQ ID NO 1823
LENGTH: 564
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APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Wogelstein, Bert
APPLICANT: Winzler, Menneth
APPLICANT: Winzler, Menneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107, 00179
CURRENT APPLICATION NUMBER: PCT/USO2/08253
CURRENT FILING DAFE: 2002-04-10
PRIOR PLILING DAFE: 2001-04-11
PRIOR PLILICATION NUMBER: 60/282,850
PRIOR PLILICATION NUMBER: 60/308,829
PRIOR PLILICA DAFE: 2001-04-11
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1894; DB 7; 1
Pred. No. 2.1e-166;
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100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100.
Matches 364; Conservative
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US-60-389-987-1823
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 320; Conservative
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CORGANISM: Homo sapiens
US-10-038-307-18
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US-10-038-307-18
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                                                                                                                                                                              EQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQL 188
                                                                                                                        99
                                                                                                          9 LGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQ 68
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Sequence 301, Application PC/TUSO208253
GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
FILE REFERENCE: 107, 00179
FILE REFERENCE: 1107, 00179
CURRENT APPLICANTON ENDOTHELIAL CELL EXPRESSION PATTITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTITLE OF INVENTION ON UNBER: CG/282, 850
PRIOR FILING DATE: 2002-04-10
PRIOR PLICATION NUMBER: 60/282, 850
PRIOR PAPLICATION NUMBER: 60/282, 850
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEO for Windows Version 4.0
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Pred. No. 4.4e-157;
5; Mismatches 8;
                                                   Score 1793; DB 1;
Pred. No. 4.4e-157;
5; Mismatches 8;
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96.1%;
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Conservative
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Best Local Similarity
Matches 342; Conserv
                                                                   Similarity
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; ORGANISM: Mus
PCT-US02-08253-194
                                                                               Matches 342;
                                                     Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEFFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Theresa L. O'KEFFE
APPLICANT: Trango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEFFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISS
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100.0%; Pred. No. 6.8e-145;
ive 0; Mismatches 0;
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAFILKEVGMKAALQVSMN 300
241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAFILKEVGMKAALQVSMN 300
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                                                                                                                Sequence 20, Application US/10038307
Sequence 20, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Horiesa L. O'KEFF
APPLICANT: Engin OKKARNAK
APPLICANT: Hodith J. HEALEY
TITLE REPREBUCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILLIA DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFWARE: FatSEQ for Windows Version 4.0
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                                                 Length 564;
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100.0%; Pred. No. 9e-144;
Live 0; Mismatches 0;
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Sequence 26, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
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Best Local Similarity 100.
Matches 318; Conservative
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CRGANISM: Homo sapiens
US-10-038-307-20
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US-10-038-307-26
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LENGTH: 564
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241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/10038307

Sequence 24, Application US/10038307

GENERAL INFORMATION:
APPLICANT: James B. ROTTWAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Good of the Composition of the Composition and Methods TITLE OF INVENTION: 193-253-99

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT PILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MATABRRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN
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Pred. No. 4.4e-144;
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100.0%; Pred. No.
0; Mismatches
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 FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 333
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Best Local Similarity 100.
Matches 318; Conservative
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Best Local Similarity 100.9
Matches 318; Conservative
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CORGANISM: Homo sapiens
US-10-038-307-24
                                                                                                             ), ORGANISM: Homo sapiens
US-10-038-307-2
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Digin OZKAYNAK
TITLE OF INVENTION: JUGALEY
TITLE OF INVENTION: THOSO 197
FILE REFERENCE: 7853-253-999
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 14
LENGTH: 543
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                   SGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQK 111
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                                    SGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRGLEELOK
                                                                                VLPGGDTYMHEGFERASEQ1YYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDL
                                                                                                                                            172 GAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTI
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98.8%; Pred. No. 6e-142;
iive 0; Mismatches 2;
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CORGANISM: Homo sapiens
US-10-038-307-14
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                                                   Methods
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100.0%; Pred. No. 6.8e-143;
ive 0; Mismatches 0;
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Pred. No. 9.9e-143;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Judith J. HEALEY
TITLE OF INVENTY TANG 197 and Tango 216 Conformery APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SED ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Theresa L. O'KEEFE
APPLICANT: ENGIN OZKATVAKA
APPLICANT: JUGITH J. HEALY
TITLE OF INVENTION: Tango 197 and Tango 216 Cor
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MATAERRALGIGFQWLSLATLVLICAGOGGRREDGGP-
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Best Local Similarity 97.2
Matches 318; Conservative
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-038-307-26
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US-10-038-307-22
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US-10-038-307-22
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Best Local Simmatches 316;
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LENGTH: 342
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RESULT 15
US-10-038-307-12
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Best Local Si
Matches 294;
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                                                                                                                                                                                                                                                                                                                                                                                          HEGFERASEQIYYENROGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                      1 MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN 60
                                                                                                                                                                                                                                                                                                                                        Compositions and Methods
                                                                                         and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
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                                                                                         Compositions
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98.4%; Pred. No. 5.1e-141;
ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                     Score 1629; DB 6;
Pred. No. 6e-142;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
TILE OF INVOINT: Tango 197
FILE OF INVOINT: Tango 197
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                  APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Judith J. HEALEY
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Con
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION NUMBER: US/20/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARRE: FASLSEQ for Windows Version 4.0
SEQ ID NO 16
US-10-038-307-16; Sequence 16, Application US/10038307; GENERAL INFORMATION:
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98.8%;
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ORGANISM: Homo sapiens
US-10-038-307-10
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CORGANISM: Homo sapiens
US-10-038-307-16
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Best Local Similarity
Matches 316; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 LAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERAS 128
                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||: | ::| || || SGRREDGGPACYGGFDLYFILLHIHHHHHHHHHHH || 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
             Sequence 12, Application US/10038307

Sequence 12, Application US/10038307

GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Horesa L. O'REFF
APPLICANT: Engin OZKANANK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 ARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 LGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQ
                                                                                                                                                                                      181 KDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVV
MATAERRALGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWN
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Pred. No. 6.3e-129;
3; Mismatches 10;
                                                                                                                                                                                                                                                                                                           299 DGLSFISSSVIITTHSSPKS 319
                                                                                                                                                                                                                                                                                          301 DGLSFISSSVIITTHCSDGS 321
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93.9%;
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CORGANISM: Homo sapiens
US-10-038-307-12
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2,

Db 298 SVIITTTHSSPKS 310

Search completed: August 9, 2002, 10:35:55 Job time: 353 sec

## (OTP2U) NNAJ8 30A9 21HT

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sequence 1, Appli
Sequence 43, Appl
Sequence 43, Appl
Patent No. 5424399
Sequence 3, Appli
Sequence 3, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gallatin, W. Mich
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953e1 Human 2 Integrin Alpha Subunit
MUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                       Sequence Seq
      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.7%; Score 166; DB 1; Lough 28.2%; Pred. No. 4.2e-09; Live 42; Mismatches 96;
US-08-605-672-2
US-08-605-672-55
US-08-605-672-99
US-08-482-293A-9
US-08-482-293A-9
US-08-943-363-9
US-08-943-363-99
US-09-193-043-2
US-09-193-043-5
US-09-193-043-9
US-09-193-043-9
US-09-193-043-9
US-09-193-043-9
US-09-193-043-9
                                                                                                                                                                                                                                                                                          PCT-US96-01314-43
5424399-2
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US-08-286-889-3
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 46, Application US/08286889 Patent No. 5470953 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1155 amino acids
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Best Local Similarity 28.2'
Matches 66; Conservative
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/Parus_COMB.pep:*
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                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08 305-652-46
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US-08 943-363-46
US-08 943-652-53
US-08 943-652-53
US-08 943-618-37
US-08 943-363-37
US-08 948-618-55
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                                                                                                                                                                                                                                                                                                                                                                                                              hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB :
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95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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                                                                                                                                                     95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
                                                                          149 IDGELHEDLFFYSE--REANRSRDLGAIVYCYGVKD-FNE-TQLARI-----ADSKDHVF 199
144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
                                                                                                                                                                                                                                                                                                                                                     Sequence 46, Application US/08362652
Sequence 46, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                               200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                         8.7%; Score 166; DB 1; Length 1155; 28.2%; Pred. No. 4.2e-09; ive 42; Mismatches 96; Indels 3
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233 South Wacker Drive, 6300 Sear Tower
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ZIP: 60606-6402
ZIP: 60606-6402
MEDIUM TYREABLE FORM:
MEDIUM TYRE EACH FORM:
COMPUTER: FLORPY disk
COMPUTER: FLORPY disk
COMPUTER: FLORPY disk
COMPUTER: FLORPY ALSE
COMPUTER: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/173,497
APPLICATION NUMBER: 08/1993
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 28.2%
Matches 66; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CITY: Chicago
STATE: Illinois
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US-08-362-652-46
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                                                                                                                                                                                             95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
                                                                                                           149 IDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 46, Application US/08485618
Sequence 46, Application US/08485618
Sequence 46, Application W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                  200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                          8.7%; Score 166; DB 1; Length 1155; 28.2%; Pred. No. 4.2e-09; Live 42; Mismatches 96; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/485,618 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 2-AUG-1994
ATTORNEY AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659,659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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INFORMATION FOR SEQ ID NO: 46:
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Best Local Similarity 28.25
Matches 66; Conservative
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US-08-485-618-46
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LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
                                                             259 TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF 315
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                            200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                          8.7%; Score 166; DB 2; Length 1155; 28.2%; Pred. No. 4.2e-09; 1.ve 42; Mismatches 96; Indels 31
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233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rc-lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRICE APPLICATION NAME: US 08/286,889
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-M0-1994
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/482, 293A
                                                                                                                                                                                                                                   RESULT 5
US-08-482-293A-46
; Sequence 46, Application US/08482293A
; Detent No. 5831029
; GENERAL INFORMATION:
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Best Local Similarity 28.23
Matches 66; Conservative
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COUNTRY: United States
ZIP: 60606-6402
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INFORMATION FOR SEQ ID NO:
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US-08-482-293A-46
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                                            149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                                   Sequence 46, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
GAPLICANT: GAllatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5817515e1 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                     | : | | : | | : | | : | | : | | 316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                       200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STATE: 1111nois COUNTRY: United States 21P: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PAPLICATION DATA:
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
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312-474-0448
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US-09-193-043-46
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; Patent No. 6251395
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COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
US-09-193-043-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-08-485-618-53
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TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                          GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                        200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                               ; Score 166; DB 2; Length 1155;
; Pred. No. 4.2e-09;
42; Mismatches 96; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago
STATE: 111inois
STATE: 111inois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RILING DATE:
FILING DATE:
FI
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REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 46, Application US/08943363 Patent No. 5837478
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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 28.2%
Matches 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                       US-08-943-363-46
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95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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Sequence 53, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CUTY: Chicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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                                                                       200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                              ; DB 4; Length 1155;
4.2e-09;
thes 96; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 28.2%; Pred. No. 4.2e-
Matches 66; Conservative 42; Mismatches
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/3504
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER PILING DATE: 1993-12-23
EARLIER PILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-08-05
EARLIER FILING DATE: 1997-00-03
NUMBER: OF SEQ. DI NOS: 114
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95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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Patent No. 5817515
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.7%; Score 166; DB 1; Best Local Similarity 28.2%; Pred, No. 4.3e-09; Matches 66; Conservative 42; Mismatches 96
                                                                                                           APPLICATION NUMBER: US/08/362,652
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AGG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                             27866/32391
                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 1161 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-362-652-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
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Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.7%; Score 166; DB 1; Length 1161; 28.2%; Pred. No. 4.3e-09; Live 42; Mismatches 96; Indels 3
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               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27866/32797
                                                                                                                                                                                 CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659 REFERENCE/DOCKET NUMBER: 27866 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300 TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312-4,
TELEFAX: 25-3856
INFORMATION FOR SEO. ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
"VPE: amino acids
"'PE: amino acids
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STATE: Illinois
COUNTR: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
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Best Local Similarity 28.2'
Matches 66; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                     FILING DATE
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149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
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Sequence 53, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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8.7%; Score 166; DB 2; Length 1161;
Best Local Similarity 28.2%; Pred. No. 4.3e-09;
Matches 66; Conservative 42; Mismatches 96; Indels 3
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233 South Wacker Drive, 6300 Sear Tower
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COMPUTER READABLE FORM:
MEDIUM TYPE FILOPPY disk
COMPUTER: FIEND COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
                                                                                                                                                                                                                                                                                  FULLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REPERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
TELEPAN: 312-474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
TOPOLOGY: 14.--
                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
US/08/482,293A
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CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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      APPLICATION NUMBER:
                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-943-363-53
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Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADSRESSE: 
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                                                                                                                 PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
FILING DATE: 5-AUG-1994
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INCRMATION:
NAME: Williams JT., JOSEPH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
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INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66; Conservative
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Best Local Similarity
Matches 66; Conserv
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STREET: 250...
TTTY: Chicago
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US-08-482-293A-53
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                           37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
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APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEB: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
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                                                                                       Length 1161;
                                                                                                                                             96; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/286,889
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                                                                                          / Match 8.7%; Score 166; DB 4; Local Similarity 28.2%; Pred. No. 4.3e-09; nes 66; Conservative 42; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECHMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application US/08286889 Patent No. 5470953 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IELEKA: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
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60606-6402
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; ORGANISM: Mus musculus US-09-193-043-53
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STATE: Illinois
COUNTRY: United
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 166; DB 2; Length 1161;
; Pred. No. 4.3e-09;
42; Mismatches 96; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 53, Application US/09193043
Patent No. 6251395
GENERALINFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
TITLE COF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
                                                                                                      FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATE: 32-DEC-1993

PRIOR APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-NG-1994

PRIOR APPLICATION DATE: 5-NG-1994

PRIOR APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION: NAME: Williams Jr., Joseph A. REFERRNCE/DOCKET NUMBER: 27866/32684

TELECOMOUNICATION INFORMATION: TELECOMOUNICATION INFORMATION: TELECOMOUNICATION INFORMATION: TELECOMOUNICATION INFORMATION: TELECOMOUNICATION INFORMATION: TELECOMOUNICATION INFORMATION FOR SEQ ID NO: 53: SEQUENCE CHARACTERISTICS: LENGTH: 1101 amino acids moreover.
                  CLASSIFICATION: 530
PRIOR APPLICATION DAPR:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
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Best Local Similarity 28.2%;
Matches 66; Conservative 47
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                                                                              DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 156
                                                                                                              157 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 207
                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Marshall, O'Toole, Gastein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STATE: Illinois COUNTRY: United States 21P: 6060-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: BATTER: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: US/08/485,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                   208 LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                   DB 1;
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8.3%; Score 159.5; DB 1;
Best Local Similarity 27.9%; Pred. No. 2.2e-08;
Matches 63; Conservative 41; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
FELECOMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AGG-1994
PRIOR APPLICATION AURIER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37, Application US/08485618
Patent No. 5728533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
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CLASSIFICATION: 435
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09ff49 arabidopsis
097566 canis famil
099864 mus musculu
091900 xenopus lae
001510 plasmodium
0923k3 mus musculu
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096c67 homo sapien
09gzfc caenorhabdi
001506 plasmodium
001508 plasmodium
                                                                  Q21281 caenorhabdi
Q964n4 caenorhabdi
O00261 homo sapien
Q966x5 homo sapien
Q96ft5 homo sapien
9p218 homo sapien
9bqu7 homo sapien
Q63870 mus musculu
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Q63001 rattus norv
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Q948g7 oryza sativ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 EIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYM 120
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bradley K.A., Mogridge J., Mourez M., Collier R.J., Young J.A.T.; "Identification of the Cellular Receptor for Anthrax Toxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 AA; 41157 MW; 8A87B13FFA7D8753 CRC64;
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Last sequence update)
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     RESULT
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096nc7 homo sapien
096cc6 homo sapien
099117 mus musculu
099ye7 rattus norv
09bpg8 halocynthia
004588 eimeria max
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044813 homo sapien
09493 homo sapien
02493 homo sapien
024913 caenorhabdi
091130 rattus norv
096877 mus musculu
                                                                                                                                                             ; Search time 102.68 Seconds
(without alignments)
620.005 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                1 MATAERRALGIGFQWLSLAT......VIIKEVPPPAEESEENKIK 368
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                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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096NC7
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Gapop 10.0 , Gapext 0.5
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sp_mammal:*
sp_mhc:*
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Maximum Match 100%
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sp_bacteriap:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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Maximum DB seq length: 200000000
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269 EKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDGSILAIALL 328
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                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC003908, AAH03908.1; -- Hypothetical protein.
                                                                                                                                                                                                                         Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012475; AAH12475.1; -.
NON_TER 1 1 2
SEQUENCE 97 AA; 10453 MW; 14F475F0B170E71A CRC64;
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61 VLLLLGAALMWWFWPLCCKVVIKDPPPPFSAPMEEEEEDPL 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      North (TremBirel, 17, Created)
01-JUN-2001 (TremBirel, 17, Last sequence update)
01-DEC-2001 (TremBirel, 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.0%; Score 286.5; DB 11;
49.0%; Pred. No. 3.4e-17;
ive 21; Mismatches 28;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:4705862) (FRAGMENT).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                  Score 391.5; DB 4;
Pred. No. 6.6e-27;
1; Mismatches 5;
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                                                                                                                                                                                        TISSUE-BREAST, AND MAMMARY ADENOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Last annotati.
HYPOTHETICAL 24.5 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 VSMNDGLSFISSSVIITTTHCSDGSILAIA 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 AA; 24505 MW;
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Best Local Similarity 49.0%
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                Local Similarity 90.0 hes 81; Conservative
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                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 VFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLC 257
                                                                                                                                              Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Ninomiya K., Wagatsuma M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamanoto J., Isono Y., Kawai Hio Y., Sato K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Sekine M., Kikuchi H., Murakawa K., Satio S., Nagahari K., Masuho Y., Sugiyama A., Sugiyama A., Kawakami B., Ranehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (Corr-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO55636; BAB709761; --
SEQUENCE 245 AA, 26111 MW, BIAE6EB0A2EBEE06 CRC64;
                                                                                           241 VRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 TYTVNETYTTSVKPVSVQLNSMLCPAPILNKAG------EWGLTVTQAGVKWHDLTH
                   241 VRGNGFRHARNYDRVLCSFKINDSVTLNERPFSVEDTYLLCPAPILKEVGMKAALQVSMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.0%; Score 574; DB 4; Length 245; ilarity 49.2%; Pred. No. 2.2e-42; Conservative 45; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                            245 AA.
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01-DEC-2001 (TREMBLrel. 19, Last annot
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Matches 120; Conserv
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                                                                                                                                                                                                                                                     361 ESEENKIK 368
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Q96EC6;
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Q96NC7;
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RESULT Q96EC6 ID Q90 AC Q91

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MEDLINE-93149203; PubMed-8426611;

MEDLINE-93149203; PubMed-8426611;

MEDLINE-93149203; PubMed-8426611;

MEDLINE-93149203; PubMed-8426611;

A Sequence of a major Eimeria maxima antigen homologous to the Eimeria art renella microneme protein Etpl00.";

MOI. Biochem. Parasitol. 57:171-174(1993).

MICHEPRO; IPR0002035; WWFA.

MICHEPRO; IPR0002035; WWFA.

MERBL; M990684; TSP1. 6.

MERPL; M00209; TSP1. 6.

MERRT; SM00209; TSP1. 6.

MERRT; SW00209; TSP1. 6.

MERRY; SW00209; TSP1. 6.

MERRT; SW00209; TSP1. 6.

MERTT; SW00209; TSP1. 6.

MER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 RDLGAIVYCVGVKDFNETQLARIA----DSKDHVFPVNDGFQALQGIIHSILKKSCIEILA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 GGRREDGG-----PACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimerlida; Eimeriidae;
Eimeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 EQIYYENROGYRT--------ASVIIALTDGELHEDLFFYSEREANRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTEGRIN ALPHA HR1.
W; 0D9108D2B05CFFAE CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MAJOR ANTIGEN HOMOLOGOUS SEQUENCE (EMP100).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.0%; Score 153.5; DB 5
Best Local Similarity 24.1%; Pred. No. 0.00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         724 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Mismatches
                         HSSP, P11215; 1A8X.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vWFA.
Fram; PF01839; FG-GAP; 5.
Pfam; PF001837; integrin_A; 1.
Pfam; PF00187; integrin_A; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 1332 INT
1332 AA; 145852 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398 GGKSAKTAG--YEMHFGENGF 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 AEPSTICAGESFOVVVRGNGF 246
   AB048261; BAB21479.1;
                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50234; VWFA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Q04588;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 DPQSLVDPIVQLQ----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 207
                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE---- 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21103187; PubMed=11160215;
Miyazawa S., Azumi K., Nonaka M.;
Cloning and characterization of integrin alpha subunits from the solltary ascidlan, Halocynthia roretzi.";
J. Immunol. 166:1710-1715(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.3%; Score 159.5; DB 11; Length 1161; 27.9%; Pred. No. 4.8e-05; tive 41; Mismatches 93; Indels 29;
                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of rat alpha D, a novel beta 2 integrin.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF021334; AAF21241.1; -.
HSSP: P11215; 1A8X.
InterPro; IPR00413; Integrin_alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 1161 AA; 126600 MW; 2258491A984A705E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 LOGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch
Gallatin W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00092; vwa; 1.
PRINTS: PR01185; INTEGRINA.
PRINTS: PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
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Pfam; PF00357; integrin_A; 1.
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01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY;
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                        ALPHA D INTEGRIN.
                                                                                                                                                                                                           NCBI_TaxID=10116;
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01-DEC-2001
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Q9BPQ8;
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Query Match
Best Local Similarity 24.7%
Matches 67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    ---ANRSRDLGAIVYCVGV-KDFNETQLARIA--DSKDHV-FP--VNDGFQALQGIIHSI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 LSAAEKLRNRGVIIVVLGVGTGVNSAECRSIAGCDTSDTVECPRYLQSNWGGVSSQINGI 228
                                                                                                                                                                                                                                   55 V-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQK 111
                                                                                                                                                                                                                                                              58 IGTSNYGKVRSFISNFAGTMPLSPDDVRVGLVTFGTSAVTRWDLSDSRAQNADLLAAAAK 117
                                                                                                                                                                                                                                                                                                                          112 VLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHEDLFFYSERE--- 164
                                                                                                   Gaps
                                                                                                                                            1 MATAERRALGIGFQWLSLATLVLICAG-----QGGRREDGGPACYGGFDLYFILDKSGS 54
                                                                                                                                                                           Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
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Translent expression of beta-galactosidase in differentiating

ROPIGE STATES OF STATES
                                                                                                                                                                                                                                                                                                                                                       43;
                                                     Length 724;
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MICRONEME PROTEIN ETMIC-1.
15B8F3C190B70F73 CRC64;
                                                                                                   Indels
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 19, Last annotation update)
MICRONEME PROTEIN ETMIC-1 PRECURSOR.
                                             7.9%; SCOLE __ 0.0001_,
25.9%; Pred. No. 0.0001_,
_***A 45; Mismatches 109;
_***A 45; Mismatches 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 LKKSCIEI----LAAEPSTI--CAGE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=HOUGHTON;
MEDLINE=92131064; PubMed=1775171;
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712 MI
74777 MW;
                                                                                                        Conservative
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37
712 AA;
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                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eimeria tenella.
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                                                            Query Match
Best Local Simi
Matches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
SEQUENCE
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SIGNAL
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14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFP-----VNDGFQ 206
                                                                                                                                                                                                                                                                             109 LOKVLPG-------GDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGEL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSV-LHHWNEIYYFVEQLAHKF-ISPQ-LRMSFIVFSTRGTTLMKLTEDREQIRQGLEE 108
                                                                                                                                                             Gaps
                                                                                                                1 MATAERRALGIGFQWLSLATLVLICAG-----QGGRREDGG--PACYGGFDLYFILDK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rowen L., Madan A., Qin S., Hall J., Dahl T., James R., Dickhoff R., Schaffer T., Ratcliffe A., Abbasi N., Loretz C., Lasky S., Hood L.; "Sequence of the mouse MHC class III region."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rowen L., Qin S., Lasky S.R., Loretz C., Dors M., Mahairas G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
COMPLEMENT FACTOR C2 (COMPLEMENT COMPONENT 2) (WITHIN H-2S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                Indels
; Score 137.5; DB 5;
; Pred. No. 0.0021;
43; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 760 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 ALQGIIHSILKKSCIEILAAEPSTI--CAGE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 QVNGIIKAACKDLAKDAVCSEWSEYGPCVGE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI 188226, C2.
InterPro; IPR00134; Chymotrypsin.
InterPro; IPR00134; Sushi_SCR_CCP.
InterPro; IPR001254; Trypsin.
InterPro; IPR002035; vWFA.
InterPro; IPR002035; vWFA.
InterPro; IPR002035; vWFA.
InterPro; IPR002035; vWFA.
InterPro; IPR00225; CHYMOTRYPSIN.
IPRNTS; PR00423; VWFADOMAIN.
SMART; SM00032; CCP. 2.
SMART; SM00020; Tryp_SPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 291-760 FROM N.A.
            7.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
STRAIN=129;
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16;
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                                                                                                                                                                                                                                                                                                                                                                               DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE-------NRQGYRTAS- 143
                                                                                                                                                                                                                                                                                                                 :| | :: :|: | :: | :: | :: | ERSQ-----DVTEVIELESASYRDHENATGTNTYEVLIRVYSMMQSQMDRLGMETSAW 371
                                                                                                                                                                                                                                                                                                                                                             144 -----VIIALTDGELHEDLFFYSEREANRSRDLGAI------VYCVGV------KD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNGFRHARNVDRV--LCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMK--AALQVS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473 GNMSANASDQERTPWQVTFKPKSKETCQGS--LISDQWVLTAAHCFHDIQMEDHHLWRVN 530
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                           41 GGFDLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLRMS--FIVFSTRGTTLMKLTE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE-20183852: pubmed-10717300;
LOVett J.L., Howe D.K., Sibley L.D.;
"Molecular characterization of a thrombospondin-related anonymous
                                                                                                                                                       Query Match 7.0%; Score 134; DB 11; Length 760; Best Local Similarity 23.5%; Pred. No. 0.0046; Matches 75; Conservative 55; Mismatches 115; Indels 7
                                                                                                                                                                        ; Pred. No. 0.0046;
55; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 765 AA; 82880 MW; 9727838CC1FE8CD4 CRC64;
                                                                                                       91C896A3EDC7D448 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
THROMBOSONDIN RELATED ADHESIVE PROFEIN HOWOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein homologue in Neospora caninum.";
Mol. Blochem. Parasitol. 107:33-43(2000).
EMBL; AF061273; ARF01565.1; -.
InterPro; IPR001969; ASP_protease.
InterPro; IPR00884; TSP1.
SMART; SM00327; VWA; 1.
PROSITE; PS50240; TRYPSIN_DOM; 2.
PROSITE; PS00134; TRYPSIN_HIS; UNRNOWN_1.
PROSITE; PS00234; TRYPSIN_SER; UNRNOWN_1.
PROSITE; PS50234; VWFA; 2.
Hydrolase; Serine protease.
SEQUENCE 760 AA; 84741 MW; 91C896A3EI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00141; ASP_PROTEASE; PROSITE; PS50092; TSP1; 6. PROSITE; PS50234; VWFA; 1. SEQUENCE 765 AA; 82880 MW; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MND-----GLSFISSSVII 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  531 VGDPTSQHGKEFLVEDVII 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00090; tsp_1; 6.
Pfam; PF00092; vwa; 1.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM0209; TSP1; 6.
SMART; SM00327; VWA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29U8J9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 ILITDGK-SSDAF---RDPAIKLRNSDVEIFAVGVKDAVDSELEAIASPPAETHVFTVED 302
                                                                                                                                                                                                                                                                         128 HWSLRANNASDKETAMQ--DVLTIPYHGGTTNTAAGLQTCNQMLFDYPREERQTVPKLVI 185
                                                                                                                                                                                                                                                                                                                                                                              TTLMKLTEDREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYRT--ASVI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVND 203
                                                                                                                                                                                                                                                                                                                                             147 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDF-NETQLARIADSKDHVFP----V 201
                                                                                                                                                72 CTSQLDICFLVDSSGSIGEAHYEE----VKQFLHAFLSKLPIGNDEVNTSLVIFSTTVHP 127
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98003048; PubMed-9344363; Wessel H., Anderson S., Fite D., Halvas E., Hempel J., SundarRaj N.; Wessel H., Anderson S., Fite D., Halvas E., Hempel J., SundarRaj N.; Type XII collagen contributes to diversities in human corneal and limbal extracellular matrices."; Invest. Ophthalmol. Vis. Sci. 38:2408-2422(1997). EMBL; U68139; AAC01506.1; F. EMBL; EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYGGFDL---YFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFST---RG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                   CYGGFDLYFILDKSGSVLH-HWNEIYYFVEQLAHKFIS-----PQLRMSFIVFSTRGTT
                                                                                                                                                                                                                             LMKL----TEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY-YENRQGYRTASVII
                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
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Length 765;
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                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56727 MW; 9B6972F44A1BD88F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
6.9%; Score 132.5; DB 5; 25.1%; Pred. No. 0.0063; tive 35; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              517 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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InterPro; IPR002035; vWFA.
Pfam; PF00041; fn3; 3.
Pfam; PF00453; vWeADOMAIN.
SMART; SM0060; FN3; 3.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, C)
01-JUN-1998 (TrEMBLrel. 06, Ls
01-DDC-2001 (TrEMBLrel. 19, Le
TYPE XII COLLAGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 NDGFQALQGIIHSILKKSC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 QTEWSQLLPSISPILKEVC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50234; VWFA; 1.
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51,
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517
517 AA;
                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-CORNEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collagen.
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SEQUENCE
  Query Match
Best Local S:
Matches 50
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Best Local 3
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043853
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63; Gaps

Indels

Length 920;

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Last sequence update)
Last annotation update)
RECEPTOR MUA-3 PRECURSOR (K08E5.3 PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 --------REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYXENRQGYR- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 THFTENDEKRNPSPKLLVRPIRQLL------GRTHTATGIRKVVRELFH-SKSGARE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 -TASVIIALTDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FN----ETQLARIA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 DSK--DHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 SKPCGDHVFQVNN-FEAVKTIQNQLQEKT----FAIEGTQTGSTSSFECEMSQBGFSAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Caenorhabditis elegans.
Elkaryota: Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                          44 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISP---QLRMSFIVFSTRGTTLMKLTED-- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lu Z., Vogel B., Hedgecock B.; "Lu Z., Vogel B.; mRNA Splicing Pattern Revealed."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
Lee J.-K., Schook L.B., Rutherford M.S.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U40072; AAB16869.1; -.
HSSP; P11215; 1A8X.
                                                                                                                                                                                                                                                                                                    102440 MW; E96CC51E350DD5AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          72;
                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                  6.8%; Score 130.5; DB
26.4%; Pred. No. 0.012;
1ve 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 3767 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                      InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWFA.
Pfam; PF01839; FG-GAP; 4.
Pfam; PF00092; Vwa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             investigating biology.";
Science 282:2012-2018(1998).
Smbl; AF139060; AAD29428-1;
EMBL; Z30974; CAA83226-2;
EMBL; Z30423; CAA83226.2; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    090113; 021340;
01-MAY-2000 (TrEMBLrel. 13, Cr
01-MAY-2000 (TrEMBLrel. 13, La
01-DEC-2001 (TrEMBLrel. 19, La
TRANSMEMBRANE CELL ADHESION RE
(FRAGMENT)
                                                                                                                                                                   PEINTS; PRO1185; INTEGRINA.
PRINTS; PRO1453; VWFADOMAIN.
SMART; SMO0191; INT_Alpha; 4.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                             26.48;
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.4%
Matches 63; Conservative
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                                                                                                                                                                                                                                                                                              920
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                                                                                                                                                                                                                                                                                                                   920 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUA-3 OR K08E5.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kershaw J.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=N2;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 HEDLFFYSERBANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8%; Score 131; DB 4; Length 660; 29.8%; Pred. No. 0.007; tive 38; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith M.;
Submitthed (JAN-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2000): CAB65984.1; -.
HSSP; P11215; 1BHQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      660
72523 MW; 3E3A10A285ECAA51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ234PIS.1 (COLLAGEN, TYPE XII, ALPHA 1) (FRAGMENT).
COL12A1.
                                                                                                                                                                         660 AA.
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                               204 GFQALQGIIHSILKKSCIEI---LAA 226
                                                               303 -FDAFQRISFELTQSICLRIEQELAA 327
                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, C. 01-NOV-1996 (TrEMBLrel. 02, L. 01-FEB-1997 (TrEMBLrel. 19, L. CD11B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003961; FN_III.
InterPro; IPR003961; vWFA.
Pfam; PF00041; fn3; 2.
Pfam; PF00042; vwa; 2.
PRINTS; PR00453; vWFADOMAIN.
SMART; SM0060; FN3; 2.
SMART; SM00327; VWA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 IHSILKKSCIEI---LAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          638 SFELTOSICLRIEQELAA 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50234; VWFA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 29.88
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         660 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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NON_TER
SEQUENCE
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Q28984
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                                                                                                                                         RESULT 12
Q9UGC3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEMBRANE CELL ADHESION RECEPTOR MUA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 HKFI--SPQLRMSFIVFSTRGTTLMKLTE--DREQIRGGLEELQKVLPG----GDTYMH- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --EGFERASEQIYYENRQGYR----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 174
                                                                                                                                                                                                                                                                                                    R PRINTS; PRO0289; UNESTWEERIN.

R PRINTS; PRO0289; UDIRECEPTOR.

R PRINTS; PRO0281; LDLRECEPTOR.

R SMART; SMO0181; EGF_CA; 1.

SMART; SMO0179; EGF_CA; 1.

SMART; SMO0192; EGF_CA; 1.

SMART; SMO0192; EGF_CA; 1.

SMART; SMO0192; EGF_CA; 1.

R SMART; SMO0102; SEA; 2.

SMART; SMO0102; SEA; 2.

R SMART; SMO0102; EGF_C; 1.

R PROSITE; PSO0101 ASX_HYDROXXL; UNKNOWN_1.

R PROSITE; PSO1187; EGF_1; UNKNOWN_1.

R PROSITE; PSO1187; EGF_2; 6.

R PROSITE; PSO108; LDLRA_2; 2.

R PROSITE; PS50068; LDLRA_2; 2.

R PROSITE; PS50064; SEA; 4.

R PROSITE; PS50024; SEA; 4.

R PROSITE; PS50024; SEA; 4.

R PROSITE; PS50024; SEA; 4.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 19, Last annotation update)
INTEGRIN BETA 2 ALPHA SUBUNIT.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 CYGGF------NNEIYYFVEQLA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.7%; Score 128; DB 5; Length 3767; Best Local Similarity 27.1%; Pred. No. 0.14; Matches 64; Conservative 31; Mismatches 75; Indels 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3767 AA; 417284 MW; 8DA3AE5EA50AEB8E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
             Interpro: IPR00152; Asx_hydroxyl.
Interpro: IPR001562; Disintegrin.
Interpro: IPR001561; BGF-1ike.
Interpro: IPR001881; BGF-Ga.
Interpro: IPR001082; BGL.
Interpro: IPR001082; SEA.
Interpro: IPR0010035; vWFA.
Ffam; PF00108; BGF; 33.
Pfam; PF001390; SEA: 2.
Pfam; PF001390; SEA: 2.
Pfam; PF00092; vwa: 1.
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SEQUENCE FROM N.A.
Fathallah D.M. Sr., Zerria K. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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25 >3767
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SEQUENCE
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09JI30;
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Q9JI30
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Search completed: August 9, 2002, 10:46:19 Job time: 842 sec

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hits satisfying chosen parameters: Total number of

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT

collagen alpha 2(V	hypothetical prote	collagen alpha 3(V	dnak protein NMB05	integrin alpha-1 c	collagen alpha 3(V	hypothetical prote	integrin alpha-1 -	probable retroelem	transcription regu	arginyl-tRNA synth	inter-alpha-inhibi	integrin alpha-E c	integrin alpha-1 c	undulin 1 - human
SUS646	T04822	CGHU3A	н81185	A45226	A37797	T47637	A55348	F84811	AF1166	E87665	JC5953	A53213	A35854	A40970
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on d	. 5	86	97.5	97	46	96.5	96	96	95.5	95.5	95.5	95.5	95.5	94
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## ALIGNMENTS

antigen Em100 - Eimeria maxima

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Antityen Emilion - Elmeria maxima (Species: Elmeria (Species: Elmeria (Species: Elmeria) (Species: Elmer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 IGTSNYGKVRSFISNFAGTMPLSPDDVRVGLVTFGTSAVTRWDLSDSRAQNADLLAAAAK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 VLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHEDLFFYSERE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.9%; Score 150.5; DB 2; Length 7 25.9%; Pred. No. 0.00039; tive 45; Mismatches 109; Indels
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Best Local Similarity 25.96
Matches 69; Conservative
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Query Match
Best Local Similarity
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A; Residues: 1-9 <SHE>
A; Residues: 1-9 <SHE>
A; Residues: 1-9 <SHE>
A; Cross-references: GB: M7624; NID: 9180018; PIDN: AAA58410.1; PID: 9553215
A; Cross-references: GB: M7624; NID: 9180018; PIDN: AAA58410.1; PID: 9553215
A; Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.
Broc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988
A; Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesi
A; Reference number: A94193; MUID: 88190151
A; Reference number: A94193; MUID: 88190151
A; Residues: 917-1042 <AR2>
A; Residue
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A; Residues: 9-1133 < HHC.
A; Residues: 9-1133 < HHC.
A; Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A; Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A; Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A; Note: part of this sequence was confirmed by protein sequencing
A; Fleming, J.C.; Pahl, H.L.; Ganzalez, D.A.; Smith, T.F.; Tenen, D.G.
A; Timmunol. 150, 480-490, 1993
A; Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in alreance number: A46526; MUID:93123748
A; Reference number: A46526
A; Status: not compared with conceptual translation
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"""."" surface glycoprotein CD11b precursor [validated] - human
N;Alternate names: complement receptor type 3 alpha chain; leukcyte adhesion protein Ma
N;Alternate names: complement receptor type 3 alpha chain; leukcyte adhesion protein Ma
eukcoyte integrin alpha chain; neutrophil adherence receptor alpham chain
C;Species: Homo sapiens (and 120 and 120 and
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A; Molecule type: machine the codon TAC for residue 1129 as Thr
A; Note: part of this sequence, including the amino end of the mature protein, was confir
B; Shelley, C.S.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A; Mitle: The promoter of the CD11b gene directs myeloid-specific and developmentally reg
A; Reference number: A41600; MUID:92073318
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A; Regidues: 1-499,501-1153 <FLE>
A; Rolecule type: DNA
A; Residues: 1-499,501-1153 <FLE>
A; Cross-references: GB:S52227; NID:9263047; PIDN:AAB24821.1; PID:9263049
A; Cross-references: GB:S52227; NID:9263047; PIDN:AAB24821.1; PID:9263049
A; Note: the last three bases of intron 13, CAG, are included in some but not all mature as Note: sequence extracted from NCBI backbone (NCBIP:121963)
A; Note: Remolad-O'Donnell, E:, Todd III, R.F.; Arnaout, M.A.
Biochim. Biophys. Acta 874, 368-371, 1986
A; Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across she reference number: A90664; MUID:87076671
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A, Recession: A31108
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-1153 <COR>
A, Oross-references: GB:103925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A, Note: part of this sequence was confirmed by protein sequencing
B, Arnaout, M.A.; Gupta, S.K.; Plerce, M.W.; Tenen, D.G.
J. Cell Biol. 106, 2153-2158, 1988
A, Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor
A, Reference number: A28915; MUID:88257215
A, Accession: A28915
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A; Residues: 17-31 <PIES
A; Experimental source: granulocytes
R; Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
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RWHOIC cell surface glycoprotein CDIIc precursor - human (2611 surface glycoprotein CDIIc precursor - human (341 surface glycoprotein CDIIc precursor - human (341 surface glycoprotein deadhesion receptor pl50,95 alpha chain (352 species: Homo sapiens (man) (352 pecies: J090 pecie
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A;Genes (GDB:ITGAM; CR3A
A;Genes (GDB:ITGAM; CR3A
A;Genes (GDB:I20599; OMIM:120980
A;Map position: 16p11.2-16p11.2
A;Map position: 16p11.2-16p11.2
A;Note: promoter contains a GATA motif and two Spl consensus binding sites
A;Note: promoter contains a GATA motif and two Spl consensus binding sites
A;Note: promoter contains a GATA motif and sites and adhesion; glycoprotein; cell adhesion; glycoprotein; cell adhesion; glycoprotein; heterodimer;
C;Neywords: alternative splicing; calcium; cell adhesion; glycoprotein colls **status predicted colls 
                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M84477; NID:g180184; PIDN:AAA51960.1; PID:g553219
C;Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac
C;Genetics:
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A;Residues: 1-834 <CO2>
A;Note: this sequence has been revised in reference A36584
A;Otte: this sequence has been revised in reference A36584
R;Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
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Blood 79, 865-870, 1992
A;iiie: Characterization of the myeloid-specific CD11b promoter.
A;Reference number: 152567; MUID:92144986
A;Accession: 152567
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C.Genetics: EMBL.78073; 2897/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1
C.Genetics:
C.Genetics: EMBL.78073; 2897/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1
C.Guperfamily: collagen alpha 1(XII) chain; fibronectin type III repeat homology; von C.Guperfamily: collagen alpha 1(XII) chain status predicted coll; connective tissue; disulficial sylfomatic signal sequence $status predicted coll; connective tissue; disulficial sylfomatic solutions and pha 1(XII) chain short splice form #status predicted colls.
F;34-3124/Product: collagen alpha 1(XII) chain short splice form #status predicted colls.
F;34-114/Domain: fibronectin type III repeat homology cWA3>
F;33-415/Domain: fibronectin type III repeat homology cWA3>
F;33-414/Domain: fibronectin type III repeat homology cWA3>
F;33-414/Domain: fibronectin type III repeat homology cWA3>
F;33-414/Domain: fibronectin type III repeat homology cWA3>
F;33-4100/Domain: fibronectin type III repeat homology cWA3>
F;34-4100/Domain: fibronectin type III repeat homology cWA4>
F;34-4100/Domain: fibronectin type III repeat homology cWA4>
F;322-4100/Domain: fibronectin type III repeat homolog
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A. Residues: 'X',1333,'O',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-251
A. Residues: 'X',1333,'O',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-251
B. Dublet, B., 'wan der Rest, 'n'
J. Biol. Chem. 262, 17724-17727, 1987
A. Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of peps
A. Reference number: $22254; MUID:88087065
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F;3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
F;32,1006,1032,1044,1512,1767,2210,2273,2532,2683/Binding site: carbohydrate (Asn) (c
R;Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A;Title: Type XII collagen: distinct extracellular matrix component discovered by cDN A;Reference number: A28037; MUID:87317590
A;Accession: A28037
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A; Residues: 2960-2976, F', 2978-3074,'AG' <GOR3>
A; Cross-references: EMBL:M1375; NID:q211649; PIDN:AAA48718.1; PID:q211650
A; Note: this sequence has been revised in reference A34485
R; Koch, M.; Bernasconi, C.; Chiquet, M.
Bur. J. Bloochem. 207, 847-856, 1992
A; Title: A major oligomeric fibroblast proteoglycan identified as a novel 1
A; Reference number: S23814; MUID:92362621
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A,Molecule type: protein
A.Residues: 2831-2832, T',2834, R',2836-2843;3002-3014 <DUB>
B,Truueb, J.; Trueb, B.
Blochim. Biophys. Acta 1171, 97-98, 1992
A,Title: The two splice variants of collagen XII share a common 5'
A,Reference number: $28811; MUID:93042014
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non-collagenous NC2 #status predicted <NC2>
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A;Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
A;Cross-references: EMBL:X67327
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F; 2509-2750/Domain:
F; 2751-2902/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F; 2899-2901/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NyAlternate names: fibrochimmeria
C:Species: Gallus gallus (chicken)
C:Species: Gallus (chick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-3124 cYAMA
A; Cross-references: GB:D00824; NID:g222810; PIDN:BAA00701.1; PID:g222811
A; Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and,
B; Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
A; Biol. Chem. 264, 1977-1977, 8, 1989
A; Title: Type XII collagen. A large multidomain molecule with partial homology to type I
A; Reference number: A34485; MUID:90062079
                                                     A; Title: cDNA cloning and complete primary structure of the alpha subunit of a leukocyte A; Reference number: $00864; MUID:88166645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  m
Y
                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-755, 'L., 757-1163 <CO3>
A; Residues: 1-755, 'L., 757-1163 <CO3>
A; Costoss-references: GB:MB1695; EMBL:Y00093; NID:9487829; PIDN:AAA59180.1; PID:9487830
A; Note: part of this sequence was confirmed by protein sequencing
C; Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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A;Residues: 2456-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g211285
A;Accession: B34485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE-- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 NPLSLLASVHOLQ----GFTYTATAIQNVVHRLFHASYGARRDATKILIVITDGKKEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 ---QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTAS-VIIALTDGELHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 LFFYSEREANRSRDLGAIVYCVGV------KDFNETQLARIAD--SKDHVFPVNDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 7.5%; Score 143.5; DB 1; Best Local Similarity 24.8%; Pred. No. 0.0027; Matches 55; Conservative 43; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collagen alpha 1(XII) chain precursor - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 2772-2792; 2846-2873 <GOR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: GDB: ITGAX; CD11C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A40020
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A, Nest Juues: 1 (14 12 12 12)
A, Cross references: GB: AF032905, GB: W/3495; NID: g2707732; PIDN: AAD03350.1; PID: g27077
A; Cross references: GB: AF032905, GB: W/3495; NID: g2707752, NCBIP: 77756)
A; Note: sequence extracted from NCBI backbone (NCBIN: 77752, NCBIP: 77756)
C; Superfamily: thrombospondin type 1 repeat homology; Von Willebrand factor type A repeat homology CWMAl>
F; 48-218-Domain: thrombospondin type 1 repeat homology CWHR2>
F; 309-371/Domain: thrombospondin type 1 repeat homology CWHR2>
F; 432-493/Domain: thrombospondin type 1 repeat homology CWHR3>
F; 494-356/Domain: thrombospondin type 1 repeat homology CWHR4>
F; 560-610/Domain: thrombospondin type 1 repeat homology CWHR6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Eimeria tenella
C;Date: 22-Apr.1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Datession: A45638
R;Tomley, F.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.
Mol. Biochem. Parasitol. 49, 277-288, 1991
A;Title: Sequence of the gene encoding an immunodominant microneme protein of A;Reference number: A45638; MUID:92131064
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C;Species: Gallus gallus (Chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A45974; S30085; S22916; S17035; S20833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 PKATNPSLAISAARSLSYSTGVTYTHYGLODA-KKLLYDTNAGARNNVPKLVLVMTDGA- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 SGSV-LHHWNEIYYFVEQLAHKF-ISPQ-LRMSFIVFSTRGTTLMKLTEDREQIRQGLEE 108
                                                                                                                                                                                              VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFK 260
                                                                                                    1 MAPLPRRRLA---PCRALSLLVGLLAASFAFSSLQPGATTSSGQDQVCTSLLDVMLVVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --GDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 -SNLPSQTRSSAAALRDAGAIVVVLGVGSGVNSSECRSIAGCSTSNCPRYLQSNWSNVTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MATAERRALGIGFQWLSLATLVLICAG-----QGGRREDGG--PACYGGFDLYFILDK
198 IHFTENDFKRNPSPRSHVSPIKQLNGRTKTASGIRKVVRELFHKTNGARENAAKILVVIT
                                                                 DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNETQLARIAD-----SKDHVFP
                                                                                                                                                                                                                                                                                                                              261 INDSVTLNEKPFSVEDTYLLCPAPILKEVG----MKAALQVSMNDGLSFISSS 309
                                                                                                                                                                                                                                                                                                                                                                       356 -SASITSN------GPLLGSVGSFDWAGGAFLXTSKDKVTFINTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagen alpha 1(XIV) chain precursor, short form 2 - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunodominant microneme protein Etp100 - Eimeria tenella
                                                                                                                                                                                                                                           Score 137.5; DB pred. No. 0.0043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 ALQGIIHSILKKSCIEILAAEPSTI--CAGE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.28;
24.78;
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Best Local Similarity
Matches 67; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues:
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A; Cross-references: EMBL:X07640; NID:952992; PIDN:CAA30479.1; PID:952983
A; Cross-references: EMBL:X07640; Discover. W.J.; Geo, C.E.; Larson, R.S.; Roberts, Proc. Ratl. Acad. Sci. U.S.A. 89; 5644-5648, 1986
A; Title: A partial genomic DNA clone for the alpha subunit of the mouse complement receptance number: I59078
A; Accession: I59078
A; A; Company: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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C;Keywords: cell adhesion; giycoprotein; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental
F;148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F;1106-1129/Domain: transmembrane #status predicted <TWM>
                        #stat
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                    F;2780,2789,2836,2842,2860,2866,2869,3004,3007/Modified site: hydroxyproline (Pro)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse N;Alternate names: complement-3 receptor alpha chain C;Species: Mus musculus (house mouse) C;Date: 30.5ep-1989 #sequence_revision 30.5ep-1991 #text_change 22-Oct-1999 C;Accession: S00551; I59078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----REQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYE-NRQGYRTASVIIALT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         QIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHED 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDRE 100
                                                                                                                                                                                                                                                                                                             ---EQELAAIRKKSYVPAKNMVFSDVTSDSFKVSWSAAGSE-- 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB: M14293; NID: 9198993; PIDN: AAA39484.1; PID: 9554193
                                                                                                                                                                                                                                                                                                                                                                                                                                  215 ILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNV---DRVLCSFKINDSVTLNEKP
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                                                                                                                         Length 3124;
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                                                                                                                                                                                              97;
                                                                                                                            7.5%; Score 143; DB 1; 26.1%; Pred. No. 0.011;
                                                                                                                                                                                       Conservative 51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 24.2
71; Conservative
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611 LTQSVCLRI-----
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                                                                                                                                                                  Local Similarity
nes 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 FSVEDTYLL 280
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Best Local S
Matches 71
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                                                                                                                                             Query Match
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Gaps

53;

Indels

Length 712;

DB 2; 108; 51

---RSKVRWNLSD 106

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----VIIALTDGELHEDLFFYSEREANRSRDLGAI------VYCVGV-----KD 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.8%; Score 131; DB 1;
llarity 23.2%; Pred. No. 0.016;
Conservative 56; Mismatches 115;
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Best Local Similarity
Matches 74; Conserv
                   :| | |
1151 NVYPCYRL 1158
   SVEDTYLL 280
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R;Trueb, J.; Trueb, B. BEL:X65122; NID:g62871; PIDN:CAA46238.1; PID:g938175
R;Trueb, J.; Trueb, B. BEL:X65122; NID:g92871; PIDN:CAA46238.1; PID:g938175
BLT. J. Blochem. 207, 549-557, 1992
A;Reference number: $22916; MUD:92339443
A;Reference number: $22916; MUD:92339443
A;Residues: $286-494, 0', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439 <TRU>A;Residues: $286-494, 'Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439 <TRU>A;Residues: $286-494, 'Q', 333-338, 1991
A;Residues: $286-494, 'Q', 333-338, 1991
A;Reference number: $17035; MUD:92037585
A;Accession: $17035
A;Accession: $17035
A;Accession: $17035
A;Accession: $17035
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin
J. Biol. Chem. 268, 12177-12184, 1993
A;Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE 155
                                                                      A:Status: preliminary
A:Wolecule type: mRNA: protein
A:Rolecule type: mRNA: protein
A:Residues: 1-1747 <GER>
A:Experimental source: embryo skin
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365)
R:Apte, S.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>
F;1554-1659/Domain: triple helical domain COL1 #status predicted <COL1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPF
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                                                                                                                                                                                        Library, March 1992
                                                         Reference number: A45974; MUID:93280195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.48;
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                                                                                                                                             submitted to the EMBL Data Li A; Reference number: $30085 A; Molecule type.
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Best Local Similarity
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Gaps

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A; Reterence number: 531211
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-416;1460-1811,1843-1888 <WAE>
A; Molecule type: mRNA
A; Residues: 1-416;1460-1811,1843-1888 <WAE>
A; Cross-references: EMBL:X70793
C; Genetics:
C; Gen
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C;Species: Caenorhabditis elegans
C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C;Accession: 842373
R;Smith, A.
Submitted to the EMBL Data Library, March 1994
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                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-1888 <TRU>
A; Cross-references: EMBD:X70793; NID:9288872; PIDN:CAA50064.1; PID:9288873
R; Waelchli, C.; Trueb, J; Ressler, B.; Winterhalter, K.H.; Trueb, B.
Bur, J. Biochem. 212, 483-490, 1993
A; Title: Complete primary structure of chicken collagen XIV.
A; Reference number: S31211; MUID:93185668
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collagen alpha 1(XIV) chain precursor, long form - chicken
C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uvery Match 6.8%; Score 130; DB 2
Best Local Similarity 25.0%; Pred. No. 0.066;
Matches 62; Conservative 44; Mismatches
                                                                                                                                                                                                        submitted to the EMBL Data Library, January 1993 A; Reference number: S78476 A; Accession: S78476
                                                                                                                                           C; Accession: S78476; S31211
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Br. Maelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.

Br. Maelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.

Br. Diochem. 212, 483-490, 1993
Br. Trueb, B.

Br. Maelchli, C.; Trueb, B.; Winterhalter, K.H.; Trueb, B.

Br. Maelchle of primary structure of chicken collagen XIV.

A; Reference number: S31211; MuID:93185668
A; Accession: S31212
A; Retais: nucleic acid sequence not shown; translation not shown
A; Residues: 1-1857 <WAE>
A; Residues: 1-1857 <WAE>
A; Residues: Br. Minh
A; Residues:
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C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Aug-1999
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                                                                                                                                                                                                    183 FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 242
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                                                                                                                                                                                                                                                                                                                               299 MND-----GLSFISSSVII 312
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531 VGDPTSQHGKEFLVEDVII 549
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Complement factor B precursor [validated] - human
N;Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; he
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragmen
C;Species: Homo sapiens (ann)
C;Date: 19-Feb-1984 #sequence_revision 05-Aug-1994 #text_change 08-Dec-2000
C;Accession: S34075; A44622; A00934; A19188; A19947; B19947; B25971; S14339; A44628;
R;Mejla, J.E.; Jahn, I.; de la Salle, H.; Hauptmann, G.
Submitted to the EMBL Data Library, March 1993
A;Reference number: S34075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U19494; NID:g632647; PIDN:AAA80217.1; PID:g632648 C;Superfamily: collagen alpha 1(XII) chain; fibronectin type III repeat homology; von F;155-236/Domain: fibronectin type III repeat homology <3FR> F;155-236/Domain: von Willebrand factor type A repeat homology <WAA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C:Species: Notophthalmus viridescens, Triturus viridescens (Eastern-Change 21-Jan-2000
C:Accession: I51027
R:Wei, Y: Yang, E.V.; Klatt, K.P.; Tassava, R.A.
Dev. Biol. 168, 503-513, 1995
A;Title: Monoclonal antibody MTZ identifies the urodele alpha 1 chain of type XII chancesion: I51027
A;Reference number: I31027; MUID:95246925
A;Reference number: I31027; MUID:95246925
A;Reference number: I51027
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                                                                                                                                                                                                                                                                             366
                                                                                                                                                                                                                                                                                                                                                                    134 ENROGYRTAS--VIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARI 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFFYSEREANRSRDLGAIVYCVGVKDFNETOLARIADSKDHVFPVN-DGFQALQGIIHSI 215
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81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 ADS--KDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGES---FQVVVRG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ICAGGGGRREDGGPACYGGFDLYFILDKSGSVL-HHWNEIYYFVEQLAHKF-ISPQLRMS
                                                              82 FIV---FSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY----Y
                                                                                                                                                                                                                                                                                                                                                                                                                              RQGLEELQKVLP - - GGDTYMHEGFERASEQIYYENRQGY - - - - RTASVIIALTDGELHED
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                                                                                                                                                                                                                                                                        315 GLVQYSSSVRQEFPLGRFHTKKDIKAAVRNM-----SYMEKGTMTGAALKYLIDNSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 FSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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Matches 57,
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A; Residues: 1-496 <JEN>
A; Cross-references: GB:J05667
A; Accession B37979
A; Molecule type: mRNA
A; Residues: 157-290, 'L', 292-496 <JE2>
A; Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1; PID:g
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                                                                                      A; Molecule type: DNA
A; Residues: 1-3051 <SMI>
A; Residues: 1-3051 <SMI>
A; Cross-references: EMBL: Z30423; NID: 9458479; PID: 9458485
C; Genetics: SMI: 16673; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1;
C; Superfamily: von Willebrand factor type A repeat homology; EGF homology; fibronectin t; F; 512-679/Domain: von Willebrand factor type A repeat homology <VWAl>
F; 744-793/Domain: EGF homology <EGF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --EGFERASEQIYYENRQGYR----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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F;1-22/Domain: signal sequence *status predicted <SIG>
F;23-496/Product: cartilage matrix protein *status predicted <MAT>
F;39-206/Domain: von Willebrand factor type A repeat homology <VWAl>
F;27-262/Domain: EGF homology <EGF>
F;273-437/Domain: von Willebrand factor type A repeat homology <VWAS>
F;75-443/Domain: von Willebrand factor type A repeat homology <VWAS>
F;6.344/Binding site: carbohydrate (Asn) (covalent) *status predicted
F;221-238,234-247,249-262/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 128; DB 2; Length 3051;
; Pred. No. 0.18;
31; Mismatches 75; Indels 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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A,Cross-references: GDB:127280; OMIM:115437
A,Rap position: 1p35-1p35
A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
C;Complex: homotrimer
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25.3%; Pred. No. 0.065;
ative 37; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.78; 27.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 64; Conservative
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Best Local Similarity
Matches 60; Conserv
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Best Local Similarity
                                                    Accession: S42373
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A.Pathway: complement alternate pathway
A.Pathway: complement C2; complement factor H repeat homology; trypsin homology;
C;Superfamily: complement C2; complement alternate pathway; duplication; glycoprotein; hyd
C;Reywords: acute phase; complement alternate pathway; duplication; glycoprotein; hyd
C;Reywords: acute phase; complement factor B *tatus experimental <MAT>
F;26-75/Domain: signal sequence *tatus predicted <SIG>
F;26-259/Product: complement factor B fragment #status experimental <BAF>
F;36-359/Product: complement factor H repeat homology <FH1>
F;103-158/Domain: complement factor H repeat homology <FH2>
F;268-458/Domain: complement factor H repeat homology <FH3>
F;268-458/Domain: von Willebrand factor Hype A repeat homology <VFA>
F;482-752/Domain: trypsin homology *status atypical <TRX>
F;37-76,62-98,103-145,131-138,165-205,191-218,470-596,511-527,599-615,656-682,695-725
F;37-76,62-98,103-145,131-138,165-205,191-218,470-596,511-527,599-615,656-682,695-725
F;329-260/Cleavage site: arbobydrate (Asn) (covalent) *status experimental
F;529-260/Cleavage site: Arg-Lys (complement factor D) *status experimental
F;526,576,699/Active site: His, Asp, Ser *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 6p21.3-6p21.3
A; Introns: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3;
A; Introns: 21/3; 99/3; 346/1; and be incompleted as a solution of an and be incompleted by the major histocompatibility complex, class III region a; Note: gene is located in the major histocompatibility complex, class III region c; Complex: complement factor B initially forms an inactive complex with complement factor c3b forming active C3/C5 convertase; Ba is released
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-764 <RES>
A;Cross-references: GB:S67310; NID:9452937; PIDN:AAD13989.1; PID:94261689
A;Cross-references: GB:S67310; NID:9452937; PIDN:AAD13989.1; PID:94261689
B;Horituchi T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Fujita, S.; Volanakis, J.E.
Myl. Immunol. 30, 1587-1592, 1993
A;Fitle: Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic of A;Reference number: 157824; MUID:94067177
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A;Molecule type: mRNA
A;Residues: 1-31, Q', 33-764 <RE25
A;Residues: 1-31, Q', 33-764 <RE25
A;Cross-references: GB:L15702; NID:g291921; PIDN:AAA16820.1; PID:g291922
C;Comment: 292-Cys has a free sulfhydryl.
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19.6%; Pred. No. 0.43;
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Best Local Similarity 19.6
Matches 66; Conservative
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A, Molecule type: protein
A, Molecule type: protein
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A; Note: binding site for carbohydrate to lysine under artificial conditions
A; Note: binding site for carbohydrate to lysine under artificial conditions
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B, Molecule type: A, Molecule type: mRNA
A; Molecule ty
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A; Residues: 339-509 cCA1>
A; Cross-references: GB:J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
A; Cross-references: GB:J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
B; Wu, L.; Morley, B.J.; Campbell, R.D.
Cell 48, 331-342, 1987
A; Title: Cell-specific expression of the human complement protein factor B gene: evidend
A; Reference number: A25971; MUID:87102880
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A; Residues: 467-546; 550-595; 752-764 <moo>
A; Note: the authors translated the codon TAC at 519 as Thr; the nucleic acid translation
B; Mole: 7. Anderson, 7. K; Davison, E.A.; Woods, D.E.
A; Anderson, 240-3412, 1984
A; Reference number: A20751; MUID: 84161997
A; Accession: A00934
A; Molecule type: protein; mRNA
A; Residues: 26-764 <moo>
A; Molecule type: protein; mRNA
A; Residues: 26-764 <moo>
A; Molecule type: protein; mRNA
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A;Molecule type: protein
A;Rolecule type: protein
A;Rolecule type: protein
A;Rolecule type: Drotein
B;Campbell, R.D.; Povrer, R.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 4464-4468, 1983
A;Title: Molecular cloning and characterization of the gene coding for human complement
A;Reference number: A19947; MUID:83273641
A;Accession: A19947
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                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-764 <MED: 72875; NID: 9297568; PIDN: CAA51389.1; PID: 9297569
A; Cross-references: EMBL: X72875; NID: 9297568; PIDN: CAA51389.1; PID: 9297569
A; Cross-references: EMBL: Ricker, A.T.; Goldberger, G.; Colten, H.R.
Proc. Natl. Acad. Sci. U.S.A. 79, 5661-5665, 1982
A; Title: Isolation of cDNA clones for the human complement protein factor B, a class A; Reference number: A4622; MUID: 83039428
A; Accession: A44622
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A; Residues: 1-99 < WUL>
A; Cross-references: GB:M15082; NID:g187699; PIDN:AAA59625.1; PID:g553534
A; Cross-references: GB:M15082; Miller, E.J.
Biochem. J. 274, 473-480, 1991
A; Title: The principal site of glycation of human complement Factor B.
A; Reference number: S14339; MUID:91174758
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A; Residues: 346-764 <CAM>
A; Cross-references: GB:J00125
A; Accession: B19947
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 2395-2871, 'S, 2873-2944 <RDS
A;Cross-references: GB:L06662; NID:g388713; PIDN:AAA89196.1; PID:g388714
B;Christiano, A.M.; Ryynaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A;Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser substance number: A55255; MUID:94224777
A;Contents: annotation
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mNA
A;Molecule type: mNA
A;Molecule type: mUI collagen
A;Molecule type: MUI colla
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A;Note: defects in this gene can result in dominant and recessive dystrophic epidermolys
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A; Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.
A; Reference number: S16316; MUID:91334380
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R; Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.; Cook, M.E.; Wright, J.;
J. Invest. Dermatol. 99, 691-696, 1992
A; Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion prot A; Reference number: 156328; MUID:93107742
A; Accession: 156328
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A; Residues: 'FER', 340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', 524-528,'C',
A; Cross-references: DDBJ:D1152; DDBJ:D13694; NID:9453698; PIDN:BAA02853.1; PID:9453699
A; Experimental source: keratinocyte
A; Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
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A;Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous
A;Reference number: 148103; MUID:93271985
A;Accession: I84686
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A;Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;
A;Note: two reported peptides cannot be reliably located
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A;Residues: 815-892,'E',894-1439 <PAR>
A;Cross-references: GB:M65158; GB:S49017; NID:9180914; PIDN:AAA96439.1; PID:9180915
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Comment: Prolines and lysines at the third position of the tripeptide repeating ed and subsequently O-glycosylated.
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collagen alpha 1(VII) chain precursor - human
N;Alternate names: procollagen alpha 1(VII) chain
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A;Cross-references: GDB:128750; OMIM:120120
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A; Residues: 1-2944 <CHR>
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A:Note: there are 118 introns
C;Complex: type VII collagen is probably a homotrimer
C;Complex: type VII collagen is probably a homotrimer
C;Function:
C;Function:
C;Function:
C;Function:
C;Function:
C;Superfamily: unassigned collagens; animal kunitz-type proteinase inhibitor homology
C;Keywords: coiled collagens; animal kunitz-type proteinase inhibitor homology
C;Keywords: coiled collagens; animal kunitz-type proteinase inhibitor homology
C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxypr
F:17-1253/Domain: animo-terminal nonhelical #status predicted cNCl>
F:17-2944/Product: collagen alpha 1(VII) chain #status predicted cNCl>
F:17-2944/Product: collagen alpha 1(VII) chain #status predicted cNCl>
F:17-294/Promain: fibronectin type III repeat homology cNNJ>
F:201-201/Domain: fibronectin type III repeat homology cNNJ>
F:208-293/Domain: fibronectin type III repeat homology cNNJ>
F:208-293/Domain: fibronectin type III repeat homology cNNJ>
F:208-25/Domain: fibronectin type III repeat homology cNNJ>
F:208-25/Domain: fibronectin type III repeat homology cNNJ>
F:208-25/Domain: fibronectin type III repeat homology cNNJ>
F:208-2119/Domain: fibronectin type III repeat homology cNNJ>
F:208-25/Domain: fibronectin type III repeat homology cNNJ>
F:208-2092/Domain: fibronectin type III repeat homology cNNJ>
F:208-2092/Domain: fibronectin type III repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 2944;
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August 9, 2002, 02:02:44; Search time 523.51 Seconds (without alignments) 4926.614 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. Total number of hits satisfying chosen parameters: 1406282 seqs, 1168085023 residues OM nucleic - nucleic search, using sw model IDENTITY\_NUC Gaport 1.0 Title: Perfect score: Sequence: Scoring table: Searched: Run on:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pending\_Patents\_NA\_New:\*

1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*
2: /cgn2\_6/ptodata/1/pna/USOG\_NEW\_COMB.seq:\*
3: /cgn2\_6/ptodata/1/pna/USOB\_NEW\_COMB.seq:\*
4: /cgn2\_6/ptodata/1/pna/USOB\_NEW\_COMB.seq:\*
5: /cgn2\_6/ptodata/1/pna/USOB\_NEW\_COMB.seq:\*
6: /cgn2\_6/ptodata/1/pna/USOL\_NEW\_COMB.seq:\*
7: /cgn2\_6/ptodata/1/pna/USOL\_NEW\_COMB.seq:\*
8: /cgn2\_6/ptodata/1/pna/USOL\_NEW\_COMB.seq:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

otion	nce 176, App nce 231, App nce 17, Appl nce 13, Appl nce 15, Appl	9, # 23, 19, 1, #	21, 111, 111, 1100, 12250 1126669, 7, 7,
Description	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	sednence Sed
ΠD	PCT-US02-08253-176 PCT-US02-08253-231 US-10-038-307-17 US-10-038-307-13 US-10-038-307-15		
DB	4477		<b>ファニュウァファウロファクタファ</b>
% Query Match Length DB	5540 5540 1674 1650 1650	1650 1056 1713 2272 1008	10047 10047 10047 10043 10047
% Query Match	98.8 98.8 87.0 86.3	86,1 86.0 86.0 86.0	82. 778. 778. 778. 778. 778. 779. 7
Score	1090.8 1090.8 960.8 952.4	950.8 949.4 949.4 949.4	9912. 8853.6 877.6 8853.6 877.
Result No.	H 0 M 4 D	6 9 9 10	11111111111111111111111111111111111111

Sequence 3023, Ap	Seguence 19015, A	Sequence 4890, Ap	Sequence 13193, A	Sequence 12581, A	Seguence 27849, A	٠.	Sequence 4089, Ap	Sequence 2836, Ap	Sequence 40629, A	Sequence 1427, Ap	Sequence 398, App	Sequence 12, Appl	Sequence 287, App	Sequence 9897, Ap	Sequence 35407, A	Sequence 252, App	Sequence 471, App	Sequence 471, App	Sequence 471, App
US-09-629-469A-3023	US-09-539-800C-19015	US-09-629-469A-4890	US-09-629-469A-13193	US-09-539-331D-12581	US-09-539-331D-27849	US-60-377-240-2177	US-60-377-240-4089	US-09-919-002-2836	US-60-360-039-40629	US-09-053-375B-1427	US-10-007-926A-398	US-10-175-525-12	US-10-116-802-287	US-60-377-240-9897	US-09-918-995-35407	US-09-930-213-252	US-09-978-403A-471	US-09-978-544A-471	US-09-978-681A-471
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277.6	189.2	113	113	84.8	82.6	39.4	38	37	36.6	36.6	36.6	36.4	36.2	36	35.8	35.8	35.6	35.6	35.6
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## ALIGNMENTS

RESULT

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<pre>process: 176 process: Application PC/TUS0208253</pre>	GENERAL INFORMATION: APPLICANT: Carson-Walter, Eleanor APPLICANT: St. Croix, Brad APPLICANT: Vogelstein, Bert APPLICANT: Vogelstein, Bert	527	CURRENT FILING DATE: 2002-04-10 PRIOR APPLICATION NUMBER: 60/282,850 PRIOR FILING DATE: 2001-04-11	PRIOR APPLICATION NUMBER: 60/308,829 PRIOR FILING DATE: 2001-08-01	NUMBER OF SEQ ID NOS: 359 SOFTWARE: FastSEQ for Windows Version 4.0	Z ID NO 1/0 LENGTH: 5540	; TYPE: DNA ; ORGANISM: Homo sapiens	Query Match 98.8%; Score 1090.8; DB 1; Length 5540; Best Local Similarity 99.8%; Pred. No. 1.2e-299; Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps		atggccacggcggagcggagcctcggcatcggcttccagtggcttcttttggccact 203	ctggtgctcatctgcgccgggcaagggggacgcagggaggacggagggtccagctgctac 120			ggcggatttgacctgtacttcatttttggacaatcaggaagtgtgctgcaccactggaat 323		gaaatctattactttgtggaacagttggctcacaaattcatcagcccacagttgagaatg 383	teetttattgtttteteeaeeegaagaacaaeettaatgaaaetgaaagaeagagaa 300	
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                                                                                                                  PATTERNS
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APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Wogelstein, Bert
APPLICANT: Kinoler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PAT
FILE REPERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/308,829
                                                                                                                                                                                                                                                                                                                      Sequence 231, Application PC/TUS0208253 GENERAL INFORMATION:
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0
                                                                           Length
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                                                                           Score 1090.8; DB 1;
Pred. No. 1.2e-299;
); Mismatches 2;
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Windows Version 4.0
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                                                                            Query Match 98.8%;
Best Local Similarity 99.8%;
Matches 1092; Conservative
FILING DATE: 2001-08-01
                                                sapiens
       NUMBER OF SEQ ID NOS:
SOFTWARE: FASTSEQ for
SEQ ID NO 231
LENGTH: 5540
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                                                   ; ORGANISM: HOMO
PCT-US02-08253-231
                                       TYPE: DNA ORGANISM:
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99.4%; Pred. No. 1.7e-260;
ive 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Con
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ 1D NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 13, Application US/10038307; GENERAL INFORMATION:
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Matches 956; Conservative
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US-10-038-307-13
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OzKAVNAK
APPLICANT: Judith J. HELEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and N
FILE REPREMENCE: 7853-233-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASTSEQ for Windows Version 4.0
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Pred. No. 7.1e-263;
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Best Local Similarity 99.8
Matches 962; Conservative
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; ORGANISM: Homo sapiens
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MESULY
10S-10-038-307-15
1 Sequence 15, Application US/10038307
2 GENERAL INFORMATION:
3 APPLICANT: James B. ROTTMAN
3 APPLICANT: Enqin OZKAYNAK
4 APPLICANT: Enqin OZKAYNAK
5 APPLICANT: Theres 1. O'KEFF
6 APPLICANT: Theres 1. HEALEY
7 TILE OF INVENTION: Tango 197 and Tango 216 Com
7 TILE OF INVENTION: Tango 197 and Tango 216 Com
7 TILE OF INVENTION: Tango 197 and Tango 216 Com
7 CURRENT APPLICATION NUMBER: US/10/038,307
1 CURRENT FILING DATE: 2002-06-28
1 NUMBER OF SEQ ID NOS: 26
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ed. No. 1.7e-260;
Mismatches 6;
                               Score 9
Pred. N
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illarity 99.4%;
Conservative 0
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for
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FastSEQ
       ; LENGTH: 1650
; TYPE: DNA
; ORGANISM: HOMO S
US-10-038-307-15
                                     Best Local Sim
Matches 956;
SOFTWARE: FE
SEQ ID NO 15
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APPLICANT: Theresa L. O'KEFE
APPLICANT: Theresa L. O'KEFE
APPLICANT: Engin OzKAYNAK
TEPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
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99.9%; Pred. No. 10
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; GENERAL INFORMATION:
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Matches 950; Conservative
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Pred. No. 4.9e-260;
); Mismatches 7;
                                                                                                                 APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Con
FILE REFRENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                               ; Sequence 9, Application US/10038307; GENERAL INFORMATION:
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99.38;
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Matches 955; Conservative
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US-10-038-307-9
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Pred. No. 1.3e-259;
0; Mismatches 1;
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Bright OXEANIMA
TITLE OF INVENTION: Tango 197 and Tango 216 of TRERERENT FILE REPRENEUT
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 193
                                                                                                                                                                                                                                                                                                       and Tango 216
                                                                                                                                                                                                                                                                       ; Sequence 19, Application US/10038307; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            86.0%; initiality 99.9%; conservative 0
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; ORGANISM: Homo sapiens
US-10-038-307-19
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950; Conserv
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US-10-038-307-19
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GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: ADILICANT: ADILICANT: THERESA TOUTH A. HEALEY
TITLE OF INVENTION: Tango 197 and Tan
FILE REFERENCE: 7853-253-999
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larity 99.5%;
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US-10-038-307-25
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Best Local Simi
Matches 952;
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                                                                                                Length 2272;
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                                                                                               Score 949.4; DB 7;
Pred. No. 1.4e-259;
0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/10/038,307 CURRENT FILING DATE: 2002-06-28 UNMBER OF SEQ ID NOS: 26 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                                86.0%;
99.9%;
                                                                                                       al Similarity 99.9
950; Conservative
                                                             ; NAME/KEY: CDS
; LOCATION: (213)...(1211)
US-10-038-307-1
                                                ORGANISM: Homo sapiens
                                   LENGTH: 2272
                                          TYPE: DNA
                                                                                                Query Match
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                                                         Compositions and
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Pred. No. 1.3e-259;
0; Mismatches 5;
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APPLICANT: Theresa L. O'KEFE
APPLICANT: Theresa L. O'KEFE
APPLICANT: APPLICANTE
TITLE OF INVENTION: Tango 197 and Tango 216 Composite OF INVENTION NUMBER: US/10/038,307 CURRENT APPLICATION NUMBER: US/10/038,307 CURRENT FILLING DATE: 2002-06-28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 1008
                                                                                                                                       RESULT 10
US-10-038-307-25
; Sequence 25, Application US/10038307
; GENERAL INFORMATION:
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Db 313 ttaatgaaactgacagaagacagaaac Oy 334 gttctgccaggaggagacacttacatgc 	Qy         694 tgtgcaggaggtcatttcaagttgtcg           Db         733 tgtgcaggaggtcatttcaagttgtcg           Qy         754 gtggcaggaggtcctttgaagttgtcagg           Qy         793 tgtgacaggtcctctgcagcttcaaga           Qy         814 ttttctgtggaagacacttattactgt           Qy         814 tttctgtggaagacacttattactgt           Qy         874 aaagctgcactccaggtcagcagaaga           Qy         874 aaagctgcactccaggtcagcatgaacg           Qy         874 aaagctgcactccaggtcagcatgaacg           Qy         934 atcaccaccacactgt           Py3 atcaccacacactgt         951           Hillilililililili         Hillilililililili           Db         973 atcaccacacacactgt           Py3 atcaccacacacactgt         950	RESULT 12 US-10-038-307-11 Squence 11, Application US/1003830; GENERAL INFORMATION: APPLICANT: James B. ROTTHAN APPLICANT: Theresa L. O'KEFFF APPLICANT: TOTOR OKANNAK TITLE OF INVENTION: TAIGO 197 and FILE REFERENCE: 7853-253-99 CURRENT FILING DATE: 2002-06-28 NUMBER OF SEQ ID NOS: 26 SOFTWARE: FastSEQ for Windows Vers SCOFTWARE: FastSEQ for Windows Vers CORRANT: 1623 TYPE: DNA CORGANISM: Homo sapiens US-10-038-307-11 Best Local Similarity 97.9%; Pre Matches 879; Conservative 0;
bb 601 gtgaatgacgctttcaatgagcctggcccggattgcggacagtaaggatcatgtttccc 612 bb 601 gtgaatgacggctttcaggctctgcaaggcatcatccactttgaagaagtcctgc 660 li	RESULT 11 US-10-038-307-21 Sequence 21. Application US/10038307 Sequence 21. Application US/10038307 Sequence 21. Application US/10038307 Sequence 21. Application US/10038307 Sequence 21. Application Sequence 21. O'KEEFE APPLICANT: Theresa L. O'KEEFE APPLICANT: Englin OZKAYMAK TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods FILE REFERENCE: 7853-253-999 CURRENT APPLICATION NUMBER: US/10/038,307 CURRENT FILING DATE: 2002-06-28 NUMBER OF SEQ ID NOS: 26 SEQ ID NO 21 LENGTH: 1047 SEQ ID NO 21 TYPE: DNA CORGANISM: Homo sapiens US-10-038-307-21	Query Match         82.6%; Score 912.4; DB 7; Length 1047;           Best Local Similarity         97.1%; Pred. No. 3.5e-249;           Matches 950; Conservative         0; Mismatches         1; Indels 27; Gaps           Db         1 atggccacggcggagcggagcgcatcggctccagtggctcctcttggccact 60           13 atggccacggcggagcggagcgcatcggctccagtggctccactttggccact 72           Qy         61 ctggtgctcatctggccgggagcgaggggacgcaggggagcgagggggggg
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Mismatches 19;
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                       gatttgacctgtacttcattttggacaaatcaggaagtgtgctgcaccactggaatgaaa
                                             tctattactttgtggaacagttggctcacaaattcatcagcccacagttgagaatgtcct
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APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION
FILE REPERBENCE: 107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2002-04-10
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PCT-US02-08253-186
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                                                                                                                       Score 853.4; DB 1;
Pred. No. 3.8e-232;
0; Mismatches 136;
                                               4.0
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4...
LENGTH: 5220
                                                                                                                        77.3%;
87.3%;
                                                                                                                       Query Match 77.3
Best Local Similarity 87.3
Matches 935; Conservative
                                                                                    musculus
                                                                                  ; ORGANISM: Mus r
PCT-US02-08253-186
                                                                                 ORGANISM:
                                                                           TYPE: DNA
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Pred. No. 3.8e-232;
); Mismatches 136; Indels 0;
                                                                                 APPLICANT: Carson-Malter, Eleanor
APPLICANT: St. Carson-Malter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELLA CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-0
NUMBER OF SEQ ID NOS: 359
NUMBER OF SEQ ID NOS: 359
                                                                                                                                  Sequence 300, Application PC/TUS0208253 GENERAL INFORMATION:
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Best Local Similarity 87.3%;
Matches 935; Conservative
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                                                                                                                       RESULT 14
PCT-US02-08253-300
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LENGTH: 5220
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    gactgatggagaactccatgaagatctctttctattcagagagggggggctaataggtc
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                                                                                                                                                                 Length 1436;
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                                                                                                                                                                Score 787; DB 5; I
Pred. No. 1.8e-213;
                                                                                                                                                                                  0; Mismatches
   APPLICATION NUMBER: JP 2000-241899
PRIOR APPLICATION NUMBER: JP 2000-24189-
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/159,590
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 19025
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 11705
LENGTH: 1436
                                                                                                                                                                71.3%;
99.3%;
                                                                                                                                                                                  Matches 801; Conservative
                                                                                                            ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (380)..(1033)
US-09-629-469A-11705
                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                Query Match
Best Local Similarity
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Search completed: August 9, 2002, 02:03:04 Job time: 10801 sec



GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 9, 2002, 01:53:53; Search time 4997.37 Seconds Run on:

(without alignments)
4779.500 Million cell updates/sec

us-09-970-076-1\_COPY\_104\_1207 Perfect score: Sequence:

IDENTITY\_NUC Gapon 10.0 , Gapext 1.0 Scoring table:

43959072 Total number of hits satisfying chosen parameters:

21979536 segs, 10817449327 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending\_Patents\_NA\_Main:\* Database :

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6/ptodata/2/pna/US6005_COMB.s 6/ptodata/2/pna/US6006_COMB.s 6/ptodata/2/pna/US6009_COMB.s 6/ptodata/2/pna/US6009_COMB.s 6/ptodata/2/pna/US6010_COMB.s 6/ptodata/2/pna/US6011_COMB.s 6/ptodata/2/pna/US6011_COMB.s 6/ptodata/2/pna/US6011_COMB.s 6/ptodata/2/pna/US6011_COMB.s 6/ptodata/2/pna/US6011_COMB.s 6/ptodata/2/pna/US6016_COMB.s 6/ptodata/2/pna/US6016_COMB.s 6/ptodata/2/pna/US6016_COMB.s 6/ptodata/2/pna/US6018_COMB.s 6/ptodata/2/pna/US6018_COMB.s 6/ptodata/2/pna/US6018_COMB.s 6/ptodata/2/pna/US6018_COMB.s 6/ptodata/2/pna/US6018_COMB.s	2_6/ptodata/2/pna/US6023_COMB.s 2_6/ptodata/2/pna/US6024_COMB.s 2_6/ptodata/2/pna/US6025_COMB.s 2_6/ptodata/2/pna/US6026_COMB.s 2_6/ptodata/2/pna/US6028_COMB.s 2_6/ptodata/2/pna/US6028_COMB.s 2_6/ptodata/2/pna/US6039_COMB.s 2_6/ptodata/2/pna/US6031_COMB.s 2_6/ptodata/2/pna/US6031_COMB.s 2_6/ptodata/2/pna/US6031_COMB.s 2_6/ptodata/2/pna/US6031_COMB.s 2_6/ptodata/2/pna/US6031_COMB.s 2_6/ptodata/2/pna/US6031_COMB.s 2_6/ptodata/2/pna/US6033_COMB.s 2_6/ptodata/2/pna/US6033_COMB.s 2_6/ptodata/2/pna/US6033_COMB.s
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 1, Appli	122	1,	23	Sequence 5, Appli	Sequence 14, Appl	45,	10	Sequence 10, Appl	Sequence 10, Appl		⋖	æ	8	œ	æ ′8	11, Ag	9264,		68, 4	204,	988,		68, 1	988,	998	7727,	763	7309,	628	Sequence 5593, Ap
QI	US-09-970-076-1	US-60-213-359-1222		US-09-918-715-231	US-09-970-076-5	PCT-US00-30045-14	PCT-US00-30045-45	PCT-US99-31025-10	US-09-223-546-10	US-09-471-179-10	US-09-599-596-10	US-09-970-076-7	PCT-US99-31025-8	US-09-223-546-8	8 US-09-471-179-8	US-09-599-596-8	US-09-796-753-11	US-09-644-871-9264	281-	-548A-6	US-09-419-553-204	448-99	US-09-770-155-204	-183-6	US-09-833-381-998	US-09-833-382-998	-77	9-644-868-7	-09-644-871-7	-09-649-163-	US-09-652-121-5593
DB	36	9	34	34	36	-	_	-	16	18	22	36	ч	16	18	22	30	25	28	17	18	19	30	30	32	32	17	25	25	25	25
% Query Match Length DB	1414	2386	5540	5540	5540	2447	2086	666	666	666	666	2112	2272	2272	2272	2272	2272	2374	2374	2459	2459	2459	2459	2459	2459	2459	2401	2401	2401	2401	2401
% Query Match	100.0	98.8	98.8	98.8	98.8	98.8	98.7	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	85.9	85.9	85.9	85.9	85.9
Score	1104	1090.8	1090.8	1090.8	1090.8	1090.6	1089.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	949.4	947.8	947.8	947.8	947.8	947.8
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/cgn2\_6/ptodata/2/pna/US6003\_COMB.seq:\* /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq:\*

•	764 721 324 781 884 841 901 901 004 001 1124 1184	RESULT 2 US-60-2122 Application US/60213359 Sequence 1222, Application US/60213359 GENERAL INFORMATION: APPLICANT: Macris, MacDonald APPLICANT: Diep, Dinh TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using TITLE OF INVENTION: Identified Thereby TITLE OF INVENTION: Identified Thereby TITLE OF INVENTION: Identified Thereby TITLE OF INVENTION: 12000-06-21 CURRENT FILING DATE: 2000-06-21 NUMBER OF SEQ ID NOS: 7924 SOFTWARE: PERL Program SEQ ID NO 1222 LENGTH: 2386 TYPE: DATE TYPE: DATE CORGANISM: Homo Sapiens FEATURE:
		Oy 121 ggcggatttgacctgtacttcatttttggacaagtaggaggaggaggaggggggccagcctgctac 120

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Query Match
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                     1021
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                         Score 1090.8; DB 60
Pred. No. 1.2e-287;
% Mismatches 2;
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                         98.8%;
99.8%;
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte
US-60-213-359-1222
                         Query Match 98.8
Best Local Similarity 99.8
Matches 1092; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Brad St. Croix
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSI
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 176
LEBGHT 5540
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Matches 1092; Conservative
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US-09-918-715-21
US-09-918-715-21
Sequence 231, Application US/09918715
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Brat Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSI
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR PAPLICATION NUMBER: 60/224,360
PRIOR PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 231
LENGTH: 5540
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ORGANISM: Homo sapiens
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   Pred. No. 1.76
); Mismatches
Score 1090.8;
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98.8%;
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Matches 1093; Conservative
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PCT-US00-30045-14
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Pred. No. 1.7e-287.0; Mismatches 2;
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APPLICANT: Bradley, Kenneth A.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor FILE REFERENCE: 960296.97745
CURRENT APPLICATION NUMBER: 0509/970,076
CURRENT FILING DATE: 2001-10-03
PRIOR PAPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER: OF SEQ ID NOS: 10
                                                                                                                             Sequence 5, Application US/09970076 GENERAL INFORMATION:
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99.8%;
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; LOCATION: (144)...(1835)
US-09-970-076-5
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SEQ ID NO 5
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INFORMATION: 28 Human Secreted Proteins
TITLE OF INFORMINE: 2000-11-01
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30 Score 1089.4; DB 1 Pred. No. 2.8e-287; 3; Mismatches Ö Ü or or or ö or equals a,t,g, n equals a,t,9, a,t,g, Query Match
Best Local Similarity 99.4%;
Matches 1090; Conservative LOCATION: (2075)
OTHER INFORMATION: n equals
NAME/KEY: SITE
LOCATION: (2079)
OTHER INFORMATION: n equals PatentIn Ver. 2.0 n equals ORGANISM: Homo sapiens NAME/KEY: SITE LOCATION: (2083) OTHER INFORMATION: n PCT-US00-30045-45 NUMBER OF SEQ ID NOS: SOFTWARE: PatentIn Ve SEQ ID NO 45 FEATURE:
NAME/KEY: SITE
LOCATION: (10)
OTHER INFORMATION: n INFORMATION: (2070)NAME/KEY: SITE NAME/KEY: SITE LOCATION: OTHER INFO TYPE: DNA 586 346 61 226 121 181 241 406 301 466 361 526 421 g Dp QΥ g Qγ g Qγ Óγ QΥ a δ g δý δ

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TITLE OF INVENTION: SECRETED PROTEINS AND
FILE OF THOWNTON: SECRETED PROTEINS AND
CURRENT APPLICATION NUMBER: US/09/223,546
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastESO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09223546 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SECRETED PROTEINS, INC.
TITLE OF INVENTION: SECRETED PROTEINS AND NUC.
TITLE OF INVENTION: SECRETED PROTEINS AND NUC.
FILE REFERENCE: 7853-173-228
CURRENT APPLICATION NUMBER: PCT/US99/31025
CURRENT PILING DATE: 1999-12-33
EARLIER PELING DATE: 1998-12-33
NUMBER OF SEQ ID NOS: 135
SEQ ID NO 10
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LENGTH: 999
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                                DB 16;
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                                Score 949.4; DB 1
Pred. No. 5e-249;
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Matches 950;
           ; TYPE: DNA
; ORGANISM: HOR
US-09-223-546-10
  SEQ ID NO 10
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                                       Sequence 10, Application US/09471179
GENERAL INFORMATION:
APPLICANT: HOITENN: Douglas
TITLE OF INVENTOR: SECRETED PROTEINS AND NUC
FILE REFERENCE: 7853-173
CURRENT APPLICATION UNDHER: US/09/471,179
CURRENT FILING DATE: 1999-12-23
PRIOR PELLOATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
                                                                                                                   NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 999
LENGTH: 999
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99.9%;
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Best Local Similarity 99.9
Matches 950; Conservative
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                            RESULT 10
US-09-471-179-10
                                                                                                                                                       TYPE: DNA
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99.9%; Pred. No. 6.8e-249;
ive 0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Young, John A.T.
APPLICANT: Collier, Reneth A.
APPLICANT: Collier, Reneth J.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrew Toxin Receptor FILE REFERENCE: 960296.97745
CURRENT APPLICATION NUMBER: 08/09/970,076
CURRENT APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 7.
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Matches 950; Conservative
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US-09-970-076-7
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TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING J
FILE REFERENCE: 09404/066010
CURRENT APPLICATION NUMBER: US/09/599,596
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH. 999
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Pred. No. 5e-249;
0; Mismatches 1; Indels 0;
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Sequence 10, Application US/09599596
GENERAL INFORMATION:
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Matches 950; Conservative
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GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceticals, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND NUC:
TITLE OF INVENTION: ENCODING THEM
FILE REFERENCE: 7853-173-28
CURRENT APPLICATION NUMBER: PCT/US99/31025
CURRENT APPLICATION NUMBER: 09/223,546
EARLIER APPLICATION NUMBER: 09/223,546
EARLIER FILING DATE: 1998-12-30
SOFTWARE: FASTED (FOR WINDOWS VERSION 4.0)
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PCT-US99-31025-8
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                                        Score 949.4; DB 1
Pred. No. 7e-249;
1; Mismatches 1
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99.9%;
                                                    Conservative
) ORGANISM: Homo sapiens

) PEATURE:

) NAME/FERY: CDS

) LOCATION: (213)...(1211)

PCT-US99-31025-8
                                        Query Match
Best Local Similarity
Matches 950; Conserv
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GENERAL INFORMATION:
APPLICANT: HOLIZMAN. DOUGLAS
APPLICANT: HOLIZMAN. DOUGLAS
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REPERENCE: 7853-173
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT APPLICATION NUMBER: 099213,546
PRIOR PILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 2272
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larity 99.9%; Pred. No. 7e-249;
Conservative 0; Mismatches
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; LOCATION: (213)...(1211)
US-09-471-179-8
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Best Local Similarity
Matches 950; Conserv
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ORGANISM: HOMO
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                                                                         APPLICANT: HOLIZAMAN, DOUGLAS
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 09404/066001
CURRENT APPLICATION NUMBER: US/09/223,546
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
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Pred. No. 7e-249;
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                                                          Sequence 8, Application US/09223546 GENERAL INFORMATION:
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99.9%;
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; LOCATION: (213)...(1211)
US-09-223-546-8
                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                            Similarity
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                                                 US-09-223-546-8
                                                                                                                                                                     TYPE: DNA
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Search completed: August 9, 2002, 01:54:14 Job time: 12956 sec

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Sequence:

Searched:

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ZIP: 22313-0299
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCES: 52
CORRESPONDENCE ADDRESS:
                  REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
FILING DATE: 26-MG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
CITY: Alexandria
STATE: VA
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
; CLONE: pTZgpt-F1s
US-08-232-463-14
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2472.460 Million cell updates/sec
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                                                                                                                                                                                                                                                                                      sequence 20, sequence 20, sequence 20, sequence 36, sequence 3, A sequence 13, sequence 13, sequence 11, A sequence 1, A sequenc
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-230-371A-20

US-09-230-371A-20

US-09-230-371A-3

US-08-021-615A-3

US-08-021-615A-3

US-09-009-556-13

US-09-009-556-13

US-09-656-13

US-09-656-13

US-08-475-690-1

US-08-33-0-1

US-08-33-0-1

US-08-33-1

US-08-487-427-25

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US-08-487-427-25
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Maximum Match 100%
Listing first 45 summaries
                                                                                                        - nucleic search, using sw model
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Maximum DB seq length: 200000000
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SEQUENCE CHARACTERISTICS:
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                                       Gaps
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0
   ch 4.3%; Score 47; DB 1; Length 7218; 1 Similarity 6.7%; Pred. No. 0.00014; 26; Conservative 199; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
APPLICANT: FALKNER, F. G.
APPLICANT: FINTENEROWERS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSE: Foley & Lardher
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ttatcaaggaggtccctccacccctgcc 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/232,463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
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          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                           Matches
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                                                                                                                                                         Length 7218;
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                                                                                                                                                         ch 3.8%; Score 41.4; DB 1; Length 7
1 Similarity 6.8%; Pred. No. 0.0094;
27; Conservative 198; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1047 TGCAGCCAAGCTCGGAATTAATTCTGTGAGCGTATGGCA 1009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/728,323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08728323A Patent No. 5948676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Boseo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
                                                                                                                                                                Query Match
Best Local Similarity 6.8%;
LENGTH: 7218 Date.
TYPE: nucleic acid
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CLASSIFICATION: 435
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                       TYPE: nucleic actu
STRANDEDNESS: sing
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                       ; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
: U.S.A.
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CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET WINBER: 45185-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
: U.S.A.
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US-08-757-669A-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/08770379
Patent No. 5849564
GENERAL INFORMATION:
Chang, Yuan
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Redelman, Isldore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37.4; DB 2; Length 3489;
Pred. No. 0.11;
0; Mismatches 91; Indels 0
                                                            0575/52268/JPW/MSC/SKS
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APPLICATION NUMBER: US/08/770,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: COOPER & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
        NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/POCKET NUMBER: 0575,
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPHONE: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER/STICS:
LENGTH: 3489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                  3.4%;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.4'
Best Local Similarity 50.3'
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: 1..3489
US-08-728-323A-1
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20908 CTCCTCGTCATCCTCGTCATCCTCGTCATCCTCGTCATCCTCGTCATCCTCGTCATC 20967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          883 ctccaggtcagcatgaacgatggcctctcttttatctccagttctgtcatcaccacc 942
                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.4%; Score 37.4; DB 2; Length 32207; Best Local Similarity 50.3%; Pred. No. 0.52; Matches 92; Conservative 0; Mismatches 91; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/08757669A
Patent No. 6183751
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
MINDER OF GENERALDIN: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/757,669A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036
COMPUTER REAABLE FORM:
CMDIUM TYPE: Floppy disk
CMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
REFERENCE/DOCKET NUMBER: 5234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-379-20
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21028 ctt 21030
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US-07-882-202A-3
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GENERAL INFORMATION:
APPLICANT: BOHENZKY, KOY A
APPLICANT: BOHENZKY, KOY A
APPLICANT: BOHENZKY, KOY A
APPLICANT: BOHENZKY, KOY A
APPLICANT: BOHENZKY, KOY B
APPLICANT: MOOFE, PARTICK S
APPLICANT: MOOFE, PARTICK S
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 45185 45 6-PCT-US
CURRENT PAPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
PRIOR FILING DATE: 1997-11-27
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATCHIN VOET: 2.0
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                                                                                                                        Length 32207;
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                                                                                                                                                     Indels
                                                                                                                                                     91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.4%; Score 37.4; DB 4;
50.3%; Pred. No. 0.52;
tive 0; Mismatches 91;
                                                                                                                        Score 37.4; DB 4;
pred. No. 0.52;
0; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-230-371A-20
; Sequence 20, Application US/09230371A
; Patent No. 6348586
          LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                           Query Match 3.4%;
Best Local Similarity 50.3%;
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.3
Matches 92; Conservative
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LENGTH: 32207
                                                                                    US-08-757-669A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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Sequence 3. Application US/07882202A

Patent No. 5374617

GENERAL INFORMATION:

APPLICANT: MOTISSEY, James H.

APPLICANT: Comp, Philip C.

TITLE OF INVENTION: Treatment of Bleeding with Modified

TITLE OF INVENTION: Tissue Factor in Combination with FVIIa

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSE: Richards, Medlock & Andrews

STREET: Lallas

CITY: Dallas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCONA.260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER PELICATION NUMBER: 09/328,111
EARLIER PELICATION NUMBER: 09/128,111
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1998-06-31
NUMBER OF SEQ ID NOS: 544
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.4%; Score 37.2; DB 4;
50.8%; Pred. No. 0.035;
Live 0; Mismatches 64;
; Sequence 368, Application US/09385982
; Patent No. 6262334
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; OTHER INFORMATION: n = A,T,C or
US-09-385-982-368
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SIATE: Da..
STATE: Texas
COUNTRY: US
-To: 75270-2197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388 gcggnngttc 397
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Best Local Similarity
Matches 66; Conserv
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928 gtcatcatcaccaccacacactgttctgacggttccatcctggccatcgcctgctgatc 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              897 GICATCATCCCCAGCACGIACGICCCGGGCACCACCAACCACGACATCGCGCTGCICCGC 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Treatment of Bleeding with Modified TITLE OF INVENTION: Tissue Factor in Combination with FVIIa NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "Coding portion of human factor VII cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 75270-2197
ZIP: 75270-2197
MEDIUM TYER FORM:
MEDIUM TYER Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.2%; Score 35.2; DB 1;
62.5%; Pred. No. 0.32;
iive 0; Mismatches 33;
                                                             OMRF B34290CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMRF B34290C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,777
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/321,777
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-008-321-777-3
Sequence 3, Application US/08321777
; Patent No. 5504067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Morrissey, James H. APPLICANT: Comp, Philip C.
                     NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: OMI
TELECOMMUNICATION:
TELEPHONE: 214-939-4500
                                                                                                               INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1440 base pairs TYPE: nucleic acid STRANDEDNESS: double
    ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.27
Best Local Similarity 62.57
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 36.1433
CTHER INFORMATION:
CTHER INFORMATION:
US-08-021-615A-3
                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Texas
                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Moriassey, James H.
APPLICANT: Comp. Philip C.
ATTLE OF INVENTION: Treatment of Bleeding with Modified
TITLE OF INVENTION: Tissue Factor in Combination with an Activator of
TITLE OF INVENTION: FVII
WINMER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.2%; Score 35.2; DB 1; Length 1440; ilarity 62.5%; Pred. No. 0.32; Conservative 0; Mismatches 33; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 36..1433
OTHER INFORMATION: /note= "Coding portion of human
OTHER INFORMATION: factor VII cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USS
ZIP: 75270-2197
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,615A
                                                      ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31,966
REFERENCE/DOCKET NUMBER: 0MRF B34290
TELEPHONE: 214-939-4500
TELEPHONE: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     988 ctgttcctgctcctagccctggctctcc 1015
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APPLICATION NUMBER: US/07/882,202A FILING DATE: 13-MAY-1992 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08021615A Patent No. 5504064 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sar
TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-882-202A-3
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Sequence 13. Application US/09009656

Sequence 13. Sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATE: APPLICATION NUMBER: US/09/009,656 FILING DATE: CONCURRENTLY Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
3.2%; Score 35.2; DB 3;
Best Local Similarity 62.5%; Pred. No. 0.32;
Matches 55; Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIPICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,920
FILICATION NUMBER: US 60/035,920
FILICATION NUMBER: US 60/035,920
ATTORNEY AGENT INFORMATION:
NAME: Hibler, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    988 etgttcctgctcctagccctggctctcc 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      957 CTGCACCAGCCGTGGTCCTCACTGACC 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Arnold, White & Durkee P.O. Box 4433
                                                                                               UTSD: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
                             NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTSD:
TELECOMMUNICATION INFORMATION:
TELEPRAN: 512/418-300
TELEPRAN: 512/418-300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 6
                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY:
US-09-009-217-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-09-009-656-13
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Sequence 13, Application US/09009217
Patent NO. 6132729
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
APPLICANT: Gao, Boning
TITLE OF INVENTION: CCMBINED TISSUE FACTOR AND
TITLE OF INVENTION: CHEMOTHERAPEUTIC METHODS AND COMPOSITIONS FOR COAGULATION
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Annold, White & Durkee
STREET: P.O. Box 4433
CITY: HOUSEON
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pred. No. 0.32;
0; Mismatches 33; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 36..1433 OTHER INFORMATION: /note= "Coding portion of human OTHER INFORMATION: factor VII cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: PATCHIL Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,217
FILING DATE: CONCULTENTLY HETEWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  988 ctgttcctgctcctagccctggctctcc 1015
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TELEPHONE: 214-939-4500
TELEPTX: 214-939-4500
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.5%
"...hes 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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COUNTRY:
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/product- "Tissue Factor"
/note- "Coding portion of human factor VIII cDNA"
/citation- ([1])
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                                                                                                                                                                                                                                                                    Length 1440;
                                                                                                                                                                                                  33; Indels
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco
                                                                                                                                                           Query Match 3.2%; Score 35.2; DB 5; Best Local Similarity 62.5%; Pred. No. 0.32; Matches 55; Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Begengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,845
FILING DATE: 07-7UN-1995
CLASSIFICATION NUMBER: 08327,690
FILING DATE: 24-0CT-1994
CLASSIFICATION UNBER: 08/065,725
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION UNBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION NUMBER: 08/065,725
FILING APPLICATION DATA:
APPLICATION NUMBER: 07/062,920
                                                                                                                                                                                                                                                                                                                      988 ctgttcctgctcctagccctggctctcc 1015
                                                                                                                                                                                                                                                                                                                                                           957 criscaccascccsresrccrcacrigace 984
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ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARTMELEE, SLEVEN W.
REGISTRATION NUMBER: 31,990
REFRENCE/DOCKET NUMBER: 1395;
TELECHMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEPHAN: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08475845 Patent No. 5788965 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berkner, Kathleen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2422 base pairs
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NAME/KEY: CDS
LOCATION: 36..1433
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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                                                                                                 PCT-US93-04493-3
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US-08-475-845-1
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Pred. No. 0.32;
0; Mismatches 33; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MOTISSBY, James.H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Truncated Tissue Factor and FVIIa or
TITLE OF INVENTION: FVII Activator for Blood Coagulation
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                       33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04493
FILING DATE: 19930512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Richards, Medlock & Andrews STREET: 1201 Elm Street, Suite 4500 CITY: Dallas
                                                                                                                                                                                                                                                                                                                                        988 ctgttcctgctcctagccctggctctcc 1015
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APPLICATION NUMBER: US 07/882202
FILING DATE: 13-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021615
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application PC/TUS9304493 GENERAL INFORMATION:
  INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                             Query Match 3.2%;
Best Local Similarity 62.5%;
Matches 55; Conservative
                    SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapi
TISSUE TYPE: BLOOD
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
                                                                                                 ; TOPOLOGY: linear
US-09-009-656-13
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75270-2197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Texas
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
PCT-US93-04493-3
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Score 35.2; DB 1; Length 2422; Pred. No. 0.46; 0; Mismatches 33; Indels 0

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| NAME/KET: CDS | LOCATION: 28..1420 | COCATION: 28..1420 | COCATION: O'THER INFORMATION: /product= "Factor VII" US-08-327-690-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.2%;
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Best Local Similarity 62.53
Matches 55; Conservative
                               MOLECULE TYPE: CDNA HYPOTHETICAL: N
TOPOLOGY: linear
                                                                                                 ANTI-SENSE: N
FEATURE:
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                                                                                                                                                               NAME/KEY: CDS
LOCATION: 28.1420
OTHER INFORMATION: /codon_start= 28
OTHER INFORMATION: /product= "Factor VII"
US-08-475-845-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Hegengaard, Claus
TITLE OF INVENTION: Modified Factor VII
WIMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION ATA:
APPLICATION NUMBER: 15-MAY-1993
CLASSIFICATION WHRE: ASSIFICATION WHRE: CAUSSIFICATION WHRE: APPLICATION WHRE: CAUSSIFICATION WHRE: APPLICATION WHRE: APPLICATION: APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         988 ctgttcctgctcctagccctggctctcc 1015
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ATTORNEY, AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE, DOOKET NUMBER: 13952
TELEFONMUNICATION INFORMATION:
TELEFAX: 415-543-5043
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2422 base pairs
TYPE: nucleic acid
""""" ANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08327690 Patent No. 5817788
          TOPOLOGY: linear MOLECULE TYPE: CDNP HYPOTHETICAL: N
                                                                                                           ANTI-SENSE: N
FEATURE:
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BG999787 MR3-HN005
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1063)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Fill-length CDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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BP 191 91006 EVRX cedex - France
Emall: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                        B1869089
BE478445
AV749755
BB649806
AW106196
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BI917586
BG951999
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BE371536
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BG999787
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BE146276
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BB620906
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AV667876
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      , mRNA sequence.
AL542724
      272
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      3304.6
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BC28183 602403057
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Copyright (c) 1993 - 2000 Compugen Ltd
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/note—Torgan: pooled brain, lung, testis; Vector:

pCMV-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA
source annonymous pool of male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (ECORV site is
elserroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NILMGC Library."

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                                             CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11448 row: n column: 07
High quality sequence stop: 804.
1. 878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                               62.0%; Score 684.6; DB 10; 95.1%; Pred. No. 2.9e-176; iive 0; Mismatches 29;
                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5179974"
/clone_lib="NiH_MGC_115"
/lab_host="DH108"
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Best Local Similarity 95.1
Matches 783; Conservative
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Wearryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 878)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, K., Sakai, K., Sano, H., Sasaki, D., Soghimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T., Tajima, Y., Tagami, M., Tagama, A., Takahashi, F., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGCATCTATTTTTTTTTTTTTVN 3'], cDNA was prepared by using trabalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /procein_id="Bab28591.1"
/db_xref="G1:12850100"
/translation="MKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENS
QGYRTASVITALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADS
KDHYFFYNDGFQALQGIHEJLFKSCIEILAARPSTLCAGESFQVVVRGNGFRHARNV
DRVLCSFKINDSVTLNEKPFAVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSV
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GLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKMPEQEYE
FPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTRFRGWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission Submitselon Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, PWR:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10, 11 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="data source:SPTR, source key:09NVP3, evidence:ISS homolog to CDNA FLJ10601 FIS, CLONE NT2RP2005000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 2.7e-175;
0; Mismatches 91;
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/db_xref="MGD:MGI:1904936"
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/clone="2810405N18"
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shibata, K. Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunato, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Ishikawa, T., Ozawa, M., Ohara, E., Matshik, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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The RIKEN Genome Exploration Research Group Phase II Team and the
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5 (bases 1 to 1614)
5 Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F.,
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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mRNA linear EST 15-SEP-2000 CDNA clone IMAGE:3948114 5',
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Bukaryotas, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryotas, Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 725)
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13 (bases 1 to 725)
14 (bases 1 to 725)
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CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM810 row: n column: 19 High quality sequence stop: 711.
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FOORI; CDNA made by oligo-dr priming. Directionally
Cloned into ECORIXAhoI sites using the following 5'
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insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
)9 a 189 C 240 g 181 t l others
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602402412F1 NIH_MGC_20 Homo sapiens CDNA clone IMAGE:4544691 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 820)
NIH-MGC http://mgc.ncl.nih.gov/.
NIH-MGC http://mgc.ncl.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs.remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory ,
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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High quality sequence stop: 815.
Location/Qualifiers
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1 (bases 1 to 963)

NIH-MGC http://mgc.ncl.nh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Confact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nh.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Information can be found through the I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 718.
                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
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Pred. No. 5.4e-149;
0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                         BG326444.1 GI:13132881
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Best Local Similarity 96.3
Matches 621; Conservative
                                                                                                                                                                                                                                  mRNA sequence.
BG326444
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VERSION
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TITLE
JOURNAL
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Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCMI230 row: a column: 15

High quality sequence stop: 659.

Location/Qualifiers

1. 964
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                                                                                                                                                                                                                                                                                                                                                                                               Score 482; DB 10;
Pred. No. 8.3e-121;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4545302"
/clone_lib="NIH_MGC_20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ф
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Best Local Similarity 98.1%;
Matches 530; Conservative
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602403057F1 NIH_MGC_20 Homo sapiens CDNA clone IMAGE:4545302 5',
                                                               8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Bukamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 964)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Conpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416
                                                                                                                                                                                                                                                                                                                                                                                                                                     651
                                                                                                                                                                                                                                                  gtcct--ttattgttttctccacccgaggaacaaccttaatgaaactgacagaagacaga 297
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                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                             ctattcagagagaggctaataggtctcgagatcttggtgcaattgtttactgtgttgg
                                                                                                                           gaaatctattactttgtggaacagtt-ggctcacaaattcatcagcccacagttgagaat
                                                                                     1 atggccacggcggagcggagagccctcggcatcggcttccagtggctcttttggccact
                                                                                                                                                                                                                               GAAATCTATTACTTTGTGGAACAGTTGGGTTCACAATTTCATCAGCCCACAGTTGAAAT
                                                                6
                                            Length 820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                               DB 10;
                                             Score 582.6; DB 10
Pred. No. 2.3e-148;
                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG281831.1 GI:13030757
                                                52.8%;
96.1%;
                                                                     Matches 683; Conservative
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BG281831
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                                                           Similarity
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                                                  Query Match
Best Local 3
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SOURCE
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TITLE
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Institutes of Health, Mammallan Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://magge.llnl.gov

Plate: LLAW8756 row: p column: 04

High quality sequence stop: 573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
601220816F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3589875 5'
                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C2ECH II (feral)"
/db_xref="taxon:10090"
/clone="IMAGE:3589875"
/clone=lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
/lab_host="DHIOB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.5%; Score 447.4; DB 10;
85.8%; Pred. No. 2.1e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                              BE369415.1 GI:9314778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   543; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                1. .638
               mRNA sequence.
BE369415
                                                                               nouse mouse
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                                            VERSION
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Matches
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ORIGIN
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AUTHORS
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/db_xref="taxon:9666"
/db_xref="taxon:9666"
/clone_lib="Hr0209"
/dev_stage="Addit"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.
18 a 150 c 127 g 128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: saimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-MRO-HT0209-280 300-106-909&t3=2000-03-286t4=1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence start: 21
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE146084 11near EST 21-JUN-2000 MRN4 11near EST 21-JUN-2000 MRN-THT0209-280300-106-909 HT0209 Homo sapiens cDNA, mRNA sequence. BE146084.1 GI:8608808
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 513)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magal, M.A., Gotafu, S., Costa, F.F.,

Nagal, M.A., Machina, W. Jr., Zago, M.A., Bordah, S., Costa, F.F.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

M. Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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631
                                                                                                     691
                                                                                                                                                       539
                                                                                                                                                                                                                   751
                              692 tatgtgcaggagagtcatttcaagttgtcgtgagaggaaacggcttccgacatgcccgca
                                                                                                                                                                                                                                                                        540 TCTGCGCGGAGAGTCCTTTCAAGTGGTCGTAAGAGGAAATGGCTTCCGACATGTCCGC-
     ttgcggacagtaaggatcatgtgtttcccgtgaatgacggctttcaggctctgcaaggca
                                                                                                          tcatccactcaattttgaagaagtcctgcatcgaaattctagcagctgaaccatccacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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                                                                                                                                                                                                                                                                                                                           599 ATGTGGACAGGGCCCCTGGGGTCTAAATAATGA 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human
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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 465)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.
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mRNA sequence.
                                                                                                               /dev_gatge="Adult"
//dev_gatge="Adult"
//note="Organ: head_neck; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 ATGGCCACGCGGAGGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTTTTGGCCACT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 teetttattgtttteteeaeeegaggaacaaeettaatgaaaetgacagaagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 atggccacggcggaggggagagcctcggcatcggcttccagtggctctctttggccact
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 420.4; DB 9; Length
Pred. No. 5e-104;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                     low stringency conditions.
                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0209"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              38.1%;
99.8%;
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Matches 421; Conservative
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1 (Dases I to 542)
1 (Dases I 
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MRO-HT0209-280300-106-b03 HT0209 Homo sapiens CDNA, mRNA sequence.
BE146075
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                           ctggtgctcatctgcgccgggcaaggggacgcagggaggatgggggtccagcctgctac 120
                                                                                                                                                                                                                                                                                                  367
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                                                                                                               126 CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTACATG
                                                                                   atggccacggcggaggggggggcctcggcatcggcttccagtggctctctttggccact
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20202663
                                   Indels
               4.9e-104;
                                     Mismatches
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High quality sequence stop: 131
               Pred. No.
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Email: asimpson@ludwig.org.br
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               99.88;
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                                          Conservative
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               Best Local Similarity
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                                          Matches
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AUTHORS
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/dy_xref="taxon:9606"
/clone_lib="HT0209"
/dev_stage="Adult"
/clone_lib="HT0209"
/dev_stage="Adult"
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Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the PUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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                                                                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MRO-HT0209-100
100-103-f09&t3=2000-01-10&t4=1)
Seq primer: puc 18 forward
High quality sequence star: 12
High quality sequence stop: 464.
Location/Qualifiers
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                                                                                        Sao Paulo-SP
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              (7), 3491-3496 (2000)
                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
              97
sequence tags
Proc. Natl. Acad. Sci. U.S.A.
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 36.2%;
Best Local Similarity 97.1%;
Matches 407; Conservative
                                                                                                                   Tel: +55-11-2704922
                                                                                                                                    Fax: +55-11-2707001
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/organism="Homo sapiens"
/db_xref="taxon:966"
/db_xref="taxon:966"
/clone_lib="Hr0209"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_l: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.
14 a 147 c 121 g 115 t
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Faz: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2-MRO-HT0209-010
500-110-f09&t3-2000-05-016.t4=1)
Seq primer: puc 18 forward
High quality sequence start: 30
High quality sequence start: 30
High quality sequence stop: 487.
                                       1 (bases 1 to 487)
Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                           Paulo-SP,
                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                          Length 487;
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Pred. No. 2.6e-94;
0; Mismatches 2;
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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99.2%;
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Matches 397; Conservative
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Length 539;

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AI466645

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BG323538.1 GI:13129975
34.5%;
86.9%;
                             419; Conservative
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BG323538
             Best Local Similarity
Matches 419; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This read is a vailable royalty-free through LLNL; contact the
This read las been verified (found to hit its original self in the
correct orientation)
Putative full length read
Vector to vector length is 709
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 539)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Onderwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Materston,R. and Wilson,R. (Phe Washlo-NCI Mouse EST Project 1999)
 360
                  100 CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGAACACTTACATG 41
   caaatccgtcaaggcctagaagaactccagaaagttctgccaggaggagacacttacatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .539,

'Organism" Mus musculus"

'strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:493999"

/clone=lib="Scares mouse embryo NbME13.5 14.5"

/sex="unknown"

/tissue_type="embryo"

/dev_stage="la15-14.5dpc total fetus"

/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                              361 catgaaggatttgaaagggccagtgagcagatttattatg 400
                                                                             quality sequence stop: 454
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High quality sequence stop: 4
POLYA=No.
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M.Fatima Bonaldo.
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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 633)
NIH-WGC http://mgc.ncl.nih.gov/.
NIH-WGC http://mgc.ncl.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          þe
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                                           Gaps
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lyttp://image.llnl.gov
http://image.llnl.gov
n column: 23
High quality sequence stop: 571.
                                                                                                                                                                                                                                                                                                                                                    304 atccgtcaaggcctagaagaactccagaaagttctgccaggaggagagacacttacatgcat
                                                                                                                                                                                                                                                                                                                                                                        484 gagagggaggctaataggtctcgagatcttggtgcaattgtttactgtgttggtgtgaaa
                                                                                                                                                                           184 atctattactttgttgtggaacagttggctcacaaattcatcagcccacagttgagaatgtcc
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                                             Indels
Score 381.2; DB 9
Pred. No. 2.6e-93;
0; Mismatches 63
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/db_xref="taxon:9606"
/clone="IMAGE:4560214"
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Query Match
Best Local Simi
Matches 376;
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          /tissue_type="remail cell adenocarcinoma"
/lab.host="DH10B (phage-resistant)"
/note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5/
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1: 8Rb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-CDNA synthesis kit
(Stratugene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIO84806 554 bp mRNA linear EST 01-OCT-1998 oz80d12.xl Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1681655 3', mRNA sequence.
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia: Eutheria: Primates; Catarrhini: Hominidae; Homo.

1 (bases 1 to 554)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nclcgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                             463
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                                                                                                                                                                                                                  34.1%; Score 376.4; DB 10; Length 693; ilarity 91.9%; Pred. No. 5.9e-92; Conservative 0; Mismatches 31; Indels 12;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 721 Std Error: 0.00
Seq primer: -40m13 fwd. Er from Amersham
High quality, sequence stop: 455.
Location/Qualifiers
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Cartilage-associat Human cDNA clone ( Human cDNA sequenc Human immune/haema Human secreted exp

Human reproductive Kaposi's sarcoma-a Kaposi's sarcoma-a Nucleotide sequenc KSHV long unique c

Genomic sequence

KSHV LUR DNA (nuc)

Human colon cancer

cDNA clone encodin cDNA clone encodin cDNA clone encodin

cDNA encoding a hu

Sequence:

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Searched:

Database

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Human secreted protein-encoding gene 4 cDNA clone HWLFR02, SEQ ID NO:14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding partner identification; chromosome 19; ss
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                                AAA75158
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AAA75162
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AAC58396
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140..1351
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  17-JUL-2001 (first entry)
sapiens
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2. (SIDSI)gcgdata/geneseq/geneseqn.embl/NA1981.DAT:*

3. (SIDSI)gcgdata/geneseq/geneseqn.embl/NA1981.DAT:*

4. (SIDSI)gcgdata/geneseq/geneseqn.embl/NA1981.DAT:*

5. (SIDSI)gcgdata/geneseq/geneseqn.embl/NA1981.DAT:*

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                                                                                                                                           Description
                      Compugen Ltd
                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                               1736436 seqs, 858457221 residues
           GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                     US-09-970-076-1_COPY_104_1207
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Listing first 45 summaries
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AAD05334
AAA47455
AAI59918
AAI58132
AAH14331
AAA190433
AAL190433
                                                      OM nucleic - nucleic search, using sw model
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Drosophila melanog Gene encoding a su Drosophila melanog Drosophila melanog Single nucleotide

Human epithin-like

Human polynucleoti Human polynucleoti

Pusarium venenatum

"Human secreted protein"

/\*tag= a /product=

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sig\_peptide mat\_peptide

Human CDNA sequenc Murine TANGO 197 c Human breast cance

0 m 4 m 9 r 80 g

Result Š. Human breast cance

Drosophila melanog

DNA encoding novel Human PRO2198 nucl

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used as food additives or preservatives
                                                         Ruben SM, Komatsoulis GA, Moore PA,
                                                                                                 Claim 1; Page 425-426; 562pp; English.
                                                                                                                                                                                                                                                               98.88;
                                   05-NOV-1999; 99US-0163581.
30-JUN-2000; 2000US-0215133.
                                                 (HUMA-) HUMAN GENOME SCI INC
                          01-NOV-2000; 2000WO-US30045
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                                                                   WPI; 2001-308778/32
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Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the invention.
                                                                                                                                                                                                                                                                                         nucleic acid molecules encoding 28 human secreted proteins for sposing, preventing, treating or ameliorating medical conditions and
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Pred. No. 0;
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780 919 840

900

480

9 0; Gaps

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Ruben SM, Komatsoulis GA, Moore PA,
                                                           Location/Qualifiers
                                                                                                                                                                                                  Claim 1; Page 449; 562pp; English.
                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                      01-NOV-2000; 2000WO-US30045.
                                                                                                                                              99US-0163581
                                                                                                                                                 30-JUN-2000; 2000US-0215133
                                                                                                166..246
/*tag= b
247..1374
                                                                   /*tag= a
                                                               .1377
                                                                                                            /*tag=
                                                                                                                                                                        WPI; 2001-308778/32.
                                                                                                                                                                           P-PSDB; AAE01469
                                                                                                                       WO200134626-A1
                                                    Homo sapiens
                                                                                                                                             05-NOV-1999;
                                                                                                 sig_peptide
                                                                                                                              17-MAY-2001
                                                                                                        mat_peptide
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healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g. radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctggtgctcatctgcgccgggcaaggggaacgcagggaggatgggggtccagcctgctac 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 atggccacggcggagcggagagccctcggcatcggcttccagtggctctttggccact
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                                                                                                                                                                                                                                                                                                                                                                 Score 1089.4;
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Best Local Similarity 99.4%;
Matches 1090; Conservative 3
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                                               Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; hreumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; cardiovascular disorder; anglogenic disorder; kidney disorder; acardiovascular disorder; anglogenic disorder; kidney disorder; anglogenic disorder; kidney disorder; anglogenic disorder; kidney disorder; candocrine disorder; pregnancy-related disorder; centoring disorder; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; chromosome 19; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Human secreted protein"
/transl_except= (pos:1828..690, aa:Xaa)
/transl_except= (pos:1123..1125, aa:Xaa)
/transl_except= (pos:1156..1158, aa:Xaa)
/transl_except= (pos:1267..1269, aa:Xaa)
/note= "Xaa equals any of the twenty naturally ocurring
L-amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
             Human secreted protein-encoding gene 4 cDNA clone HWLFR02, SEQ ID NO:45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Mature human secreted protein"
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                                                                                                                                        1125
                                                                                                                                                                                 1020
                                                                                                                                                                                                                     1185
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                                                       tgtccagcgcctatcttaaaagaagttggcatgaaagctgcactccaggtcagcatgaac 1065
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                                                                                                                                                                                 tgtccagcgcctatcttaaaagaagttggcatgaaagctgcactccaggtcagcatgaac
                                                                                                                                          gatggcctcttttttatctccagttctgtcatcatcaccaccacactgttctgacsgt
                                                                                                                                                                                                                                                                                   tggttctggcccctctgctgcactgtgattatcaaggaggtccctccacccctgccgag
                                                                                                                         Location/Qualifiers
213..1214
/*tag= a
/product= TANGO 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human TANGO 197 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 4; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA47455 standard; cDNA; 2272
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chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachexia and autoimmune diseases e.g. mysathemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO 128, 137, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                 Length 2272;
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                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                               Sequence 2272 BP; 638 A; 554 C; 558 G; 522 T; 0 other;
                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                  Score 949.4; DB 21
Pred. No. 2.5e-280;
                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                    cellular disorders can be treated.
                                                                                                                                                                                                                                                                  86.0%;
                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                   Similarity
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data for this patent did not form part of the printed
                                             360 A; 354 C; 399 G; 289 T; 0 other;
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Best Local Similarity 99.8%;
Matches 805; Conservative (
            Note: The sequence specification.
                                             Sequence 1402 BP;
  S disorders.
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                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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tgtccagcgcctatcttaaaagaagttggcatgaaagctgcactccaggtcagcatgaac
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Yang Y,
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Xue AJ,
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Wang Z, Wehrman T, Xi
Zhou P, Goodrich R,
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2000US-0552317.
2000US-0598042.
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 Length 1402;
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                            Indels
 DB 22;
Score 803.8; DB 22
Pred. No. 8.8e-236;
0; Mismatches 2;
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                                                           Human polynucleotide SEQ ID NO 335.
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Wang Z, Wehrman T, Xi
Zhou P, Goodrich R,
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; 2000US-0552317.
; 2000US-0598042.
; 2000US-0698042.
; 2000US-0633450.
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                        (first entry)
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P-PSDB; AAM38976.
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19-OCT-2000;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and
the encoded polypeptides (AAM38642-AAM42213) with nootropic,
the encoded polypeptides (AAM38642-AAM42213) with nootropic,
immunosuppressant and cytostatic activity. The polypucleotides are useful
c in gene therapy. A composition containing a polypeptide or polynucleotide
c in gene therapy. A composition containing a polypeptide or polynucleotide
c of the invention may be used to treat diseases of the peripheral nervous
c system, such as peripheral nervous injuries, peripheral nervous
c calised neuropathies and central nervous system diseases, such as
c localised neuropathies and central nervous system diseases, such as
c lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
c lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
cutilisation of the activities such as: Immune system suppression,
c attivity, cancer diagnosis and therapy, drug screening,
assays for receptor activity, arthritis and inflammation, leukaemias and
c no contained the c
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treating disorders
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Novel nucleic acids and polypeptides, useful for such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 335; 10078pp; English
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Wang

Ren F, W Zhang J;

Qian XB, Yang Y,

nen R, Ma Y, ( {u C, Xue AJ, Drmanac RT;

Chen R, Xu C, Dp οy g òγ

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primer; detection; diagnosis; antisense therapy; gene therapy; ss
                                                                    Human cDNA sequence SEQ ID NO:11705.
              BP.
              AAH14331 standard; cDNA; 1436
                                                                                                                                                                                99JP-0248036.
                                                                                                                                                               2000EP-0116126
                                                     (first entry)
                                                                                                                                                               28-JUL-2000;
                                                                                                                           EP1074617-A2
                                                                                                                                                                                29-JUL-1999;
27-AUG-1999;
                                                                                                           Homo sapiens
                                                    26-JUN-2001
                                                                                          Human;
RESULT
                                   ;
0
                                                                                                                                               ctggtgctcatctgcgccgggcaaggggacgcagggaggatgggggtccagcctgctac 120
                                                                                                                               Gaps
                                                                                                            Length 1609;
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                                                                                                                               Indels
                                                                                                             22;
                                                                                                            72.8%; Score 803.8; DB 22;
larity 99.8%; Pred. No. 9.5e-236;
Conservative 0; Mismatches 2;
                                                                                                                       al Similarity
805; Conserv
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Query Match

Best Local Matches 8(

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Ωp ŏ 682 900 742 9 802 720 862

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TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; Crohn's disease; chronic myelogenous leukemia; cancer; liver disease; Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia; autofimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus erythematosus; transgenic animal; diagnosis; prophylatic; therapeutic; mouse; ds.
                      503 catgaaaggatttgaaaagggccagtgagcagatttattatgaaaacagacaagggtacagg
                                                                                                                    563 acagetagegteateattgetttgaetgatggagaaetecatgaagatetetttttetat
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/product= TANGO 197
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                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide comprises one of the Complementary strand of a polynucleotide which comprises one of ilgonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, and per therapy. The primers are useful for synthesising polynucleotides, the full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13631 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to AAH3632 to AAH3646 to AAH3632 to AAH3632 to AAH3632 to AAH3646 to AAH3642 to AA
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                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
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                                                                                                                                          Saito K, Y. Otsuki T;
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Pred. No. 1.3e-230;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID 11705; 2537pp + CD ROM; English.
                                                                                                                                          Hayashi K, S
A, Nagai K,
                                                                                                                                          hikawa T,
Wakamatsu
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                                                                                                                                        Nishikawa
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99.3%;
2000JP-0118776.
                    02-MAY-2000; 2000JP-0183767, 09-JUN-2000; 2000JP-0241899
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                                                                                             (HELI-) HELIX RES INST
                                                                                                                                                                                                                 WPI; 2001-318749/34
                                                                                                                                        Ota T, Isogai T,
Ishii S, Sugiyama
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Best Local Similarity
11-JAN-2000;
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(first entry)

07-DEC-2001

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                                                                                            Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's diseases of septiminary arthritis, Lyme's disease, cachexia and autoimmune diseases e.g. myasthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transpenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology; for diagnostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range
Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 453.2; DB 21;
Pred. No. 6.1e-128;
0; Mismatches 53;
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                                                                    209pp; English
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90.18;
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                                                                      Claim 1; Fig 27;
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Matches 485;
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The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
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                     polynucleotide 11500
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100.0%; Pred. No. 1.3e-96;
ive 0; Mismatches 0;
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                                              Human; breast cancer; cell marker; cytostatic;
                                                                                                                                                                                                                                                                            MEDICINE INC
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2000US-0192099.
2000US-0193480.
2000US-0205230.
2000US-0211315.
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Matches 349; Conserv
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09-JUN-2000;
25-JUL-2000;
                         Human breast
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                                                                           Homo sapiens
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llarity 100.0%; Po
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20000S-0192099.
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24-MAR-2000;
29-MAR-2000;
15-MAY-2000;
09-JUN-2000;
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Best Local Simi
Matches 346;
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                                                                                                         Human; breast cancer; cell marker; cytostatic; ss.
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                                                                                       Human breast cancer expressed polynucleotide 590.
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Pred. No. 2.5e-96;
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100.0%; Pred. No.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 189; 3695pp; English.
                             AAL08133 standard; cDNA; 355
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24-MAR-2000; 2000US-0192099.
29-MAR-2000; 2000US-0193480.
15-MAY-2000; 2000US-0205230.
09-JUN-2000; 2000US-0211315.
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                                                                                                                              Homo sapiens
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Human breast cancer expressed polynucleotide 18335.
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Pred. No. 1e-95;
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gtgtgaaagatttcaatgagacacagctggcccggattgcggacagtaaggatcatgtgt 180
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Matches 627; Conserv
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TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; coedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; schemic heart disease; hydrocephalus; brain hernlation; latrogenic disease; inflammation; meningitis; haraheimer's Disease, cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
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AAA75157-59 encode human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 260 polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular adhesion in proliferation, modulate cellular adhesion, modulate the proliferation, differentiation, and/or function of cells matrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or creat disorders associated with the ovaries, and cerebral cerebral condema, hydrocephalus, brain hernititis, Alzheimer's Disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral concers, hydrocephalus and encephalitis, and treat hepatic disorders in twas presents esquence does not appear in the specification; it was concerted and except and version and encephalitis, and treat hepatic disorders.
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Disclosure; Page -; 175pp; English.
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Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,

2000-579269/54 P-PSDB; AAB18456

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TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoietic associated disease; atelectasis; pulmonary congestion; ocdema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain herniation; iatrogenic disease; inflammation; meningitis; hzaheimer's Disease, cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
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AAA75157-59 encode human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 262, and TANGO 267. The TANGO CEC describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO CEC polypeptides can be used to modulate cellular adhesion. The cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, computate the proliferation differentiation, and/or function of cells and hematopoletic associated diseases and disorders, treat bone marrow, blood that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoletic associated diseases and disorders, sphen associated diseases, modulate the proliferation disorders sphen associated diseases, modulate the proliferation, differentiation, as ischemic heart disease, modulate the proliferation, differentiation, as ischemic heart disease, modulate the proliferation, differentiation, differentiation, disorders succiated diseases or disorder. They may also be used to creat disorders associated diseases or disorder. They may also be used to treat disorders associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, bacherial and viral meningitis, alzheimer's Disease, cerebral cancers, obsertail and viral meningitis, alzheimer's Disease, cerebral cancers, hote: the present sequence does not appear in the specification; it was created using information provided.
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Pred. No. 3.5e-94;
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                                                                                                                                                            Disclosure; Page -; 175pp; English.
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58.1%;
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Matches 626; Conservative
                                                                                                                     for treating cancer
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Fraser CC;

Sharp JD,

Holtzman DA,

Barnes TM,

(MILL-) MILLENNIUM PHARM INC

01-MAR-2000; 2000WO-US05226

01-MAR-1999;

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TANGO 266; TANGO 216;; TANGO 261; TANGO 267;
cellular proliferation; cellular differentiation; cellular adhesion;
von Willebrand factor-associated disorder; cell trafficking; cancer;
hematopoietic associated disease; atelectasis; pulmonary congestion;
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
intestinal disorder; spleen associated disease; renal disorder;
anticovascular disorder; ischemic heart disease; hydrocephalus;
brain hernlation; iatrogenic disease; inflammation; meningitis;
Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
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                                   781 gcagagaaagaggcaaagatatccaggtcacttgggggctagtgtttattgtgttgtgtgt
                                                                      541 aaagatttcaatgagacacagctggcccggattgcggacagtaaggatcatgtgtttccc
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                                                                                          cDNA clone encoding a human TANGO 216 polypeptide.
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/product= "TANGO 216"
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08-SEP-2000

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ARA75157-59 encode human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 262, and TANGO 267. The TANGO 260 escribes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular aproliferation, modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate the proliferation of proliferative disorders, such as cancer, that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, understand disorders, spleen associated diseases, modulate the proliferation of cellular intestinal disorders, spleen associated as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, brinn beintations, intercents and cerebral oedema.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.1%; Score 343; DB 21; 58.1%; Pred. No. 3.5e-94;
                                                                                                                                                                                                                                                                                                                                           Disclosure; Page -; 175pp; English.
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P-PSDB; AAB18457.
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AAA75160-62 encode murine TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO 262 ellupar dependes can be used to emodulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, modulate cell adhesion in proliferation, and/or functions, and cell trafficking and/or migration, and/or function of cells that appear in the bone marrow, and leukcytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, plumary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as inchmic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage casociated diseases or disorder. They may also be used to cartilage associated diseases or disorder. They may also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders. note: the present sequence does not appear in the specification; it was
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US-09-970-076-1 1414 Title: Perfect score:

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IDENTITY\_NUC Gapop 10.0 ; Gapext 1.0 Scoring table:

2812564 Total number of hits satisfying chosen parameters:

1406282 seqs, 1168085023 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Database

Pending\_Patents\_NA\_New:\*

1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

tion	ce 176, App	ce 231, App		H	ce 13, Appl	15,	23,	19,	25,	o,	ce 21, Appl	급	ce 11, Appl	186	300,	98, A			(A		ce 3023, Ap	ce 669, App	ce 5, Appli	6	47,
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## ALIGNMENTS

RESULT Sequence Seque	PCT-USO2-08253-176  PCT-USO2-08253-176  Sequence 176, Application PC/TUSO208253  GENERAL INFORMATION: APPLICANT: Carson-Walter, Eleanor APPLICANT: St. Croix, Bard APPLICANT: St. Croix, Brad APPLICANT: Winzler, Renneth TITE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS FILE REFERENCE: 1107.00179 CURRENT FILING DATE: 2002-04-10 PRIOR APPLICATION NUMBER: 60/282,850 PRIOR FILING DATE: 2001-04-11 PRIOR FILING DATE: 2001-04-11 PRIOR FILING DATE: 2001-04-11 PRIOR FILING DATE: 2001-08-01 PRIOR FILING DATE: 2001-08-01 PRIOR FILING DATE: 2001-08-01 SEQ ID NO 176 SOFTWARE: FastSEQ for Windows Version 4.0 SSOFTWARE: FastSEQ for Windows Version 4.0 TYPE: DNA CORGANISM: Homo sapiens	Match 84.4%; Score 1193.8; DB 1; Length 5540; Cocal Similarity 99.8%; Pred. No. 9.1e-160; es 1195; Conservative 0; Mismatches 2; Indels 0; Gaps	1 aggacccgcgaggaagggcccgcggatggcgcgtccctgagggtcgtggcgagttcgcgg 60	61 agcgtgggaaggagcggacctgctctcccqggctgcgggccatggccacggcggagcg 120 	1] gagagccctcggcatcggcttccagtggctctctttggccactctggtgctcatctgcgc 180	31 cgggcaaggggacgcagggagatggggtccagcctgctacggcgatttgacctgta 240 	11 cttcattttggacaaatcaggaagtgtgctgcaccactggaatgaaatctattacttgt 300 
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APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Beth
TITLE OF INVENTION: EMPOTHELIAL CELL EXPRESSION |
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
                                                                                                                                                                                                                                                     Sequence 231, Application PC/TUS0208253 GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-08-01
PRIOR PLING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.;
SEQ ID NO 231
LENGTH: 5540
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                                      LENGTH: 5540
TYPE: DNA
CRGANISM: Homo sapiens
PCT-USO2-08253-231
                                                               Query Match
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APPLICANT: Theresa L. O'KEEFE
FILE REFERENCE: TS63-233-999
CURRENT APPLICATION: Tango 197 and Tango 216 Conformer FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENTH: 1674
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ORGANISM: Homo sapiens
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APPLICANT: Theresa L. O'KEFE
APPLICANT: Theresa L. O'KEFE
APPLICANT: Dudith J. Healey
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION NOWBER: 2020-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FRSESEQ FOR WINDOWS Version 4.0
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Pred. No. 7.7e-140;
0; Mismatches 1;
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Best Local Similarity 99.9%;
Matches 1053; Conservative 0
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; LOCATION: (213)...(1211)
US-10-038-307-1
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US-10-038-307-1
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Length 1674;
         Indels
DB 7;
    Pred. No. 3.2e-127
         0; Mismatches
Score 962.8;
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     Similarity 99.8
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Matches 964;
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Pred. No. 9.3e-126;
0; Mismatches 6;
RESULT 5
US-10-038-307-13
Sequence 13, Application US/10038307
Sequence 13, Application US/10038307
Sequence 13, Application US/10038307
Sequence 13, Application US/10038307
SEQUENCH: James B. ROTTMAN
APPLICANT: James L. O'KEEFE
TITLE OF INVENTION: Tango 197 and Tango 216 (
FILE REFERENCE: 7653-253-99
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 13
LENGTH: 1650
LENGTH: 1650
                                                                     and Tango 216
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99.48;
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                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-10-038-307-13
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nes 956; Conserv
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Pred. No. 1.3e-125;
0; Mismatches 1;
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216
FILE REFRENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 23
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ORGANISM: Homo sapiens
US-10-038-307-23
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Pred. No. 9.3e-126;
0; Mismatches 6;
                                                                                                                                                                                                                                  Sequence 15, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
SAPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: TOUGIL JO. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 (
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: TastSEQ for Windows Version 4.0
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CORGANISM: Homo sapiens
US-10-038-307-15
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Best Local Simi.
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GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Theresa L. O'KEEFE
TITLE OF INVENTION: Tango 197 and Tango 216
FILE REFRENCE: 7853-253-99
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
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US-10-038-307-19
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                                                              Score 951.4; DB 7;
Pred. No. 1.3e-125;
0; Mismatches .1;
        4.0
         Version
  26
Windows
                                                                67.3%;
99.9%;
                                                                               Conservative
                                   ; ORGANISM: Homo sapiens
US-10-038-307-19
  NOS:
                                                                 Query Match
Best Local Similarity
Matches 952; Conserv
  SEQ ID NO
FastSEQ 1
NUMBER OF SEQ
SOFTWARE: FASTS
SEQ ID NO 19
LENGTH: 1713
TYPE: DNA
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Pred. No. 1.6e-125;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                      APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 of TITLE OF INVENTION: Tango 197 and Tango 216 of TITLE OF INVENTION NUMBER: US/10/038,307
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ 1D NOS: 26
SEQ 1D NOS: 26
SEQ 1D NOS: 26
SEQ 1D NOS: 26
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ilarity 99.3%;
Conservative
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CORGANISM: Homo sapiens
US-10-038-307-9
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US-10-038-307-9
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Pred. No. 1.5e-125;
0; Mismatches 5; Indels
          Compositions
                                                                       Sequence 25, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
TILE OF INVENTION: Tango 197 and Tango 216 Corp.
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEC ID NOS: 26
NUMBER OF SEC ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.5%;
Matches 954; Conservative
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US-10-038-307-25
                                                    RESULT 9
US-10-038-307-25
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APPLICANT: ISOGAI, TAKAO
APPLICANT: NISHIKAWA, TETSUO
APPLICANT: HAYASHI, KOJI
APPLICANT: SAITO, KAORU
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US-09-629-469A-11705
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Sequence 2.1, Application US/10038307

GENERAL INFORMATION:
REPLICANT: James B. ROTTWAN

APPLICANT: Endin OZKAYNAK

APPLICANT: Endin OZKAYNAK

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and TITLE OF INVENTION: Tango 197

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT FILING DATE: 2002-06-28

NUMBER OF SEQ 1D NOS: 26

SOFTWARE: FASELSEQ for Windows Version 4.0
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Pred. No. 2.2e-120;
0; Mismatches 1;
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al Similarity 97.1%;
952; Conservative
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US-10-038-307-21
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SEQ ID NO 21
LENGTH: 1047
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Pred. No. 7.9e-114;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/10038307
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Com
FILE REFERENCE: 7853-253-999
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 1623
TYPE: DNA
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Best Local Similarity 97.9%;
Matches 879; Conservative
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; ORGANISM: Homo sapiens
US-10-038-307-11
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US-10-038-307-11
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99.3%; Pred. No. 5.7e-117;
ive 0; Mismatches 5;
      APPLICANT: INAMA, TOMOYASU
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: WAKAMTSU, AI
APPLICANT: WAKAMTSU, AI
APPLICANT: WAGAL, KEITCHI
APPLICANT: OTSUKI, TETSUJI
TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FUL
FILE REFERENCE: 084335/0123
CURRENT APPLICATION NUMBER: US/09/629,469A
CURRENT APPLICATION NUMBER: US/09/629,469A
PRIOR APPLICATION NUMBER: JP 1999-208-27
PRIOR PILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR PELICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-06-01
PRIOR PELICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-06-02
PRIOR PELICATION NUMBER: JP 2000-241899
PRIOR FILING DATE: 2000-06-09
PRIOR PELICATION NUMBER: GO/183,322
PRIOR PILING DATE: 1999-10-18
PRIOR PELING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 60/183,322
PRIOR FILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-18
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Matches 904; Conservative
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SEQ ID NO 11705
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NAME/KEY: CDS
; LOCATION: (380)..(1033)
US-09-629-469A-11705
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SEQUENCE 186, APPLICATION:
APPLICANT: GESTSON WHALEY, Eleanor
APPLICANT: St. CTOIX, Brad
APPLICANT: St. CTOIX, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Wogelstein, Bert
APPLICANT: Wogelstein, Bert
APPLICANT: WOGELSTEIN, BOTH
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATT
TITLE OF INVENTION: ENDOTHELIAL
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: POT/USO2/08253
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/388,829
PRIOR FILING DATE: 2001-04-11
SPRIOR PRICE FEASEQ FOR WINDOWS VERSION 4.0
SOFTWARE FEASESQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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Pred. No. 7.1e-112;
); Mismatches 136;
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ilarity 87.3%;
Conservative
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es 935; Conserv
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CRGANISM: Mus n
PCT-US02-08253-186
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PCT-US02-08253-186
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Best Local S
Matches 935
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                                                                                                                                                                                                                                                       Length 5220;
                          APPLICANT: Carson-Walter, Eleanor
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: PCT/US02/08253
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR PILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
SPRIOR FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                     Score 853.4; DB 1;
Pred. No. 7.1e-112;
0; Mismatches 136;
:r-USO2-08253-300
Sequence 300, Application PC/TUS0208253
GENERAL INFORMATION:
                                                                                                                                                                                                                                                     60.4%;
87.3%;
                                                                                                                                                                                                                                                   Query Match 60.4
Best Local Similarity 87.3
Matches 935; Conservative
                                                                                                                                                                                                          ORGANISM: Mouse
PCT-US02-08253-300
                                                                                                                                                                            SEQ ID NO 300
LENGTH: 5220
                                                                                                                                                                                                  TYPE: DNA
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Search completed: August 9, 2002, 02:02:44 Job time: 10781 sec

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets or results. These databases were split into to two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, .rapm and .rapn

The Pending database search results should not be left in the case because they contain data that is confidential.

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

- nucleic search, using sw model

OM nucleic

Run on:

August 8, 2002, 22:18:18 ; Search time 4997.37 Seconds (without alignments) 6121.569 Million cell updates/sec

Title:

US-09-970-076-1

Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

43959072 Total number of hits satisfying chosen parameters:

21979536 segs, 10817449327 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2\_6/ptodata/2/pna/US095\_\_\_\_\_OMB.seq: /cgn2\_6/ptodata/2/pna/US095\_\_\_COMB.seq: /cgn2\_6/ptodata/2/pna/US096A\_COMB.seq: /cgn2\_6/ptodata/2/pna/US096B\_COMB.seq: /cgn2\_6/ptodata/2/pna/US096E\_COMB.seq: /cgn2\_6/ptodata/2/pna/US096E\_COMB.seq: /cgn2\_6/ptodata/2/pna/US097\_\_COMB.seq: /cgn2\_6/ptodata/2/pna/US097\_COMB.seq: /cgn2\_6/ptodata/2/pna/US097\_COMB.seq: /cgn2\_6/ptodata/2/pna/US098A\_COMB.seq: /cgn2\_6/ptodata/2/pna/US098B\_COMB.seq: /cgn2\_6/ptodata/2/pna/US098B\_COMB.seq: /cgn2\_6/ptodata/2/pna/US098B\_COMB.seq: /cgn2\_6/ptodata/2/pna/US099A\_COMB.seq: /cgn2\_6/ptodata/2/pna/US099B\_COMB.seq: /cgn2\_6/ptodata/2/pna/US099B\_COMB.seq: /cgn2\_6/ptodata/2/pna/US099B\_COMB.seq: /cgn2\_6/ptodata/2/pna/US099B\_COMB.seq: /cgn2\_6/ptodata/2/pna/US099C\_COMB.seq: /cgn2\_6/ptodata/2/pna/US099C\_COMB.seq: /cgn2\_6/ptodata/2/pna/US090C\_COMB.seq:\* 

/cgn2\_6/ptodata/2/pna/US6003\_coMB.seq:\* /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq:\*

the number of recult	ŭ
: /cgn2_6/ptodata/2/pna/US6035_COMB.seq:*	74:
: /cgn2_6/ptodata/2/pna/US6034_COMB.se	73:
: /cgn2_6/ptodata/2/pna/US6033_COMB.se	72:
: /cgn2_6/ptodata/2/pna/US6032_COMB.se	71:
: /cgn2_6/ptodata/2/pna/US6031_COMB.se	70:
: /cgn2_6/ptodata/2/pna/US6030_COMB.se	: 69
: /cgn2_6/ptodata/2/pna/US6029_C	68:
: /cgn2_6/ptodata/2/pna/US6028_COMB.se	. 29
: /cgn2_6/ptodata/2/pna/US6027_COMB.se	99
: /cgn2_6/ptodata/2/pna/US6026_COMB.se	65:
: /cgn2_6/ptodata/2/pna/US6025_C	64:
: /cgn2_6/ptodata/2/pna/US6024_COMB.se	63:
: /cgn2_6/ptodata/2/pna/US6023_COMB.s	62:
: /cgn2_6/ptodata/2/pna/US6022_COMB.se	61:
: /cgn2_6/ptodata/2/pna/US6021_COMB.se	90:
: /cgn2_6/ptodata/2/pna/US6020_COMB.se	59:
: /cgn2_6/ptodata/2/pna/US6019_COMB.se	58:
: /cgn2_6/ptodata/2/pna/US6018_COMB.se	57:
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: /cgn2_6/ptodata/2/pna/US6016_COMB.s	55:
: /cgn2_6/ptodata/2/pna/US6015_COMB.se	54:
: /cgn2_6/ptodata/2/pna/US6014_COMB.se	53:
: /cgn2_6/ptodata/2/pna/US6013_	52:
: /cgn2_6/ptodata/2/pna/US6012_COMB.se	51:
: /cgn2_6/ptodata/2/pna/US6011_COMB.se	50:
: /cgn2_6/ptodata/2/pna/US6010_COMB.	49:
: /cgn2_6/ptodata/2/pna/US6009_	48:
: /cgn2_6/ptodata/2/pna/US6008_COMB.se	47:
: /cgn2_6/ptodata/2/pna/US6007_COMB.s	46:
: /cgn2_6/ptodata/2/pna/US6006_COMB.	45:
gn2_6/ptodata/2/pna/US600	44:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1, Appli Sequence 1222, Ap			ι,	Sequence 14, Appl	Š	,,	Q.			Sequence 8, Appl1	Sequence 11, Appl	÷	435	Sequence 68, Appl	204,		204,	ĸ,	998,	988,	7727,		Sequence 7309, Ap			7873,	7727,	Seguence 188, App	Sequence 1757, Ap
TD (II)	US-09-970-076-1	-09-918-715	US-09-918-715-231	US-09-970-076-5	Ţ	PCT-US00-30045-45	US-09-970-076-7	PCT-US99-31025-8	US-09-223-546-8	US-09-471-179-8	US-09-599-596-8	US-09-796-753-11	US-09-644-871-9264	US-09-710-281-4357	US-09-329-548A-68	US-09-419-553-204	16-448-99	-770-155-2	US-09-780-183-68	19-833-381-9	09-833-382-9	-371-168-7	39-644	US-09-644-871-7309	-649-163-6	-652-121-5	US-09-652-127-7873	-801-833	-09-668-337-18	US-09-625-102-1757
DB	36	34	34	36	~	٦	36	٦	16	18	22	30	25	28	17	18	19	30	30	32	32	17	25	25	25	25	25	31	56	24
Query Match Length DB	1414	5540	5540	5540		2086		2272	2272	2272	2272	2272	2374	2374	2459	2459	2459	2459	2459	2459	2459	2401	2401	2401	2401	2401	2401	2401	2485	2397
Query Match	100.0	84.4	84.4	84.4	84.4	84.3	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.3	74.3	74.3	74.3	74.3	74.3	74.3	72.5	68.1
Score	1414		٠.		1193.6	1192.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1052.4	1050.8	1050.8	1050.8	1050.8	1050.8	1050.8	1050.8	1025.8	963
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361 caccogaggaacaacttaatgaaactgacagaagacagaacaaatcogtcaaggcct	1081 cctgctgatcctgctcctagcctggctcctcctggtggtgttctggccctctg 114 1081 cctgctgatcctgttcctgctcctagcctggctctcctggtggttctggccctctg 114 1081 cctgctgatcctgttcctgctcctagcctggctctcctctggtggttctggccctctg 114 1081 ctgcactgtgattatcaaggaggtccctccacccctgcgagagaga
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octgotgatcotgttcotgctcotagcoctggctctcctctggtggttctggccctctg 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 176, Application US/09918715

SERENEAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Berd St. Croix
APPLICANT: Berd St. Croix
APPLICANT: Berd St. Croix
APPLICANT: Renneth Kinzler
TILLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REPERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/282,850
SPRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
SPRIOR FILING DATE: 2000-04-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 84.4%;
Best Local Similarity 99.8%;
Matches 1195; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-176
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                                                                   APPLICANT: Lal, Freeti
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Toloride Sequence Databases, and Single Nucleotide Polymor
TITLE OF INVENTION: Toloride Thereby
FILE REPERENCE: 6x-0015 P
CURRENT APPLICATION NUMBER: US/60/213,359
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 7924
SOFTWARE: PERL Program
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                                                                                                                                                                                                                                                                                                                                                           Score 1193.8; DB 60; Lengt
Pred. No. 5.6e-131;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
COTHER INFORMATION: Incyte ID No: 243308.2
US-60-213-359-1222
                            Sequence 1222, Application US/60213359
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
                                                                                                                                                                                                                                                                                                                                                             84.48;
99.88;
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.8
Matches 1195; Conservative
                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                               SEQ ID NO 1222
                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541
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US-UY-YLB-/1D-431
Sequence 231, Application US/09918715
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Bert Vogelstein
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107 00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR PALICATION NUMBER: 60/224,599
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
SUMBER OF SEQ ID NOS: 358
SOFTWARE: FESTSEQ for Windows Version 3.0
SEQ ID NO 231
LENGTH: 5540
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Pred. No. 5.1e-131;
0; Mismatches 2;
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larity 99.8%;
Conservative
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US-09-918-715-231
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Matches 1195;
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Pred. No. 5.1e-131;
); Mismatches 2;
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APPLICANT: Bradley, Kenneth A.
APPLICANT: Graller, Robert J.
APPLICANT: Graller, Robert J.
APPLICANT: Graller, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor
FILE REFERENCE: 960296.9745
CURRENT APPLICATION NUMBER: US/09/970,076
CURRENT FILING DATE: 2000-110-03
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09970076 GENERAL INFORMATION:
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99.8%;
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Best Local Similarity 99.8
Matches 1195; Conservative
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; LOCATION: (144)..(1835)
US-09-970-076-5
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ORGANISM: HOMO
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US-09-970-076-5
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; Sequence 45, Application PC/TUS0030045
; GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TILE OF INVENTION: 28 Human Secreted Proteins
FILE REPREBUCE: PS708PCT
CURRENT APPLICATION NUMBER: PCT/US00/30045
; CURRENT FILING DATE: 2000-11-01
PRIOR PRICATION NUMBER: 60/163,581
PRIOR PILING DATE: 1999-11-05
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 201
; SOGTWARE: PatentIN Ver. 2.0
; SEQ ID NO 45
LENTH: 2086
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LOCATION: (2070)
OTHER INFORMATION: D
NAME/KEY: SITE
LOCATION: (2075)
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OTHER INFORMATION:
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INFORMATION:
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OTHER INFORMATION:
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LOCATION: (2083)
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PCT-US00-30045-45
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                                                                               APPLICATE: Human Genome Sciences, Inc.
APPLICATE: Human Genome Sciences, Inc.
TITLE OF INVENTION: 28 Human Secreted Proteins
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PS708PCT
CURRENT APPLICATION NUMBER: PCT/US00/30045
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/163,581
PRIOR APPLICATION NUMBER: 60/215,133
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 201
SOFTWARE: PatentIn Ver: 2.0
                                                                                                                                                                                                                                  Score 1193.6; DB 1;
Pred. No. 5.9e-131;
); Mismatches 4;
                                                                 Sequence 14, Application PC/TUS0030045 GENERAL INFORMATION:
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99.78;
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pcr-us00-30045-14
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Matches 1196;
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                                                                                                                                                                    APPLICANT: Young, John A.T.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Bradley, Kenneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor
FILE REFERENCE: 960296, 97745
CURRENT APPLICATION NUMBER: 05/9970,076
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 7.
SEQ ID NO 7.
                                                                                                                                                      Sequence 7, Application US/09970076 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (113)..(1111)
US-09-970-076-7
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Best Local Similarity
Matches 1053; Conserv
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ADDITIONAL INCOMPATION: SECRETED PROTEINS AND NUCT
TITLE OF INVENTION: SECRETED PROTEINS AND NUCT
TITLE OF INVENTION: SECRETED PROTEINS
TITLE OF INVENTION: ENCODING THEM
FILE REFERENCE: 7853-173-228
CURRENT APPLICATION NUMBER: PGT/US99/31025
CURRENT FILING DATE: 1999-12-33
EARLIER FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FASLSEQ for Windows Version 4.0
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 8
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GENERAL INFORMATION:
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LOCATION: (213)...(1211)
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ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (213)...(1211)
US-09-471-179-8
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 1053; Conserv
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Pred. No. 2e-114;
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   US-09-223-546-8

Sequence 8, Application US/09223546

GENERAL INFORMATION:
FILLE OF INVENTION: SECRETED PROTEINS AND NURTIER REFERENCE: 09404/066001

CURRENT APPLICATION NUMBER: US/09/223,546

CURRENT FILING DATE: 1998-12-30

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 3.0
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Matches 1053; Conservative
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; LOCATION: (213)...(1211)
US-09-223-546-8
                                                                    LENGTH: 2272
TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 2272
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Pred. No. 2e-114;
0; Mismatches
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US-09-471-179-8

SQUENCE 8, Application US/09471179

GENERAL INFORMATION:
APPLICANT: HOITEMAN DOUGLAS

TITLE OF INVENTION: SECRETED PROTEINS AND NUC
FILE REFERENCE: 7853-173

CURRENT APPLICATION NUMBER: US/09/471,179

CURRENT APPLICATION NUMBER: 09/223,546

PRIOR PRICH APPLICATION NUMBER: 09/223,546

PRIOR FILING DATE: 1998-12-30

NUMBER: OF SEQ ID NOS: 135

SEQ ID NO 8

SEQ ID NO 8
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; Sequence 8, Application US/09599596
; GENERAL INFORMATION:
    APPLICANT: Holtzman, Douglas
; TITLE OF INVENTION: SECRETED PROTEINS AND NUC
FILE REPERENCE: 09404/06601
    CURRENT APPLICATION NUMBER: US/09/599,596
    CURRENT APPLICATION NUMBER: 09/223,546
    PRIOR APPLICATION NUMBER: 09/223,546
    PRIOR FILING DATE: 1998-12-30
    NUMBER OF SEQ ID NOS: 22
    SOFTWARE: FASTSEQ for Windows Version 3.0
    SEQ ID NO 8
    LENGTH: 2272
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (213)...(1211)
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Score 1052.4; DB
Pred. No. 2e-114;
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99.9%;
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                           Sequence 11, Application US/09796753 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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                                               Score 1052.4; DB Pred. No. 2e-114; 0; Mismatches
                                                 74.48;
99.98;
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Best Local Similarity 99.9
Matches 1053; Conservative
; NAME/KEY: CDS
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US-09-796-753-11
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Sequence 4357, Application US/09710281
SPERRAL INFORMATION: John J.
APPLICANT: Hunter, John J.
APPLICANT: Shyjan, Andrew W.
APPLICANT: Stbdal, Hilde
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
CURRENT APPLICATION NUMBER: US/09/710,281
CURRENT FILING DATE: 2000-11-10
PRIOR FILING DATE: 1999-11-09
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SOFTWARE: FastSEQ for Windows Version 4.0
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|larity 99.9%;
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ORGANISM: Homo sapiens
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Matches 1053; Conserv
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US-09-710-281-4357
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APPLICANT: HOLIZAMAN, DOUGJAS A.
APPLICANT: PAD, YANG
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOR
TITLE OF INVENTION: THEREOR
TITLE OF INVENTION: THEREOR
TITLE OF INVENTION: US/09/644,871
CURRENT APPLICATION NUMBER: US/09/644,871
CURRENT FILING DATE: 2000-08-28
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9739
SOFTWARE: FASTSEQ FOR Windows Version 4.0
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Best Local Similarity 99.9
Matches 1053; Conservative
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US-09-644-871-9264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Bradley K.A., Mogridge J., Mourez M., Collier R.J., Young J.A.T.; "Identification of the Cellular Receptor for Anthrax Toxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Vertebrata; Euteleostom1;
Vertebrata; Euteleostom1;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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100.0%; Pred. No. 4.6e-127;
ive 0; Mismatches 0;
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EMBL; AF421380; AAL26496.1;
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Oggye8 halocynthia
O04588 eimeria max
O43811 eimeria ten
O70550 mus musculu
Ogudj9 neospora ca
O43853 homo sapien
O20894 sus scrofa
O20894 sus scrofa
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096nc7 homo sapien
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096ec6 homo sapien
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                                                                                                                                    9, 2002, 10:46:19; Search time 102.68 Seconds
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                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                       hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                 562222 seqs, 172994929 residues
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1 GQGGRREDGGPACYGGFDLY.....
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368 AA

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ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ 180 181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 240

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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STRAIN-SPRAGUE-DAWLEY:
O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G Gallatin W.M.;
Cloning of rat alpha D, a novel beta 2 integrin.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF021334; AAF21241.1;
HSSP; P11215: 1A8X.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR000413; Integrin_alpha.
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                           Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012475; AAH12475.1; -.
                                                                                                                                              SEQUENCE 97 AA; 10453 MW; 14F475F0B170E71A CRC64;
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Last annotation update)
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Pred. No. 9.2e-27;
0; Mismatches 4;
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[1]
SEQUENCE FROM N.A.
TISGUE-BREAST, AND MAMMARY ADENOCARCINOMA;
Strausberg R.; AND MAMMARY ADENOTATION CONTRACTOR
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PROSITE; PS50234; VWFA; 1.
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Pfam; PF00357; integrin_A; 1.
Pfam; PF00092; vwa; 1.
PRINTS; PR01188; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
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ilarity 95.1%;
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01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
ALPHA D INTEGRIN.
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Matches 63; Conserv
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nes 78; Conserv
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:4705862) (FRAGMENT).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                           Query Match
37.4%; Score 574; DB 4; Length 245;
Best Local Similarity 49.2%; Pred. No. 1.4e-42;
Matches 120; Conservative 45; Mismatches 67; Indels
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Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last annot
CDNA FLJ31074 FIS, CLONE HSYRA2001476.
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MEDLINE-93149203; PubMed-8426611;
Pasamontes L.E., Hug D., Huembelin M., Weber G.;
Pasamontes L.E., Hug D., Huembelin M., Weber G.;
Sequence of a major Eineria maxima antigen homologous to the Eineria tenella microneme protein Etp100.";
Mol. Blochem. Parasitol. 57:171-174(1993).
EMBL; M99058; AAA29076.1; -.
InterPro; IPR000884; TSP1.
InterPro; IPR0002035; vWFA.
Pfam; PF00092; vwa; 1.
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MEDLINE=92131064; PubMed=1775171;
Tomley F.M., Clarke L.E., Kawazoe U., Dijkema R., Kok J.J.;
Tomley F.M., Clarke L.E., Kawazoe U., Dijkema R., Kok J.J.;
"Sequence of the gene encoding an immunodominant microneme protein of Eimeria tenella.";
Mol. Biochem. Parasitol. 49:277-288(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 CTRLLDVMLVVDESGSIGTSNYGKVRSFISNFAGTMPLSPDDVRVGLVTFGTSAVTRWDL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 ELHEDLFFYSERE-----ANRSRDLGAIVYCVGV-KDFNETQLARIA--DSKDHV-FP- 174
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                                                                                                                                                                                                        Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 CYGGFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 TEDREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75808 MW; AC2A0E7A346A7E9E CRC64;
                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MAJOR ANTIGEN HOMOLOGOUS SEQUENCE (EMP100).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 -VNDGFQALQGIIHSILKKSCIEI----LAAEPSTI--CAGE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 YLQSNWGGVSSQINGIIKAACKDLAKDAVCSEWSEYGPCEGE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MICRONEME PROTEIN ETMIC-1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.0%; Score 139; DB 5; L
26.6%; Pred. No. 0.0012;
tive 40; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00453; VWFADOMAIN.
SMART; SM0209; TSP1; 6.
SMART; SM00327; VWA; 1.
PROSITE; PS50092; TSP1; 5.
PROSITE; PS50234; VWFA; 1.
SEQUENCE 724 AA; 75808 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 59; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5802;
                                                                                                                                                                                                                                                                    NCBI_TaxID=5804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Elmeria tenella
                                                                                                                                                                                  Eimeria maxima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   043981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eimeria
                                                                                                                                                                                                                                              Eimeria
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043981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDLGAIVYCVGVKDFNETQLARIA---DSKDHVFPVNDGFQALQGIIHSILKKSCIEILA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GGRREDGG-----PACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-HEMOCYTE;

PEDLINE-21103189;

Miyazawa S., Azumi K., Nonaka M.;

"Cloning and characterization of integrin alpha subunits from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRI---QLQGYTTYTGRALQKVIRDFDDAYIGNKQVLLLLTDGQAKDNKLILP--NANRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN 31 1332 INTEGRIN ALPHA HRI.
SEQUENCE 1332 AA; 145852 MW; 0D9108D2B05CFFAE CRC64;
                                                                                                     323 LRSIQRQLQEK----IFAIEGTQSRSSSSFQHEMSQEGFSSALTSD 364
                                                         182 LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Halocynthia roretzi (Sea squirt).
Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTEGRIN ALPHA HRI PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.0%; Score 153.5; DB 5; 24.1%; Pred. No. 0.00015; ative 42; Mismatches 81;
                                                                                                                                                                                                                                                                        PRT; 1332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              solitary ascidian, Halocynthia roretzi.";
J. Immunol. 166:1710-1715(2001).
EMBL; ABO48261; BAB21479.1; -.
RSSP; PI1215; 1A8X.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01839; FG-GAP; 5.
Pfam; PF0018357; integrin_A; 1.
Pfam; PF00092; vwa; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWEADOMAIN.
SMART; SM00191; INT_Alpha; 5.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGKSAKTAG--YEMHFGENGF 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEPSTICAGESFQVVVRGNGF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 24.1*
"The 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50234; VWFA; 1
                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30
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Length 724; Indels

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Neospora caninum.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida; Sarcocystidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 GNGFRHARNVDRV--LCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMK--AALQVS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 -----VIIALTDGELHEDLFFYSEREANRSRDLGAI------VYCVGV------KD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372 KEIRHTIILLIDGK--SNMGDSPKKAVTRIRELLSIEQNRDDYLDIYAIGVGKLDVDWKE 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :| | :: :| | :: | | :: | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 | 371 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 GHLNLYYLLDASQSVTEKDFIFKKSAELMVERIFSFEVNVSVALITFASQPKTIMSILS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 DREQIRGGLEELQKVLPGGDTYMHEGFERASEQIYYE------NRQGYRTAS- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 GGFDLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLRMS--FIVFSTRGTTLMKLTE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.7%; Score 134; DB 11; Length 7 Best Local Similarity 23.5%; Pred. No. 0.0035; Matches 75; Conservative 55; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00327; VWA; 1.
PROSITE; PS50240; TRYPSIN_DOM; 2.
PROSITE; PS50240; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
PROSITE; PS50234; VWEA; 2.
Hydrolase; Serine Protease.
Hydrolase; Serine Protease.
T60 AA; 84741 MW; 91C896A3EDC7D448 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 19, Last annotation update)
THROMBOSPONDIN-RELATED ADHESIVE PROTEIN HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          765 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00092; vwa; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00032; CCP; 2.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | | |: |||
531 VGDPTSQHGKEFLVEDVII 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 MND-----GLSFISSSVII 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neospora.
NCBI_TaxID=29176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9U8J9
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             SA NAME OF STREET OF STREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rowen L., Madan A., Qin S., Hall J., Dahl T., James R., Dickhoff R., Schaffer T., Ratcliffe A., Abbasi N., Loretz C., Lasky S., Hood L.; "Sequence of the mouse MHC class III region."; submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 TEDREQIRQGLEELQKVLPG------GDTYMHEGFERASEQIYYENRQGYR-- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 CYGGFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISPQ-LRMSFIVFSTRGTTLMKL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 CTSLLDVMLVVDESGSIGTSNFRKVR@FIEDFVNSMPISPEDVRVGLITFAT----- 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Musinae; Mus
MCBI_TaxID=10090;
                                                                                                          A Relleher W., Tomley F.W.;

A Relleher W., Tomley F.W.;

Transient expression of beta-galactosidase in differentiating sporozoites of Eimeria tendella.";

Mol. Biochem. Parasitol. 97:21-31(1998).

R EMBL; AF032905; AAD03300.1; -. 37:21-31(1998).

R InterPro; IPR00084; TSP1.

R InterPro; IPR00084; TSP1.

R Pfam; PF00090; tsp_1; 6.

R Pfam; PF00092; vwar 1.

R PRINTS; PR00453; VWFADOMAIN.

R SWART; SM00309; TSP1; 6.

R PROSITE; PS50034; VWFA: 1.

R PROSITE; PS50034; VWFA: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 712;
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01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-AUG-1901 (TrEMBLrel. 19, Last annotation update)
COMPLEMENT FACTOR C2 (COMPLEMENT COMPONENT 2) (WITHIN H-2S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rowen L., Qin S., Lasky S.R., Loretz C., Dors M., Mahairas Hood L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
MICRONEME PROTEIN ETMIC-1.
15B8F3C190B70F73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 P-----VNDGFQALQGIIHSILKKSCIEILAAEPSTI--CAGE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 PRYLQSNWSNYIQQVNGIIKAACKDLAKDAVCSEWSEYGPCVGE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.8%; Score 134.5; DB 5; 24.6%; Pred. No. 0.0029; tive 40; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 291-760 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN 37 712 M. SEQUENCE 712 AA; 74777 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.0%,
Best Local Similarity 24.6%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                  SEQUENCE FROM N.A.
                                                                                                       MEDLINE=99094493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         070350;
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16;

Gaps

74;

Length 760;

14;

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128 HEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 ILITDGK-SSDAF---RDPAIKLRNSDVEIFAVGVKDAVDSELEAIASPPAETHVFTVED 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 ITLMKLTEDREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYRT--ASVI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 DREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYRT--ASVIIALTDGEL 127
                                                                                                                                  120 IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVND 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFST---RGTTLMKLTE 71
                                                                                                                13 CYGGFDL---YFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFST---RG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                    29;
                                                       DB 4; Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 660;
                                                       Query Match 8.6%; Score 131.5; DB 4; Length Best Local Similarity 29.6%; Pred. No. 0.0035; Matches 61; Conservative 39; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72523 MW; 3E3A10A285ECAA51 CRC64;
               56727 MW; 9B6972F44A1BD88F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ234P15.1 (COLLAGEN, TYPE XII, ALPHA 1) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.5%; Score 131; DB 4;
29.8%; Pred. No. 0.0054;
tive 38; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                            660 AA
                                                                                                                                                                                                                                                                                          178 GFQALQGIIHSILKKSCIEI---LAA 200
                                                                                                                                                                                                                                                                                                                    303 -FDAFQRISFELTQSICLRIEQELAA 327
                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50234; VWFA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
517 5
517 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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SECUENCE
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 NON_TER
SEQUENCE
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б
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                                                                                                                                                                                                                                                                                                                                                                                                                                   128 HWSLRANNASDKETAMQ - - DVLTIPYHGGTTNTAAGLQTCNQMLFDYPREERQTVPKLVI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDF-NETQLARIADSKDHVFP----V 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wessel H., Anderson S., Fite D., Halvas E., Hempel J., SundarRaj N.,
"Type XII collagen contributes to diversities in human corneal and
limbal extracellular matrices.";
Invest. Ophthalmol. Vis. Sci. 38:2408-2422(1997).
EMBL. 108139; AACO1506.1;
InterPro; IPR003961; FN_III.
InterPro; IPR003961; FN_III.
InterPro; IPR00241; fin3: 3.
Pfam; PF00041; fin3: 3.
Pfam; PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                               13 CYGGFDLYFILDKSGSVLH-HWNEIYYFVEQLAHKFIS-----PQLRMSFIVFSTRGTT 65
          Lovett J.L., Howe D.K., Sibley L.D.;
Lovett J.L., Howe D.K., Sibley L.D.;
"Molecular characterization of a thrombospondin-related anonymous protein homologue in Neospora caninum.";
MOI. Biochem. Parasitol. 107:33-43(2000).
EMBL; AFO61273; AAF01565.1; -.
InterPro; IPR001969; Asp_protease.
InterPro; IPR000884; TSP1.
InterPro; IPR002035; vWFA.
Pfam; PF00090; tsp_l; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TYPE XII COLLAGEN (FRGMENT).
TYPE XII COLLAGEN (FRGMENT).
FUND sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                       Length 765;
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                               765 AA; 82880 MW; 9727838CC1FE8CD4 CRC64;
                                                                                                                                                                                                                                                                                       8.6%; Score 132.5; DB 5;
25.1%; Pred. No. 0.0048; 3tive 35; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            517 AA
                                                                                                                                                   PRINTS: PRO0453: VWFADOMAIN.
SMART: SM00209; TSP1: 6.
SMART: SM00327; VWA: 1.
PROSITE: PS00141; ASP_PROTEASE; UNKNOWN_1.
PROSITE: PS50092; TSP1: 6.
PROSITE: PS50234; VWFR: 1.
SEQUENCE 765 AA; 82880 WW; 9727838CC1F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
 MEDLINE=20183852; PubMed=10717300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-CORNEA;
MEDLINE-98003048; Pubmed-9344363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 NDGFQALQGIIHSILKKSC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 QTEWSQLLPSISPILKEVC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0453; VAFADOMAIN.
SMART; SM00060; FN3; 3.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                   Best Local Similarity 25.18
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                         Query Match
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TRANSMEMBRANE CELL ADHESION RECEPTOR MUA-3 PRECURSOR (K08E5.3 PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUA-3 OR KOBE5.3.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
TISSUE-MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
                                                                                                                                                                  8.3%; Score 128; DB 11; Length 221;
44.2%; Pred. No. 0.0022;
7ative 12; Mismatches 17; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                      243 EKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCSDG
                                                                                                                                                                                                                                                             SIRAIN-NZ, Landercock E.; Lud Z., Vogel B., Hedgecock E.; "Mud Z., Vogel B., Hedgecock E.; "MRS Splicing Pattern Revealed."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nersum u.n.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases
                                                  the EMBL/GenBank/DDBJ databases
                                            Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC003908; AAH03908.1; -.
Hypothetical protein.
NON TER
SEQUENCE 221 AA; 24505 MW; 31AB702E42E9CEB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                              PRT; 3767 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR000152; Asx_hydroxyl.
Interpro; IPR00152; Disintegrin.
Interpro; IPR001561; EGF-like.
Interpro; IPR001881; EGF_Ca.
Interpro; IPR002192; LDL_recept_A.
Interpro; IPR002082; SEA.
Interpro; IPR002082; SEA.
Interpro; IPR000082; SEA.
Interpro; IPR000082; SEA.
Interpro; IPR000082; SEA.
Interpro; IPR000082; SEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    investigating biology.";
Science 282:2012-2018(1998).
EMBL; AF139060; AAD29428-1;
EMBL; 230974; CAA83226-2; JOINED.
HSSP; P01130; LLDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF_CA; 1.
EGF_like; 45.
LDLa; 4.
SEA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00289; DISINTEGRIN. PRINTS; PR00261; LDLRECEPTOR. PRINTS; PR00453; VWFADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00057; Idl_recept_a; Pfam; PF01390; SEA; 2. Pfam; PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00181; EGF; 51.
SMART; SM00179; EGF_CA; 1
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                         Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SM00001;
SM00192;
SM00200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239
                                                                                                                                                                                                                                                                                                                                                                                  Q9UA13; Q21340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FRAGMENT)
                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                   09UA13
                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                         Q9UA13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 -TASVIIALTDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FN----ETQLARIA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYR- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 THETENDEKRNPSPKLLVRPIRQLL------GRTHTATGIRKVVRELFH-SK$GARE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISP---QLRMSFIVFSTRGTTLMKLTED-- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 DSK--DHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 SKPCGDHVFQVNN-FEAVKTIQNQLQEKT----FAIEGTQTGSTSSFECEMSQEGFSAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                          Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.5%; Score 130.5; DB 6; Length 920; 26.4%; Pred. No. 0.0093; Live 41; Mismatches 72; Indels 63
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Lee J.-K., Schook L.B., Rutherford M.S.;

Lee J.-K., Schook L.B., Rutherford M.S.;

Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.

REMBL: 040072; AAB16869.1;

RIGEPTO: 1PR000413; Integrin_alpha.

RIGEPTO: 1PR000413; Integrin_alpha.

R Pfam; PF001839; FGG-GAP; 4.

R Pfam; PF001839; FGG-GAP; 4.

R Pfam; PF00183; INTEGRINA.

R PRINTS; PR00453; VWFADOMAIN.

R SMART; SM00191; Int_alpha; 4.

SMART; SM00197; VWA; 1.

R PROSITE: PS50234; VWFA; 1.

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102440 MW; E96CC51E350DD5AC CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                 Sus scrofa (Pig).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                           920 AA
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01-JUN-2001 (TrEMBLrel. 17, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotation
HYPOTHETICAL 24.5 KDA. PROTEIN (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                             Created)
                                                                                                                                             PRT;
                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, 01-FEB-1997 (TrEMBLrel. 02, 01-DEC-2001 (TrEMBLrel. 19, CD11B (FRAGMENT).
                          186 IHSILKKSCIEI---LAA 200
                                                         638 SFELTQSICLRIEQELAA 655
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Best Local Similarity 26.4%
Matches 63; Conservative
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                                                                                                                                               PRELIMINARY;
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TRANSMEMBRANE CELL ADHESION RECEPTOR MUA-
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCT-2001 (TrEMBLrel. 19, Last annotation update)
101-DEC-2001 (TrEMBLrel. 19, Last annotation update)
101FECRIN BETA 2 ALPHA SUBUNIT.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
MARIMALIA; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
MCBI_TaxID=10116;
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PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS50068; LDLRA_2; 2.
PROSITE; PS50034; LDLRA_2; 2.
PROSITE; PS50234; VWFA; PS50234; VWFA; PS50234; VWFA; PS50234; VWFA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.3%; Score 128; DB 5; Length 3767; Best Local Similarity 27.1%; Pred. No. 0.11; Matches 64; Conservative 31; Mismatches 75; Indels 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fathallah D.M. Sr., Zerria K. Jr., Fathallah D.M. Sr., Zerria K. Jr., Cloning of the rat CD11b cDNA sequence."; Cloning of the rat CD11b cDNA sequence."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF266393; AAF81280.1; Interpro; IRR000413; Integrin_alpha. Interpro; IRR0020413; Integrin_alpha. Interpro; IRR002035; vWFA. Ffam: PF001839; FG-GAP; 5.
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3767 AA; 417284 MW; 8DA3AE5EA50AEB8E CRC64;
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PROSITE; PS50234; VWFA; 1.
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PRINTS; PR00453; VWFADOMAIN.
SWART; SM00191; Int_alpha; 5.
SWART; SM00327; VWA; 1.
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SM00327; VWA; 1.
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Length 1151;

Score 123; DB 11; Pred. No. 0.058;

8.0%;

Query Match Best Local Similarity

Search completed: August 9, 2002, 10:46:21 Job time: 844 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Desnick, Robert J.
APPLICANT: Bishop, David F.
APPLICANT: Ioannou, Yiannis A.
APPLICANT: Wang, Anne M.
TITLE OF INVENTION: CLONING AND EXPRESSION OF BIOLOGICALLY
TITLE OF INVENTION: ACTIVE ALPHA-N-ACETYLGALACTOSAMINIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
ELLCATION NUMBER: US/07/602,608 FILING DATE: 24-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6%; Score 51.6; DB 1;
                                       US-08-665-966-9
US-09-041-780-9
US-09-182-816-22
US-09-182-816-22
US-09-471-528-22
US-09-471-528-22
US-09-471-528-22
US-09-634-530-22
US-08-514-014-7
US-08-933-823-7
US-08-897-340-1
US-08-993-228-3
US-08-993-228-3
US-08-993-228-3
US-08-993-228-3
US-08-993-228-3
US-08-993-228-3
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1155 Avenue of the Americas
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: COLUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 693-(
TELECHONE: (212) 790-9090
TELEPAN: (212) 869-8864/9741
TELERX: 66141 PENNE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2158 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: Gouble
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Patent No. 5382524
                       11454
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CORRESPONDENCE ADDRESS:
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STATE: New York
COUNTRY: U.S.A.
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STREET: 11
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US-07-602-608-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
US-07-602-608-1
Query Match
(without alignments)
3166.719 Million cell updates/sec
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Sequence 6, Appli
Sequence 595, Appli
Sequence 1, Appli
Sequence 15, Appli
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Sequence 17, Appli
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Sequence 37, Appl
Patent No. 5196333
Sequence 10, Appl
Sequence 16, Appl
Sequence 10, Appl
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                                                                                                                                                                                                                                                                                                                           Sequence 49,
Sequence 49,
                                                                                                                                                                         ; Search time 109.68 Seconds
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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                                                  Compugen Ltd.
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US-08-342-411A-1

US-09-248-335-25

US-08-232-463-14

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US-08-621-493-3

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US-08-965-173-3

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US-08-461-697-75

US-08-484-105-17

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US-08-248-335-35

US-08-484-105-17

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US-09-195-666A-16
US-09-309-592-10
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                       GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match I
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51.6
50.8
50.8
49.8
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Maximum DB s
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                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
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                                                                                                                                                                         Run on:
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RESULT 3
US-08-631-097-8
US-08-631-097-8
Sequence 8, Application US/08631097
TITLE OF INVENTION: Tumor Suppressor Genes,
TITLE OF INVENTION: Proten Encloded Thereby, and Use of Said Genes and Protein NUMBER OF SEQUENCES:
SUPPRESSOR ADDRESS:
CORRESPONDENCE ADDRESS:
SUPPRESSOR OF SEQUENCES OF SEQUENCES OF SECUENCES O
2025 CACIGGGAGTGAGGGTCACAAAGGAGACCTIGGCTCCCTCAGGTCACAAAAACCTGIT 2084
                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myers, P.C.
1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Wigman, Cohen, Leitner, & SIREET: 900 17th Street, N.W., Suite CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/631,097
FILING DATE: 12-Apr-96
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11598
FILING DATE: 12-Oct-94
FILING DATE: 12-Oct-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Cohen, Herbert
REGISTRATION NUMBER: 25,109
REFERNEC/EDCKET NUMBER: 0744.057
TELEPHONE: (202)463-7700
TELEPHONE: (202)463-7700
TELEFAX: (202)473-6915
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 3829 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANELLE: not applicable
IMMEDIATE SOURCE:
ILIBRARY: not applicable
CLONE: not applicable
CLONE: not applicable
CLONE: not applicable
CHROMOSOME/SEGMENT: not applicable
MAP POSITION: not applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN: not applicable INDIVIDUAL ISOLATE: not applicable DEVELOPMENTAL STAGE: not applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not applicable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Genomic DNA HYPOTHETICAL: NO
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STRANDEDNESS: double
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FRAGMENT TYPE: D
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                2025 CACTIGGGAGTIGAGGGTCACAAAGGAGCCTTGGCTCCCTCAGGTCACCAATAAACCTGTT 2084
                                                                                                                                                                                                                                                                 Score 51.6; DB 1; Length 2158;
Pred. No. 0.00038; J. Mismatches 49; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Desnick, Robert J.
APPLICANT: Dashok, David F.
APPLICANT: Tashok, David F.
APPLICANT: Tashok, Manis A.
APPLICANT: Wang, Anne M.
TITLE OF INVENTION: CLONING AND EXPRESSION OF BIOLOGICALLY
TITLE OF INVENTION: ACTIVE ALPHA-N-ACETYLGALACTOSAMINIDASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New YORK
COUNTRY: New YORK
COUNTRY: U.S.A.

ZIP: 10036
COMPUTER: Eloppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
CONFERNT APPLICATION NUMBER: US/08/261,578
FILING DATE: 17-JUN-1994
CLEASIFICATION NUMBER: US/07/602,608
FILING DATE: 34-0CT-1990
ATPLICATION NUMBER: US/07/602,608
FILING DATE: 24-0CT-1990
ATPLICATION NUMBER: US/07/602,608
FILING DATE: 24-0CT-1990
ATPLICATION NUMBER: US/07/602,608
FILING DATE: 34-0CT-1990
ATPLICATION NUMBER: US/07/602,608
FILING DATE: US/07/602,008
FILING DATE: US/07/602,009
TELEFRAX: (212) 869-8864/9741
TELEFRAX: (212) 869-8864/9741
TELEFRAX: (212) 869-8864/9741
TELEFRAX: GALA PERNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2138 Dasse PAIRS
TENDAMENDNESS: double
                                      Best Local Similarity 62.3%; Pred. No. 0.00038;
Matches 81; Conservative 0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08261578 Patent No. 5491075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.6%;
Best Local Similarity 62.3%;
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
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; LOCATION:
US-08-261-578-1
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US-08-261-578-1
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RESULT 6
US-08-342-411A-1
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NAME/KEY: in claim 1(vi) starting at triplet in position 201-203
NAME/KEY: and ending at the triplet 3018-3020
LOCATION: not available seperiment.
IDENTIFICATION METHOD: experiment.
IDENTIFICATION METHOD: in specification
OTHER INFORMATION: prevention of IFN- induced
OTHER INFORMATION: programmed cell death
US-08-631-097-8
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                                                                                                                                                                                                                                                     3.6%; Score 50.8; DB 2; Length 3829; 74.4%; Pred. No. 0.00083; tive 0; Mismatches 22; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08810712G

Patent No. 6160106

GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co. LTD

TITLE OF INVENTION: Tumor Suppressor Genes, Proteins
FILE REFERENCE: sequencelist
CURRENT APPLICATION NUMBER: US/08/810,712G

CURRENT FILING DATE: 1997-03-03

EARLIER APPLICATION NUMBER: PCT/US94/11598

EARLIER PRING DATE: 1994-10-12

NUMBER OF EQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 50.8; DB 4;
Pred. No. 0.00083;
0; Mismatches 22
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US-08-998-416-595/c
Sequence 595, Application US/08998416
; Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pollmann, Rainer
APPLICANT: Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
3.6%;
Best Local Similarity 74.4%;
Matches 64; Conservative C
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Matches 64; Conservative
not applicable
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; LOCATION: (201)..(3020)
US-08-810-712-6
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ORGANISM: Homo sapiens
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UNITS:
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APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Rebisching, Contine
APPLICANT: Rebisching, Contine
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49.8; DB 4; Length 6 Pred. No. 0.00063; 0; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/998,416

FILING DATE: 24-DEC-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: CH 0016/97

FILING DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Me19s, J. TIMOCHY

REGISTRATION NUMBER: PF/5-30306/A/CGC1976

TELECOMMUNICATION INFORMATION:

TELEPAATION NUMBER: PF/5-30306/A/CGC1976

TELECOMMUNICATION INFORMATION:

TELEPAATION SEQUENCE: 319-541-8689

INPORMATION FOR SEQ ID NO: 595:

SEQUENCE CHARACTERISTICS:

LENGTH: 658 base pairs

TTYPE: NUCLEI Cacid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwalls Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/08342411A; Patent No. 5639616; GENERL INFORMATION:
APPLICANT: LIAO, Shutsung
APPLICANT: SONG, Ching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
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Best Local Similarity 51.6%;
Matches 114; Conservative
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; ORGANISM: PAG1408RP
US-08-998-416-595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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1011 CCATACGCTCACAGATTAATTCCGAGCTTGGCTGCAGGTCGAGGGAGCTTGCGATXXYY 1070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            852 gcaacgtggacagggtectctgcagcttcaagatcaatgactcggtcacactcaatgaga 911
                                                                                  1336 attomamtoccmatgtottamcattcmatamatagotatatgmamatcmamamamamama 1395
                                                                                                       3.3%; Score 47; DB 1; Length 7218; 6.7%; Pred. No. 0.012; ive 199; Mismatches 164; Indels
Length 1279;
Score 47; DB 3; Length 127
Pred. No. 0.0049;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALINER, F. G. TITLE OF INVENTION: RECOMBINANT FOULPOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDENCE S. DORRESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
NAME: ABOUT NUMBER: 29,768
RECISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.78; F. 199;
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TELEPHONE: (703)836-9300
                                                                                                                                                                                1396 aaaaaaaaaaaaaaaaaa 1414
                                                                                                                                                                                                         (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 899149
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
           Query Match 3.34
Best Local Similarity 74.74
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
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US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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US-08-232-463-14
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US-09-248-335-25

is sequence 25, Application US/09248335

sequence 25, Application US/09248335

patent No. 6096504

GENERAL INFORMATION:

APPLICANT: O'KEEF, DANIEL

ITLE OF INVENITON: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES

TITLE OF INVENITON: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES

FILE REFERENCE: CL-1128-A

CURRENT PILING DATE: 1999-02-10

SEALIER APPLICATION NUMBER: 08/924 759

BARLIER APPLICATION NUMBER: 1997-September-05

NUMBER OF SEQ ID NOS: 74

SEQ ID NO 25

LENGRIH: 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.4%; Score 48.4; DB 1; Length 1898; Best Local Similarity 68.4%; Pred. No. 0.0025; Matches 67; Conservative 0; Mismatches 31; Indels 0
                                                                                                                                                                                                                                                              MEDIUM TYPE: FLOPPY GISA

COMPUTER: IBM PC COMPAILABLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,411A

FILING DATE: 18 NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: KITCHELL, BARBARA S.
REFERENCE/TOCKET NUMBER: ARCD154

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1898 bases palits
TITLE OF INVENTION: UBIGUITOUS NUCLEAR RECEPTOR:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOREY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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CRGANISM: maize
US-09-248-335-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , NAME/KEY:
; LOCATION:
US-08-342-411A-1
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972 gcatgaaagctgcactccaggtcagcatgaacgatggcctctcttttatctccagttctg 1031
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                                                                                             912 agocottttotgtggaagacacttatttactgtgtccagcgcctatcttaaaagaagttg 971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREES Howson and Howson STREET: Spring House Corporate Center, PO Box 457 CITY: Spring House STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 3, Application US/08265087; Patent No. 5571515; GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: SCOTE, Phillip APPLICANT: Trinchieri, Giorgio TITLE OF INVENTION: Compositions and Method; TITLE OF INVENTION: IL-12 as an Adjuvant NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1152 ttatcaaggaggtccctccacccctgcc 1180
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST51AUSA
TELECHONE: 215-540-9206
TELECHONE: 215-540-9206
TELECHONE: 215-540-9206
TELETRAX: 215-540-9206
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 424
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; LOCATION:
US-08-265-087-3
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US-08-265-087-3
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Score 46.8; DB 1; Length 1364; Pred. No. 0.0057; 0; Mismatches 22; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Scott, Phillip
APPLICANT: Trinchieri, Giorgio
ITILE OF INVENTION: Compositions and Methods for Use of
TITLE OF INVENTION: IL-12 as an Adjuvant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,493
FILING DATE: 25-MR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/265,087
FILING DATE: 17-JUN-1994
ATPONEY/AGENT INPORMATION:
ATTORNEY/AGENT INPORMATION:
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0.0057;
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Patent No. 5723127
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INFORMATION FOR SEQ ID NO: 3:
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LENGTH: 1364 base pairs
                                                                                    60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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101..859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
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Best Local Similarity
Matches 60; Conserva
    Query Match
Best Local Similarity
Matches 60; Conserv
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; LOCATION:
US-08-621-493-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-621-493-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1364;
                                                              TITLE OF INVENTION: Compositions and Methods for Use of
                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46.8; DB 4; Length 1 Pred. No. 0.0057; 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                       COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/260,173
FILING DATE: 01-Mar-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: CURROWN
FILING DATE: CURROWN
APPLICATION NUMBER: 08/265,087
FILING DATE: 17-JUN-1994
APPLICATION NUMBER: 08 08/229,282
FILING DATE: 18-APR-1994
ATORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: WST51AUSA
REFRENCE/DOCKET NUMBER: WST51AUSA
TELEPHONE: 215-540-9206
TELEPHONE: 215-540-9218
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                        IL-12 as an Adjuvant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 101..859
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/965,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUN-1994
18-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application PC/TUS9412883
GENERAL INFORMATION:
APPLICANT:
                                APPLICANT: Scott, Phillip
Trinchieri, Giorgio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1393 aaaaaaaaaaaaaaaaaaaa 1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1364 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 3.3%;
Best Local Similarity 73.2%;
Matches 60; Conservative
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 19477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
PCT-US94-12883-3
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Patent
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Pred. No. 0.0057;
0; Mismatches 22; Indels
                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
GAPPILCANT: Scott, Phillip
APPLICANT: Trinchieri, diorgio
TITLE OF INVENTION: Compositions and Methods for Use of
TITLE OF INVENTION: IL-12 as an Adjuvant
                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,493
FILING DATE: 25-WAR-1996
APPLICATION NUMBER: 08/265,087
FILING DATE: 17-UN-1994
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REGISTRATION NUMBER: 31,215
REJERHONE: 215-540-9206
TELEFAX: 215-540-9206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WST51AUSA
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEM PC compatible
COMPUTER: PEM PC COMPATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                              Sequence 3, Application US/08965688 Patent No. 5976539
            3.3%;
illarity 73.2%;
Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                 CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
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, LOCATION:
US-08-965-688-3
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US-08-965-688-3
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DESCRIPTION: Tobacco CCaMK cDNA and deduced amino-acid
DESCRIPTION: sequence
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bachettira W. Poovalah, Zhihua Liu,
APPLICANT: Shameekumar Patil, Daisuke Takezawa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein-coding sequence (not including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Klarquist Sparkman Campbell Leigh
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Dow, Alan E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-45000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (563) 228-7391
TELEFAX: (563) 228-9446
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                              2505 aaaaaaaaaaaaaaaaaaaaaaaa 2530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/655,352 FILING DATE:
                                                                                                                                         United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,449
FILLING DATE: October 14, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                           US-08-655-352-10
; Sequence 10, Application US/08655352
Patent No. 6077991
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
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LENGTH: 1776 base pairs
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CORRESPONDENCE ADDRESS:
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; LOCATION:
US-08-655-352-10
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** APPLICANT: BAXTER, ROBERT C.; WOOD, WILLIAM I.

** TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION

** OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN BP53

** NUMBER OF SEQUENCES: 58

** CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46.8; DB 6; Length 2:
Pred. No. 0.0077;
0; Mismatches 62; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version SOFTWARE: #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/12883 FILING DATE: Concurrently Herewith
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                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BARBARA S. KITCHELL
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD154P--
TELECOMMUNICATION INFORMATION:
TELECHONE: (512) 418-3000
TELEPHONE: (713) 789-2679
                                                                                                                                                                                                                                                                                                                      FILING DATE: CONCULTENTLY HEREWITH CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152,003
FILING DATE: 10-NOV-1993
CLASSIFICATION:
                                      E: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/171,623
FILING DATE: 22-MAR-1988
                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELER: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: DNA (genomic)
PCT-US94-12883-3
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OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                CORRESPONDENCE ADDRESS:
                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity
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                                                                                                             COUNTRY: Ur
                                        ADDRESSEE:
                                                                                                 STATE:
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Search completed: August 9, 2002, 00:23:01 Job time: 7954 sec

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DT (9H6X2; Q9NVP3; DT (1-MAR-2002 (Re DT 01-MAR-2002 (Re DT 01-MAR-2004 (RE DT 01-MAR-200
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                                                                                             9, 2002, 10:47:01; Search time 31.3 Seconds (without alignments) 697.694 Million cell updates/sec
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P10323
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               Compugen Ltd
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GenCore version Copyright (c) 1993 - 2000
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WASP_MOUSE
EBN2_EBV
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FMN1_MOUSE
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PC15_HUMAN
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Maximum Match 100%
Listing first 45 summaries
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CSP_PLABE
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CMG2_HUMAN
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1 MATAERRALGIGFOWLSLAT.
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Maximum DB seq length: 200000000
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homo sapien
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herpes simp
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Q13164
P10210
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008808
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043516
013349
P40603
P28955
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                                                       MK07_HUMAN
VP40_HSV11
FYB_MOUSE
DIAL_MOUSE
ZAP3_MOUSE
WAIP_HUMAN
ITAD_HUMAN
APG_BRANA
TEGU_HSVEB
                                     PRP2_MOUSE
EXTN_MAIZE
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EDDD -> NKIK (IN ISOFORM 2).
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                                                                                                                       Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing SIGNAL 1 32 POTENTIAL.
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EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                             MISSING (IN ISOFORM 4).
B118A00AD5DF2233 CRC64;
                                                                                                                                                                             CYTOPLASMIC (POTENTIAL). VWFA.
                                                                                                                                                                                                                                                                                                MISSING (IN ISOFORM 3)
                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 3025; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.6e-176;
Matches 564; Conservative 0; Mismatches 0;
     modified and this statement is not removed.
              entities requires a license agreement (Sk
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                     ISOFORM 4
                                                                                                                                                                        POTENTIAL
                                            EMBL; AF279145; AAK52094.1; -.
EMBL; AK025429; BAB15128.1; ALT_INIT.
EMBL; AK001463; BAA91707.1; ALT_FRAME.
EMBL; BC012074; AAH12074.1; -.
                                                                                                                                                                                                                                                                                                                                         62789 MW;
                                                                                                InterPro; IPR002035; vWFA.
SMART; SM00327; vWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                          564 AA;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RA Kawai J., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Ahinadawa A., Shibata K., Yoshino H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Ouackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Ouackenbush J.,
RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Mashima J., Mazazarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Mang K.H., Weitz C., Whittaker C., Wilming L.,
RA Havashizaki Y., Hoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havashizaki Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=21443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Antrax toxin receptor precursor (Tumor endothelial marker 8).
ATR OR TEM8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE ATR FAMILY. SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                               562 AA.
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EMBL; AK013005; BAB28591.1; ALT_INIT.
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MEDLINE-21085660; PubMed=11217851;
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                                                                                        541 PPPPQAPPPNRAPPPSRPPRPSV
                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
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                                                                                            SEQUENCE FROM N.A.

MEDLIN=21539596; PubMed=11683410;

MEDLIN=21539596; PubMed=11683410;

MEDLIN=21539596; PubMed=11683410;

MEDLIN=21539596; PubMed=11683410;

MAXWell S.A., Davis G.E.;

"Differential gene expression during capillary morphogenesis in 3D collagen matrices: regulated expression of genes involved in basement membrane matrix assembly, cell cycle progression, cellular differentiation and G-protein signaling.",

J. Cell Sci. 114:2755-2773(2001).

SUBUNIT: Seems to bind to collagen type IV and laminin.

SUBCELLULAR LOCATION: Type I membrane protein (Probable).

SUMILARITY: BELONGS TO THE ATR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 AERRALGIGFQWLSLATLVLICAGQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEI 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSFISSSVIITTHCSDGSILAIALLILFLLLALALLWWFWPLCCTVIIKEVPPPAEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAPILLARY MORPHOGENESIS PROTEIN-2 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.0%; Score 1060; DB 1; Length 386; 45.3%; Pred. No. 1.5e-57; 1ve 58; Mismatches 84; Indels 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (P
0F9B2D6688EAB17A CRC64;
                                           Craniata; Vertebrata; E
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. CYTOPLASMIC (POTENTIAL).
    01-MAR-2002 (Rel. 41, Last annotation update)
Capillary morphogenesis protein-2 precursor (CMG-2).
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                           Signal
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY040326; AAK77222.1; -. PROSITE; PS50234; VWFA; 1.
                                          Chordata; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ψ.
                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 45.3
Matches 219; Conservative
                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44
211
386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     34
34
216
237
                                                                       NCBI_TaxID=9606;
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TRANSMEM
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GRCINFTRVKNSQPAKYPLNNTYHPSSPPAAPIYTPPPPAAP
                                                                                                                                                                                                                     HCPPPAPSAPTPPIPSPSTLPPPPQAPPPNRAPPSRPPP
RPSV -> RFGWRLTICLGSKHVHPGRHDKGPETPLLKQA
WMFSSFLERAFO (IN ISOFORM 2).
6AC92049B4BB4F7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPSAPTPPIPSIPSTLPPPPOAPP 548
                                                                                                                                                                                                                                                                                                                                                                                                               LAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERAS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQL 188
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                       LGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQ 68
                                              Signal; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                             ARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRH
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                                                                                            POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
AWFA.
ASP/GLU-RICH (HIGHLY ACIDIC).
PRO-RICH.
N-LINKED (GLCNAC. .) (POTENTI
N-LINKED (GLCNAC. .) (POTENTI
N-LINKED (GLCNAC. .) (POTENTI
                                                                                                                                                                                                                                                                                                    Length 562;
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                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                      ANTRAX TOXIN RECEPTOR
                                                                                                                                                                                                                                                                                                    Score 2901; DB 1;
Pred. No. 5.4e-169;
7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
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                                                                                                                                                                                                                                                              62308 MW;
                                                                                                                                                                                                                                                                                                    95.9%;
MGD; MGI:1919432; Atr.
InterPro; IPR002035; vWFA.
PROSITE; PS50234; vWFA: 1.
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3340
3340
2013
3562
562
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164
562
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Matches 538; Conserv
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182
260
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P58335;
                                            Receptor; SIGNAL
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TRANSMEM
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CARBOHYD
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VARSPLIC
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DOMAIN
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NONTRIPLE-HELICAL SEQUENCES.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINAL TISSUE
                                                                                                                                                                                                                                                                                                                                                           Yamagata M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka H., Nishida Y., Obara M., Kimata K.; Tranaka H., Tanaka M., Kimata K.; The complete primary structure of type XII collagen shows a chimeric molecule with reiterated fibronectin type III motifs, von Willebrand factor A motifs, a domain homologous to a noncollagenous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95370352; PubMed=7642694;
MEDLINE-95370352; PubMed=7642694;
MCOCH M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;
Koch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;
Large and small splice variants of collagen XII: differential
expression and ligand binding.";
J. Cell Biol. 130:1005-1014(1995).
-i. FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
CONTAINING FIBRILS, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE
SUBRACE OF THE FIBRILS, AND THE COLL AND NC3 DOMAINS MAY BE
LOCALIZED IN THE PERFERBILLAR MATRIX.
-i. SUBUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 KDa OF
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                              318 ETEEPIRP------RPPRPKPTHQPPQTKWYTPIKGRLDALWALLRRQYDRVSLMRPQ 369
                423 QEYEFPEPRNLINNMRRPSSPR------KWYSPIKGKLDALWVLLRKGYDRVSVMRPQ 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-1283 FROM N.A. (SHORT FORM), AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gordon M.K., Gerecke D.R., Dublet B., van der Rest M., Olsen B.R.; Type XII collagen. A large multidomain molecule with partial homology to type IX collagen."; J. Biol. Chem. 264:19772-19778(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  end.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 2456-3124 FROM N.A., AND SEQUENCE OF 2772-2794 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 2960-3076 FROM N.A.
MEDLINE-87317590; PubMed=3476925;
Gordon M.K., Gerecke D.R., Olsen B.R.;
"Type XII collagen: distinct extracellular matrix component discovered by cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The two splice variants of collagen XII share a common Blochim. Blophys. Acta 1171:97-98(1992).
                                                                                                                                                                 CAIC_CHICK STANDARD; PRT; 3124 AA. P13944; Q04509; 01-JAN-1990 (Rel. 13, Created) 01-NOV-1997 (Rel. 15, Last sequence update) 01-NAR-2002 (Rel. 41, Last annotation update) collagen alpha 1(XII) chain precursor (Fibrochimerin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 84:6040-6044(1987).
                                                                                                                                                               3124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93042014; PubMed=1420368;
Trueb J., Trueb B.;
                                                                                                                                                                                                                                                                                                                                                STRAIN-WHITE LEGHORN;
MEDLINE-92011862; PubMed=1918137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90062079; PubMed=2584192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell Biol. 115:209-221(1991).
                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
                                                                                                  370 EGD 372
                                                                          475 PGD 477
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                    1- TISSUES SPECIFICITY: TYPE XII COLLAGEN IS PRESENT IN TENDONS,
1IGAMENTS, PERICHONDRIUM, AND PERIOSTEUM, ALL DENSE CONNECTIVE
1IGAMENTS, PERICHONDRIUM, AND PERIOSTEUM, ALL DENSE CONNECTIVE
1ISSUES CONTAINING TYPE I COLLAGEN.
1 SEQUENCE DEFINES FIVE DISTINCT DOMAINS, TWO TRIPLE-
1 DOMAINS (NCL, NC2, AND NC3).
1 PTW. THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT
1 EACH END.
1 PTW. THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT
1 GACH END.
2 INTERPREPARED, CHONDROITIN-SULFATED (BY SIMILARITY).
3 SINILARITY: EBLONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
3 SIMILARITY: CONTAINS 4 WWFA DOMAINS.
3 SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
3 SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
FORM OF COLLAGEN XII MAY CONTAIN HOMOTRIMERS OF EITHER THE LONGER OR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTEOGLYCAN. THE LARGE ISOFORM HAS MORE RESTRICTED EXPRESSION IN EMBRYONIC TISSUE THAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   natrix; Connective tissue; Repeat; Hydroxylation; Collagen; Signal; Glycoprotein; Alternative splicing. 24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLLAGEN ALPHA 1(XII) CHAIN. FIBRONECTIN TYPE-III 1.
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FIBRONECTIN TYPE-III 4
FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 7
FIBRONECTIN TYPE-III 7
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FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
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EMBL; X61024; CAA43358.1; -
EMBL; M17375; AA448118.1; -
EMBL; J05137; AA48618.1; -
EMBL; X6727; CA44744.1; -
PIR; A28037; A28037.
PIR; A34485.
HSSP; P17301; 1A0X.
InterPro; IPR003067; Collagen.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FN_III.
InterPro; IPR003129; TSPN.
InterPro; IPR003129; TSPN.
InterPro; IPR003129; TSPN.
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pfam; pr00041; fn3; 17.
pfam; pr00041; fn3; 17.
pfam; pr00022; wva; 4.
prints; pr00004; pr17*pEIII.
prints; pr00004; pr17*pEIII.
prints; pr00060; FN3; 17.
SWART; SW00050; FN3; 17.
SWART; SW00210; TSPN; 1.
SWART; SW00327; VWA; 4.
pr0SITE; pS50234; VWFA; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-F. NACAREBUSIS, / HALO.

STRAIN-F. NACAREBUSIS, / HALO.

X MEDLINE-90094551; PubMed-2689458;

Betl H., Mengele R., Wenzl S., Engel J., Sumper M.;

Erl H., Mengele R., Wenzl S., Engel J., Sumper M.;

Erl H., Mengele R., Wenzl S., Engel J., Sumper M.;

the cellular compartment.";

J. Cell Biol. 109:3493-3501(1989).

L. J. Cell Biol. 109:3493-3501(1989).

- :- FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS

C. :- FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS

C. :- FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS

C. COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS

C. COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS

C. COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS

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C. CONTAINS THE THAN DEWARD THE POLYPEPTIDE CHAINS

C. CONTAINS THE PROMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF HYDROXYPROLINE RESIDUES.
2643 EVKKIFYGSFHKVHIVVTSSNVKIYIDCSEILEKPIKEAGNITTDGYEILGKLLKGDRRS 2702
                                                                                                                                                                                                                                         2821 PCLPGRSGTPGLPGPPGPVGPPGERGFTGKDGPTGPRGPPGPAGAPGVPGVAGPSGKPGK 2880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469 SVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPPSA 528
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                                                                                                                                                2703 ATLEIONFDIVCSPVWTSRDRCCDLPSMRDE--AKCPALPNACTCTQDSVGPPGPPGPPG
                                                                                                                       501 -----YHTSSPPPAPIYTPPPAPHCPPPP-------YHTSSPPPAPHCPPPP
                                                                                                                                                                                                      ------PDSRPPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
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A52216400A031421 CRC64;
                                         469 SVMRPQPGD-----TGRCINFTRVKNNQPAKYP-LNNA-
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14.2%; Pred. No. 3.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 19, Last sequence update) (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               529 PTPPIPSPPSTLPPPPQAPPNRAPPPSRPPPRPS 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sulfated surface glycoprotein 185 (SSG 185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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NCBI_TaxID=3067;
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Best Local Similarity
Matches 42; Conserv
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01-OCT-1996
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P21997;
                                                                                                                                                                                                                                                                                   562 P 562
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SEQUENCE
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SSGP_VOLCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 KLT--EDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY-YENRQGYRTASVIIALTD 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 GELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQAL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKPFSVEDTYLLCPAPILKEVGMKAALQ-VSMNDGL-----SFISSSVIITTT 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 CYGG-FDLYFILDKSGSV-LHHWNEIYYFVEQLAHKF--ISPQ-LRMSFIVFSTRGTTLM 93
                                                                                                                                                                                                WITH 2 IMPERFECTIONS.

NONHELICAL REGION (NCI).

ASC/LUS-RICH (ACIDIC).

AGC/LUS-RICH (BASIC).

TO CHONDROITIN SULFATE (POTENTIAL).

TO CHONDROITIN SULFATE (POTENTIAL).

TO CHONDROITIN SULFATE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | :: | | : | | : | | EKIQDNLVJFVCETATSTCPLIYLEGYTSP----------GFKMLESYNLT
                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC...) (POTENTIAL).
M-SING (IN SHORT ISOFORM).
T -> S (IN REF. 4).
D -> E (IN REF. 4).
P -> A (IN REF. 2).
V -> F (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2602 QITDRDYKPQVGV------VLDPGSKVLSFFNKDTRGEVQTVTFD----ND
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                                                                                                                                                            NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION (COL1)
                                                                                                                         TRIPLE-HELICAL REGION (COL2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> AG (IN REF. 3).
094285AFE7F346CF CRC64;
                                                            FIBRONECTIN TYPE-III 18.
  FIBRONECTIN TYPE-III 15.
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-III 17.
                                                                                                  NONHELICAL REGION (NC3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.6%; Score 200.5; DB 1;
Best Local Similarity 21.8%; Pred. No. 0.00022;
                                                                                                                                           WITH 1 IMPERFECTION.
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                                                                                                                                                                                                                                                                                                                                                                                   32
1006
1006
1004
11512
1210
2273
2232
2683
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11258
2759
2759
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2206
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2901
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(Rel. 29, (Rel. 29, 1) (Rel. 39, 1)
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                                                                                                                                                                                                                                                                                                                                                                 306 AA;
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                                                                                                                                                                                                                                                                                                 Hydroxylation.
SIGNAL
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01-JUN-1994
30-MAY-2000
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Q05859;
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FM14_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                502 HTSSPPPAPIYTPPPPAPHCPPPPSAPTPPIPSPPSTLPPPPQAPPPNRAPPPSRPPR 561
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
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                                                                                                                                                                                                                                                                           Owenia fusiformis.

Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata; Sabellida; Oweniidae; Owenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECTENCE FROM N.A. Chen J., Varner J.E.;
Chen J., Varner J.E.;
An extracellular matrix protein in plants: characterization of genomic clone for carrot extensin.";
EMBO J. 4:2145-2151(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=90147742; PubMed=2105723;
Bakalara N., Collet J., Planells R., Thouveny Y., Fontes M.;
Bakalara in invertebrate genomes of sequences characterized lrepetition of the triplet CCPurine.";
Biochem. Biophys. Res. Commun. 166:66-73(1990).
PIR; A34043; A34043.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 197.5; DB 1
Pred. No. 9.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                           P21260; P21261;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                 Hypothetical proline-rich protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 AA
            273 PPPPSPPRRPPSPS 307
                                                                                                                                                     141 AA
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SEQUENCE OF 264-306 FROM N.A.
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                                                                                                                                                        STANDARD;
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116
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                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6347;
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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DEVELOPMENTAL STAGE: THIS IS THE ISOFORM FOUND IN THE APICAL
ECTODERMAL RIDGE AND THE MESENCHYMAL COMPARTMENT OF THE DEVELOPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352 KEVPPP---PAEESEEEDDDGLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      409 KLEKAKNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRV 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPPAPIYTPPPPAPHCPPPPP-- 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 -KYKYKSPPPPTPVYKYKSPPP------PTPVYKYKSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 306;
                                                                                                                                                                                            EMBL; X02873; CAA26632.1; -.
EMBL; M1221; AAA33137.1; -.
PIR; A24354; A24354.
Repeat; Cell wall; Glycoprotein; Signal; Structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             527 ---SAPTPPIPSPPSTLPPPP----QAPPPNRAPPP---SRPPPR 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 XKYKSPPPPMHSPPPWX TKSPPPPMHSPPPPWK 292
                                                                                                                                                                                                                                                                                                                                               EXTENSIN.
AEC944007F0938DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     6.3%; Score 191.5; DB 1;
26.1%; Pred. No. 5.3e-05;
3ve 18: Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 КЅРРРКНЅРАРЕННҮКҮКЅРРРРКНГРАРЕННҮ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Formin 1 isoform IV (Limb deformity protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1206 AA
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MEDLINE=92112033; PubMed=1339380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                        32
306 EX
34225 MW;
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Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              locus.
  RANGE STATE 
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457 LWVLLRKGYDRVSVMRPQPGDTGR------CINFTRV---KNNQPAKYPLNNAYH 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           634 TSSSSQQKISPPAPPTPPPLPPPLIPPPPLPPCLGPLPPAPPIPPVCPVSPPPPPPPP 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 PPPPAEESEEEDDDGLP-------KKKWPTVDASYYGGRGVGGIKRMEVR 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                478 PPPKTKDTEEK--VGLKYTEAEYQAAILHLKREHKEEIETLQAQF-----ELKTFHIR 528
                -i- PTM: PHOSPHORYLATED ON SERINE AND POSSIBLY THREONINE RESIDUES.
-i- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 1 (FH1) DOMAIN.
-i- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 2 (FH2) DOMAIN.
-i- SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY FAMILY. CAPPUCCINO SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 188.5; DB 1; Length 1206;
Pred. No. 0.0004;
); Mismatches 76; Indels 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear protein; Developmental protein; Alternative splicing; Phosphorylation; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4DFB38CB52BD8EE7 CRC64;
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01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Formin 1 isoforms I/II/III (Limb deformity protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIPSPPSTLPPPPQAPPP-----NRAPPPSRPPRP 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FH1 (PRO-RICH).
FH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1468 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                                          EMBL; X62379; CAA44244.1; -.
PIR; S24407; S24407.
MGD; MGI:101815; Fmn.
InterPro; IPR003104; FH2.
InterPro; IPR001265; Formin.
Pfam; PF02181; FH2; 1.
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SMART; SM00498; FH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  644 74 759 116 1043 111 635 63 751 751 751 751
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Q05860;
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Best Local S
Matches 69
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 90:5554-5558(1993).

Proc. Natl. Acad. Sci. U.S.A. 90:5554-5558(1993).

Proc. Natl. Acad. Sci. U.S.A. 90:5554-5558(1993).

Involved in Maintaining Specific Differentiated States.

II III AND IV (AC 06859); ARE PRODUCED BY ALTERNATIVE SPLICING.

A VARIATION IN SPLICING IS SEBN AMONG DIFFERENT TISSUES AND DIFFERENT SIZE TRANSCRIPTS EXIST WITHIN ANY ONE TISSUE.

II III AND IV (AC 06859); ARE PRODUCED BY ALTERNATIVE SPLICING.

A VARIATION IN SPLICING IS SEBN AMONG DIFFERENT TISSUE.

ILMB, OWARY, BRAIN, SMALL INTESTINE, SALIVARY GLAND AND HARDERIAN GLAND. IT IS PRESENT IN THE DEVELOPING LIMB BUD, THE PROTEIN SECONDANTAINS TREEDOMINANTLY IN THE POSTERIOR REGION. DURING COMPARTMENT, PREDOMINANTLY IN THE POSTERIOR REGION. DURING THE EPITHELIAL COMPARTMENT OF THE PRONEHROS AND MESONEPHROS.

THE EPITHELIAL COMPARTMENT OF THE PRONEHROS AND MESONEPHROS.

THE EPITHELIAL COMPARTMENT OF THE PRONEHROS AND MESONEPHROS.

THE EPITHELIAL SECONDAINS I FORMIN HOMOLOGY I (FH1) DOMAIN.

IS IMILARITY: SELONGS TO THE FORMIN HOMOLOGY FAMILY. CAPPUCCINO SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93296176; PubMed-8516300; Vogt T.F., Jackson-Grusby L., Rush J., Leder P.; "Formins: phosphoprotein isoforms encoded by the mouse limb deformity
                                                                                            Woychik R.P., Maas R.L., Zeller R., Vogt T.F., Leder P.; "'Pormins': proteins deduced from the alternative transcripts of the limb deformity gene"; Ilimb deformity gene"; Nature 346:850-853(1990).
                                                                                                                                                                                                                                                                                           MEDLINE-97224459; PubMed-9119367;
Wang C.C., Chan D.C., Leder P.;
"The mouse formin (Fmn) gene: genomic structure, novel exons, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METR. S11515; S11515.
METR. S11515; S11515.
METR. S1101815; Fmn.
InterPro: IPR0031045; Formin.
Pfam: PF02181; FH2: 1.
PRINTS: PR00828; FORMIN.
SNART: SN00498; FF12: 1.
Nuclear protein; Developmental protein; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COILED COIL (POTENTIAL).
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SEQUENCE FROM N.A.
TISSUE-Kidney, and Testis;
MEDLINE-90363291; PubMed-2392150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation; Coiled coil.
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                                                                                                                                                                                                                                                                                                                                                                                                  genetic mapping.";
Genomics 39:303-311(1997).
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970
11378
11378
864
892
925
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861
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911
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                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Glycosylated polyproline II rods-with-kinks as a structural motif in plant hydroxyproline-rich glycoproteins."; Blochemistry 40:2978-2987(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91017504; PubMed=1699225;
Adair W.S., Apt K.E.;
"Cell wall regeneration in Chlamydomonas: accumulation of mRNAs encoding cell wall hydroxyproline-rich glycoproteins.";
Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-:- FUNCTION: Major component of the outer cell wall W6 (crystalline)
                                                                                                                                                                                                                                                                                                         TSS------CP--PPPAPIYTPPPPAPH--------CP--PPPPSAPTP 531
                                                                                                                                                                                             398 WGEKGSTEEGAKLEKA-KNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDA 456
                                                                                                                                                                                                                                                                ----KKKWPTVDASYYGGRGVGGIKRMEVR 397
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydomonas reinhardtii.
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                            LWVLLRKGYDRVSVMRPQPGDTGR------CINFTRV---KNNQPAKYPLNNAYH
                                                                                                                                                                S., Drees J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    GP1_CHLRE STANDARD; PRT; 555 AA.

GPFQ6; Q03927; Teated)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last senuctation update)
01-MAR-2002 (Rel. 41, Last annotation update)
vegetative cell wall protein gpl precursor (Hydroxyproline-rich)
                                                                                                                       97;
                                                                                                                                                                                                                  -GEHALVT -- ARLEEAIENLKOQLEKRREGCEEMRDVCISTDDDCSPKAFRN----
                                                                                                 DB 1; Length 1468;
                                                                                                                          Indels
              MISSING (IN ISOFORM IB).
MISSING (IN ISOFORM II).
IA -> SV (IN ISOFORM III).
MISSING (IN ISOFORM III).
MISSING (IN ISOFORM III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
PubMed=11258910;
Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz
Goodenough U.W.;
                                                                                                                                                                                                                                                                                                                                           PIPSPPSTLPPPPQAPP-----NRAPPPSRPPRP 562
                                                                                                                                                                                                                                                                                                                                                           920 PIPVPPSDGPPPPPPPPPPNVLALPNSGGPPPPPPP 960
                                                                                          6.2%; Score 188.5; DB 1;
24.6%; Pred. No. 0.0005;
... mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Associates with GP2 and GP3.
-!- PTM: N-glycosylated and O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                  555 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL PRELIMINARY SEQUENCE FROM N.A.
                                                                                                                                                   PPPPAEESEEDDDGLP------
     977 981 E
1252 1287 N
625 722 I
626 627
628 1468 I
1468 AA; 163809 M
                                                                                                                            Conservative
                                                                                                                  Local Similarity
les 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycoprotein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3055;
                                VARSPLIC
VARSPLIC
VARSPLIC
                                                                 SEQUENCE
                                                                                                        Query Match
                   VARSPLIC
                                                                                                                                                                                                                                                                                                                                                  532
                                                                                                                                                      355
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last pronotation update)
Wiskott-Aldrich syndrome protein family member 2 (WASP-family protein member 2) (Verprolin homology domain-containing protein 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              507 PPAPIYTPPPPAPHCPPP---PPSAPTPPIPSPPSTLPPPPQAPPNRAPPPSRPPRRP 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 PPFPANTPMPPSPPSPPSPPAPPTPPSPSPPSPSPPSPPSPAPVPSSPAPPSPAPSPPS 337
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  general actin
complex.";
                                                                                                                                                                                         VEGETATIVE CELL WALL PROTEIN GP1.
49 X 5 AA APPROXIMATE PPSPX REPEATS.
POLY-PRO.
N-LINED (GLCNAC. . ) (POTENTIAL).
M; 6A584A9046550ZF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                             Score 187.5; DB 1; Length
Pred. No. 0.00019;
4; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Machesky L.M., Insall R.H.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=T-cell lymphoma; MEDLINE=99310608; PubMed=10381382; Suetsugu S., Miki H., Takenawa T., Identification of two human WAVE/SCAR homologues as regulatory molecules which associate with the Arp2/3 (Piochem. Blophys. Res. Commun. 260:296-302(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497 AA
send an email to license@isb-sib.ch)
                                                                                                                                                                                   POTENTIAL.
                                                                                  orrocaltens, Parky, Interpro, IPR003802, Pistil_extensin. Interpro, IPR003965, P_rich_extensn. PRINTS, PR01217, PRICHEXTENSN. PRINTS, PR01218, PSTLEXTENSIN.
                                EMBL; AF309494; AAG45420.1; -
EMBL; M58496; AAA69706.1; ALT_SEQ
GlycoSuiteDB; Q9FPQ6; -
                                                                                                                                                                                                                                                                                                                  W.
                                                                                                                                                                                                                                                                                                                                                                    6.28;
                                                                                                                                                                   Signal.
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                                                                                                                                                                                                                                                                                                                  54219
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                       29
339
339
399
455
                                                                                                                                                                   Glycoprotein; Repeat;
SIGNAL 1 29
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40
309
309
455
493
555 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                           34;
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                                                                                                                                                                                                                                                                CARBOHYD
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V -> G (IN REF. 1).

K -> K (IN REF. 1).

R -> K (IN REF. 1).

R -> K (IN REF. 1).

P -> TS (IN REF. 1).

PF -> TS (IN REF. 1).

PF -> TS (IN REF. 1).

SS -> GP (IN REF. 1).

SS -> GP (IN REF. 1).

I -> V (IN REF. 1).

SS -> GP (IN REF. 1).

I -> V (IN REF. 1).

I -> P (IN REF. 1).
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WH2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54094 MW;
                                                                                                                                                                                                                                  InterPro; IPR003124; WH2.
                                                                                                                                                                                                                                                    Pfam; PF02205; WH2; 1.
SMART; SM00246; WH2; 1.
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497
497 AA;
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74
93
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DOMAIN 20
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15;
                                                                                                                                                            356 PPPAEESEEEDDDGLPKKKWPTVDASYY-----GGRGVGGIKRMEVRWGEKGSTE 405
                                                                                                                                       406 EG-----AKLEKAKNARVKMPEQEYEFPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWV 459
                                                                                                                                                                                                                                       ---ENVDASSYPPPSQSDSASSPSPSFSEDNLPPPPAREFSYPVDNQRGSGLAGPKRSSVV 295
                                                                                                                                                                                                                                                                          502 HTSSPPPA-PIYTP-----PPPAPHCP--------PPPSAPT- 530
                                                                                                     130 PPPLNNLTPYRDDGTEALKFYT-DPSYFFDLWKKKMLQDTRDIMKEKRKH-RKEKKDNPN 187
                                       Gaps
                                                                                                                                                                                                        LLRKGYDRVSVMRPQPGDTGRCINFTRVKNNQPA-----KYPLNN------AY
                                 92;
6.2%; Score 187; DB 1; Length 497; 26.5%; Pred. No. 0.00018; ive 27; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                ------PPIPSPPS----TLPPPPQAPPNRAPPPSRPPP 560
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                 Best Local Similarity
Matches 75; Conserv
                                 75;
 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Extracellular matrix.
THE PROPERSING CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H-A-P-P.
H-A-P-P.
2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428 PEPRNLINNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTGRCINFTRV 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488 KNNQPAKYPLNNAYHTSSPPPAPIYTPPPPA----------PHCPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              525 PPS-----APTPPI---PSPPSTLPPPP---QAPPPNRAPPPSRPPS 563
                                                                        Extensin precursor (Cell wall hydroxyproline-rich glycoprotein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79;
                                                                                                                                                                        6.1%; Score 185.5; DB 1; Length 620; 29.7%; Pred. No. 0.00028; ive 10; Mismatches 34; Indels 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONTAINS THE SER-PRO(4) REPEATS.

3 X APPROXIMATE TANDEM REPEATS.
641DD2278AB28524 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S06733; S06733.
Repeat; Cell wall; Glycoprotein; Signal; Structural protein;
Hydroxylation.
                                  01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
           620 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65406
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Matches 52; Conservative
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620
73
151
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148
229
229
236
205
620 AA;
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                                              01-JAN-1990
16-OCT-2001
          EXTN_TOBAC
P13983;
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EXTN_TOBAC
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Kwan S.P., Hagemann T.L., Radtke B.E., Blaese R.M., Rosen F.S.;
The figuration of mutations in the Wiskott-Aldrich syndrome gene and
characterization of a polymorphic dinucleotide repeat at DXS6940,
adjacent to the disease gene. ";
Proc. Natl. Acad. Sci. U.S.A. 92:4706-4710(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kolluri R., Shehabeldin A., Peacocke M., Lamhonwah A.-M., Teichert-Kuliszewska K., Weissman S.M., Siminovitch K.A.; "Identification of WASP mutations in patients with Wiskott-Aldrich syndrome and isolated thrombocytopenia reveals allelic heterogeneity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLIND=95315993; PubMed=7795648; Villa A., Notarangelo L., Macchi P., Mantuano E., Cavagni G., Brugnoni D., Strina D., Patrosso M.C., Ramenghi U., Sacco M.G., Ugazzio A., Vezzoni P.; "X-linked thrombocytopenia and Wiskott-Aldrich syndrome are allelic diseases with mutations in the WASP gene."; Nat. Genet. 9:414-417(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAŘIANTS WAS F-27; I-48; M-75; L-86; H-86; K-131; C-187 AND K-477.
MEDLINE-96133286; PubMed-8528199;
                                                                                                                                                                                                                                                                                                                                                                                                             Hagemann T.L., Kwan S.-P.; "The identification and characterization of two promoters and the complete genomic sequence for the Wiskott-Aldrich syndrome gene."; Biochem. Biophys. Res. Commun. 256:104-109(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n.,
                                                                                                                                                                  TISSUB=T-cell;
MEDLINE=94349367; PubMed=8069912;
Derry J.M.J., Ochs H.D., Francke U.;
"Isolation of a novel gene mutated in Wiskott-Aldrich syndrome.";
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Derry J.M.J., Kerns J.A., Weinberg K.I., Ochs H.D., Volpini V., Estivill X., Walker A.P., Francke U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blechschmidt K., Nyakatura G., Strom T.M., Drescher B., Menzel Meingl A., Rosenthal A.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS WAS K-31; M-75; P-82; C-86; H-86; C-97; K-133; E-476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "WASP gene mutations in Wiskott-Aldrich syndrome and X-linked thrombocytopenia.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [9]
VARIANTS WAS TRP-43; MET-45; MET-75 AND CYS-86.
                      P42768, O9UNJ9;
01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MR-2002 (Rel. 41, Last annotation update)
Wiskott-Aldrich syndrome protein (WASP).
                 502 AA
                                                                                                                                                                                                                                              MEDLINE-95094263; PubMed-8001129;
Derry J.M.J., Ochs H.D., Francke U.;
Cell 79:923-923(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at the WAS locus.";
Hum. Mol. Genet. 4:1119-1126(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hum. Mol. Genet. 4:1127-1135(1995).
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99167346; PubMed-10066431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96133285; PubMed-8528198;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=95273432; PubMed=7753869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS WAS VAL-56 AND GLU-236
                     STANDARD;
                                                                                                                                                                                                                   Cell 78:635-644(1994)
                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                     NCBI_TaxID=9606;
                     WASP_HUMAN
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ERRATUM
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LIGAND.

DISEASE: DEFECTS IN WAS ARE THE CAUSE OF WISKOTT-ALDRICH SYNDROME DISEASE: AN X-LINKED RECESSIVE IMMUNOBETICIENCY CHARACTERIZED BY ECZEMA, THROMBOCYTOPENIA, RECURRENT INFECTIONS, AND BLOODY ECZEMA, THROMBOCYTOPENIA, RECHRS BEFORE AGE 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: POSSIBLE REGULATOR OF LYMPHOCYTE AND PLATELET FUNCTION.
MAY BE INVOLYED IN SIGNALING PATHWAYS WITH CYTOSKELETAL FUNCTION.
-i- SUBUNIT: BINDS TO CDC42, RAC, NCK, FYN, SRC KINASE FGR, BTK, ABL,
WIP, AND TO THE P85 SUBUNIT OF PLC-GAMMA.
-i- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE THYMUS. ALSO
FOUND, TO A MUCH LESSER EXTENT, IN THE SPLEEN.
-i- DOMAIN: THE WHI (WASP HOMOLOGY 1) DOMAIN MAY BIND A PRO-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88378988; PubMed-9713366; Rachard B.D., Giliani S., Faccheti F., Blanzuoli L., Vermi W., Notarangelo L.D., Giliani S., Frorini M., Fasth A., Stewart D.M., Nelson D.L.; "Defective actin polymerization in EBV-transformed B-cell lines from patients with the Wiskott Aldrich syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     El-Hakeh J., Rosenzweig S., Oleastro M., Basack N., Berozdnik L., Molina F., Rivas E.M., Zelazko M., Daniellan S.; Mulskott-Aldrich syndrome in Argentina: 17 unique, including nine novel, mutations."; Hum. Mutat. 19:186-187(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS WAS ARG-73; MET-75; CYS-83; CYS-86 AND LYS-133.
MEDLINE-99374925; PubMed-10447259;
Lemahleu V., Gastier J.M., Francke U.;
"Novel mutations in the Wiskott-Aldrich syndrome protein gene and their effects on transcriptional, translational, and clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [11]
MEDLINE-98350091; PubMed-9683546;
MEDLINE-98350091; PubMed-9683546;
MACCATHY Morrogh L., Gaspar H.B., Wang Y.-C., Katz F., Thompson L.
Layton M., Jones A.M., Kinnon C.;
"Absence of expression of the Wiskott-Aldrich syndrome protein in peripheral blood cells of Wiskott-Aldrich syndrome patients.";
Clin. Immunol. Immunopathol. 88:22-27(1998).
                                                                                                                                                                                                                                                                                                    VARIANTS WAS LVS-31 AND MET-45.
MEDLINE=97253413; PubMed=9098856;
Ariga T., Yamada M., Sakiyama Y.,
Aniga T., Yamada W., Sakiyama Y.,
Aniga T., Yamada W., Sakiyama Y.,
Aniga T., Yamada W., Sakiyama Y.,
Sayidrome and determination of the family members' carrier status
using three different methods.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIARRHEA, DEATH USUALLY OCCURS BEFORE AGE 10.

-!- DISEASE: DEFECTS IN WAS ARE THE CAUSE OF ISOLATED X-LINKED THROMBOCYTOPENIA (XIT). XIT IS CLINICALLY MILD WITH SMALL PLATELETS AND SUBCLINICAL LEUKOCYTE ABNORMALITIES.
-!- SIMILARITY: CONTAINS 1 GBD DOMAIN.
-!- SIMILARITY: CONTAINS 1 WHI DOMAIN.
MEDLINE=97272113; PubMed=9126958;
Remold-O'Donnell E., Cooley J., Shcherbina A., Hagemann T.L.,
Kwan S.-P., Kenney D.M., Rosen F.S.;
"Variable expression of WASP in B cell lines of Wiskott-Aldrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98992074; PubMed-9445409; Parolini O., Rasmann G., Haas O.A., Pawlowsky J., Gadner Knapp W., Holter W.; "X-linked Wiskott-Aldrich syndrome in a girl."; New Engl. J. Med. 338:291-295(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS WAS HIS-52 AND TRP-70.
                                                                                                                                                                                                   syndrome patients.";
J. Immunol. 158:4021-4025(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pediatr. Res. 41:535-540(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pathol. 185:99-107(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS WAS LYS-133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Calcium-dependent cell-adhesion protein. Essential for maintenance of normal retinal and cochlear function.
SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).
TISSUE SPECIFICITY: Expressed in brain, lung, kidney, spleen and restis. Found also in the inner and outer synaptic layers, and the nerve fiber layer in adult and fetal retinas. Found in the supporting cells, outer sulcus cells and spiral ganglion of fetal
                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Fetal brain;

MEDLINE-13800012; PubMed-11487575;

MEDLINE-13800012; PubMed-11487575;

Alagramam K.N., Yuan H., Kuehn M.H., Murcia C.L., Wayne S.,

Srisailpathy C.R.S., Lowry R.B., Knaus R., Van Laer L., Bernier F.P.,

Schwartz S., Lee C., Morton C.C., Mullins R.F., Ramesh A.,

Van Camp G., Hagemen G.S., Woychik R. P., Smith R.J.H.;

"Mutations in the novel protocadherin PCDH15 cause Usher syndrome type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISEASE: Defects in PCDH15 are the cause of Usher syndrome type 1F (USH1P). Usher syndrome type 1 is a autosomal recessive disorder characterized by congenital profound sensorineural hearing loss. constant vestibular dysfunction and prepubertal onset of retinitis spignentosa leading to blindness. Usher syndrome is the most common cause of combined deafness and blindness in developed countries. SIMILARITY: CONTAINS IL CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11398101;
Ahmed Z.M., Riazuddin S., Bernstein S.L., Ahmed Z., Khan S.,
Griffith A.J., Morell R.J., Friedman T.B., Riazuddin S., Wilcox E.R.;
"Mutations of the protocadherin gene PCDH15 cause Usher syndrome type
                Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                      PC15_HUMAN STANDARD; PRT; 1955 AA. 0960U1; 0960T8; 01-MAR-2002 (Rel. 41, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hum. Mol. Genet. 10:1709-1718(2001).
                                                                                                     381 LPPPPPGAGGPPMPPPPPPPPP 405
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Pfam; PF00028; cadherin; 10.
PROSITE; PS00232; CADHERIN_1; 3.
PROSITE; PS50268; CADHERIN_2; 10.
                                                                    -LPPPPQAPPNRAPPPSRPPRPS
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                                                                                                                                                                                                                                                                            Protocadherin 15 precursor
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MIM; 605514; -.
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PC15_HUMAN
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 488 KNNQPAKYPL--NNAYHTSSPPPAPI-YTPPPPAPHCPPPPPSAPTPPIPSPPST---- 539
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/FTIG-VAR_O08105.
/FTIG-VAR_008105.
/FTIG-VAR_008106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISSING (IN THROMBOCYTOPENIA) /FTId=VAR_005824.
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/FTIG-VAR_012710.
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RanBP1_WASP.
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                                                                                                                                                                        AF115549; AAD26691.1; -. AF196970; AAF06804.1; -.
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                                                                                                                                                                                                                                                                                        Pfam; PF00786; PBD; 1.
Pfam; PF00568; WH1; 1.
Pfam; PF02205; WH2; 1.
SMART; SM00285; PBD; 1.
SMART; SM00461; WH1; 1.
SMART; SM00461; WH1; 1.
RART; PS50108; GBD; 1.
REPEAT; Dissemitation.
                                                                                                                                                        AAC50140.1;
                                                                                                                                    U18935; AAA60381.1;
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InterPro; IPR000697:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----QPGDTGRCI--NFTRVKNNQP
        Signal; Multigene family; Vision; Deafness; Retinitis pigmentosa;
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(POTENTIAL).
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16-0CT-20101 (Rel. 40, Last annotation update)
16-0CT-20101 (Rel. 40, Last annotation update)
Plasmodium berghei (strain Anka).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.0%; Score 182; DB 1; Length 1955; 28.9%; Pred. No. 0.0017;
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L -> Q (IN REF. 2).

Q -> R (IN REF. 2).

Q -> Q (IN REF. 2).

W, 5592CF30F64FF082 CRC64;
                                                         PROTOCADHERIN 15.
EXTRACELLULAR (POTENTIAL)
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POLY-PRO.
N-LINKED (GLCNAC. ..) (
N-LINKED (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                         -!- MISCELLANDOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
-!- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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                 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 X 8 AA REPEATS.
17 X 2 AA REPEATS OF P-Q.
0EC240EE35681AF8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pram; PF00090; tSP_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
PROSTIE: PSS0092; TSP1; 1.
Malaria; Sporozoite; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S07873; OZZQBK.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
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347 AA;
[1]
SEQUENCE FROM N.A.
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August 9, 2002, 10:47:04; Search time 31.3 Seconds (without alignments) 411.936 Million cell updates/sec
                                                                                                                                                                                             US-09-970-076-8
1728
1 MATAERRALGIGFOWLSLAT.....TTHCSLHKIASGPTTAACME 333
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                        105224 seqs, 38719550 residues
                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence:
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Post-processing: Minimum Match 0% '
Maximum Match 100%
Listing first 45 summaries

105224

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ption	Q9h6x2 homo sapien	2 mus m	5 homo	omod 6	omod o	2 homo	gallu	5 mus mus	snw	mus	homo sa	gallu	caenor	P21941 homo sapien	notophi	galli	homo	рошо	рошо	mus m	Q02788 mus musculu	mus	O89029 mus musculu	mus m	homo sa	gallu	homo sa	homo	302 oryct		195	6893 plasm	P12110 homo sapien
SUMMARIES	ID	ATR_HUMAN	ATR_MOUSE	CMG2_HUMAN	ITAD_HUMAN	ITAM HUMAN	ITAX_HUMAN	CA1C_CHICK	ITAM_MOUSE	CA1C_MOUSE	CO2_MOUSE	CA1C_HUMAN	CA1E_CHICK	YNX3_CAEEL	CAMA_HUMAN	CA1C_NOTVI	MTN3_CHICK	MTN2_HUMAN	CFAB_HUMAN	CA17_HUMAN	CFAB_MOUSE	CA26_MOUSE	CAMA_MOUSE	MTN4_MOUSE	MTN2_MOUSE	ITAH_HUMAN	CAMA_CHICK	MTN4_HUMAN	MTN3_HUMAN	CA1C_RABIT	ROP_DROME	x173_BORBU	TRAP_PLAFA	CA26_HUMAN
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ф	Query Match	95.4	89.9	ᅼ	9.5	8.4	•		•		•	•																	5.9	٠	•		5.7	5.7
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P12111 homo sapien P58079 caulobacter O9K014 caulobacter O9K014 gallus gall P15989 gallus gall P15989 pallus gall P15989 pallus gall P56199 homo sapien O9nxO2 homo sapien P53710 bos taurus P18614 rattus norv O43405 homo sapien
CA36_HUMAN HUTI_CAUCR HUTI_CAUCR ITA1_CHICK CA36_CHICK ITAE_HUMAN ITAE_HUMAN ITA2_HUMAN ITA2_BOVIN ITA1_BOVIN ITA1_BOVIN
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# ALIGNMENTS

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coved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                            NEKPFSVEDTYLLCPAPILKEVGMKAALOV -> SKSLOSP
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                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                    WVSSTSGFKEGNSHPCLPARPHT (IN ISOFORM 3).
                                                                                                                                                                                                                              MISSING (IN ISOFORM 3).
DGSILAIALLILFLL -> LHKIASGPTTAACME (IN
                                                                                                Glycoprotein; Signal; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
EDDD -> NKIK (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
41. Antrax toxin receptor precursor (Tumor endothelial marker 8).
ATR OR TEM8.
                                                                                                                                                                                                                                                                                  Length 564;
                                                                                                                                                   ASP/GLU-RICH (HIGHLY ACIDIC). PRO-RICH.
                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                            B118A00AD5DF2233 CRC64;
                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                     (IN ISOFORM 4)
                                                                                                               ANTRAX TOXIN RECEPTOR
                                                                                                                                                                                                                                                                                  Query Match 95.4%; Score 1649; DB 1; I
Best Local Similarity 100.0%; Pred. No. 2.8e-128;
Matches 318; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    562 AA
  modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                               [SOFORM 4).
                                                                                                                                 POTENTIAL.
                                        EMBL, AK025429; BAB15128.1; ALT_INIT.
EMBL, AK001463; BAA91707.1; ALT_FRAME.
EMBL, BC012074; AAH12074.1; -.
                                                                                                                                                                                                                                                      MISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                             62789 MW;
                                   EMBL; AF279145; AAK52094.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 DGLSFISSSVIITTHCS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 DGLSFISSSVIITTHCS 318
                                                                         InterPro; IPR002035; vWFA.
                                                                                  SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                Receptor; Transmembrane; SIGNAL 1 32
                                                                                                                                                                                                368
564
297
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343
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09C252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              RP SEQUENCE OF 88-562 FROM N.A. (ISOFORM 2).

RX SARAN-C57BL/G3; IISSUBE-Embryo;

RX KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alawa T., Lawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alawa T., Matuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matudi F., Sizuki R., Gissi C., King B., Kochiwa H.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schimul L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,

RA Blake J., Bolfelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Bolfelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mondberts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Sakamoto N.,

RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Nyanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Wayashiw-Poris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO-RICH.

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

GRCINFTRVKNSQPAKYPLNNTYHPSSPPPAPIYTPPPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                        Kinzler K.W., St Croix B.; "Cell surface tumor endothelial markers are conserved in mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASP/GLU-RICH (HIGHLY ACIDIC).
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                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
MEDINE=21443268; PubMed=11559528;
Carson Walter E.B., Watkins D.N., Nanda A., Vogelstein.
Kinzler K.W., St Croix B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
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-!- SIMILARITY: BELONGS TO THE ATR FAMILY.
-!- SIMILARITY: CONTAINS 1 WWFA DOMAIN.
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EMBL; AK013005; BAB28591.1; ALT_INIT.
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InterPro; IPR002035; vWFA.
PROSITE; PS50234; VWFA; 1.
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HCPPPAPSAPTPPIPSPPSTLPPPPQAPPNRAPPPSRPPP
               RFRGWRLTICLGSKHVHPGRHDKGPETPLLKQA
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basement
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                                                                                                                                                                                                             69 LAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERAS 128
                                                                                                                      Gaps
                                                                                                                                                                               7 LGAGLRGLCVAALVLVCAGHGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQ 66
                                                                                                                                                                                                                                                                                                                                                    9 LGIGFQWLSLATLVLICAGQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQ
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-21539596; PubMed-11683410;
A BELl S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S.,
A Maxwell S.A., Davis G.E.;
Maxwell S.A., Davis G.E.;
Collagen matrices: regulated expression of genes involved in base membrane matrix assembly, cell cycle progression, cellular membrane matrix assembly, cell cycle progression, cellular differentiation and G-protein signaling.";
L. J. Cell Sci. 114:2755-2773(2001).
C -1 SUBCELLULAR LOCATION: Type I membrane protein (Probable).
C -1 SIMILARITY: BELONGS TO THE ATR FAMILY.
C -1 SIMILARITY: CONTAINS I VWFA DOMAIN.
                                                                                                                                                                 .;
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                                                                                          Length 562;
                               WMFSSFLERAFQ (IN ISOFORM 2).
6AC92049B4B4F7C CRC64;
                                                                                                                      7; Indels
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Capillary morphogenesis protein-2 precursor (CMG-2).
Homo sapiens (Human).
                                                                                        Score 1553; DB 1;
Pred. No. 2.2e-120;
5; Mismatches 7;
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                 RPSV ->
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                                            62308 MW;
                                                                                        89.9%;
96.1%;
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Best Local Similarity 96.1
Matches 298; Conservative
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P58335;
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interaction With VCAMI.
MEDLINE-90059842; PubMed-9841932;
Grayson M.H., Van der Vieren M.,
Grayson M.H., Van der Vieren M.,
Hoffman P.A., Staunton D.E., Bochner B.S.;
"alphadbeta2 integrin is expressed on human eosinophils and functions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a human
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Noti J.D., Johnson A.K., Dillon J.D.;
Structural and functional characterization of the leukocyte integrin
gene CD11d. Essential role of Spl and Sp3.";
J. Biol. Chem. 275:8959-8969(2000).
                                                                                                                                                                                                                                                                                                                                                                                        123 GFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T.,
Staunton D.E., Gallatin W.M.;
"A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
                                                                                                                                                                                                                                                                                                  63 YYEVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHE 122
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96257236; pubMed-8666289; Wong D.A., Davis E.M., LeBeau M., Springer T.A.; "Cloning and chromosomal localization of a novel gene-encoding beta 2-integrin alpha subunit.";
                                                                                                   POTENTIAL)
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                 CAPILLARY MORPHOGENESIS PROTEIN-2. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                Length 386;
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                                                                  CYTOPLASMIC (POTENTIAL). VWFA.
                                                                                                 N-LINKED (GLCNAC. . .) (
0F9B2D6688EAB17A CRC64
                                                                                                                                                                                                   57;
                                                                                                                                                                   DB 1;
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                                                                                                                                                                  551.5; DB No. 4e-38;
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Pred.
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MEDLINE=96111956; PubMed=8777714;
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53.8%;
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Best Local Similarity 53.88
Matches 114; Conservative
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         ASSOCIATES WITH BETA-2.

ASSOCIATES WITH BETA-2.

ASSOCIATES WITH BETA-2.

SUBCELULAR LOCATION: Type I membrane protein.

ISSUE SPECIFICITY: EXPRESSED MODERATELY ON WYELOMONOCYTIC CELL

ISSUE SPECIFICITY: EXPRESSED MODERATE BLOOD LEUKOCYTES AND STRONGLY ON

LINES AND SUBSETS OF PERIPHERAL BLOOD LEUKOCYTES AND STRONGLY ON

TISSUE-SPECIALZED CELLS, INCLUDING MACROPHAGES FOAM CELLS WITHIN

ATHEROSCLEROTIC PLAQUES, AND ON SPLENIC RED PULP WACROPHAGES.

DOMAIN: THE INTEGRIN LOMAIN (INSERT) IS A WHFA DOMAIN. INTEGRINS

WITH I-DOMAINS DO NOT UNDERGO PROTESSE CLEAVAGE.

SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.

SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
                                                                                                MEDLINE-99770002; PubMed=10438935;
MEDLINE-99770002; PubMed=10438935;
Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a binding interface between I domain and VCAM-1.";
J. Immunol. 163:1984-1990(1999).
I. FUNCTION: INTEGRIN ALPHA-D.BETA-2 IS A RECEPTOR FOR ICAM3 AND VCAM1. MAY PLAY A ROLE IN THE ATHEROSCLEROTIC PROCESS SUCH AS CIERARING LIPOPROFIENS FROM PLAQUES AND IN PHAGOCYTOSIS OF BLOOD-CLEARING AND ALLANDERS AND ALLANDERS AND PLAGUES AND IN PHAGOCYTOSIS OF BLOOD-CLEARING AND ALLANDERS AND ALL
                                                                                                                                                                                                                                                            BORNE PATHOGENS, PARTICULATE MATTER, AND SENESCENT ERYTHROCYTES FROM THE BLOOD.
                                                                                                                                                                                                                                                                                                    SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-D
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Signal; Repeat; Calcium;
as an alternative ligand for vascular cell adhesion molecule 1 (VCAM-1).";
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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FG-GAP 2.
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EMBL: U40274: AAB60634.1; --
EMBL: U40277: AAB60635.1; --
EMBL: U40277: AAB60635.1; --
EMBL: U40277: AAB60638.1; --
EMBL: U40279: AAB60638.1; --
EMBL: U40279: AAB60638.1; --
EMBL: AC1079: AAB60638.1; --
EMBL: AC1079: AAB60638.1; --
EMBL: AC1079: AAB60638.1; --
HSSP: P11215; 1A8X.-
InterPro: IPR000413: Integrin_alpha.
InterPro: IPR000413: Entegrin_alpha.
InterPro: IPR00035; vWFA.
Integrin_A: PF00395; vWA.1.
PFUNTS: PR001185: INTEGRINA.
PRINTS: PR001185: INTEGRINA.
PRINTS: PR00191: Int_alpha.
SMART: SM00191: Int_alpha.
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                                                J. Exp. Med. 188:2187-2191(1998).
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Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;
The human leukocyte adhesion glycoprotein Mac-1 (complement receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1999 (Rel. 11, Created)
01-JUL-1996 (Rel. 34, Last sequence update)
01-OCT-2002 (Rel. 41, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CE-3 alpha chain) (CDllb) (Leukocyte adhesion receptor MO1)
ITCAM OR CR3A OR CD11B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 ERASEQIYYENRQGYRTA-SVIIALIDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 LTVVTQLFHHKNGARKSAKKILIVITDGQKYKDPLEYSD-VIPQAEKAGIIRYAIGVGHA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 LAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLP----GGDTYMHEGF 124
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 IGFQWLSLATLVLICAGQGGRREDGGPAC-YGGFDLYFILDKSGSV-LHHWNEIYYFVEQ
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(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                      POTENTIAL)
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GHPW -> ATP (IN REF. 2).

LS L -> V (IN REF. 2).

LS L -> V (IN REF. 2).

126885 MW; F296AlA35455D77D CRC64;
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Matches 70; Conserv
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EMBL;
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      PARTER NO PROPERTY NO PROPERTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
MEDLINE-95171458; PubMed=7867070;
Lee J.O., Rleu P., Arnaout M.A., Liddington R.;
"Crystal structure of the A domain from the alpha subunit of integrin CR3 (CD11b/CD18).";
Cell 80:631-638(1995).
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Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway for
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"Anthon acid sequence of the alpha subunit of human leukocyte adhesion
receptor Mol (complement receptor type 3).";
J. Cell Biol. 106:2153-2158(1988).
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                                                                                                                  SEQUENCE FROM N.A.

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leukocyte adhesion glycoprotein Mol: chromosomal localization and homology to the alpha subunits of integrins.";

Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-9 FROM N.A. MEDLINE-92073318; PubMed=1683702; Shelley C.S., Armaout M.A.; "The promoter of the CD11b gene directs myeloid specific and developmentally regulated expression.";
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Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991)
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MEDLINE-98362595; Pubmed-9687375;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-88257215; PubMed-2454931;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunol. 150:480-490(1993).
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SEQUENCE OF 9-1153 FROM N.A.
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JOINED. JOINED, JOINED

AAB24821.1;

AAB24821.1

S52169; S52170;

AAB24821.1;

S52165;

552167;

AAB24821.1; AAB24821.1;

S52180;

S52181; S52184;

S52189; S52191; \$52192; 552203; \$52212; S52216;

AAB24821. AAB24821.

AAB24821.1 AAB24821..

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S52219; S52220;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LECOLULIAR SUPPLIATION OF STREET CONTROL OF STREET STREET STREET SUBJILITY SUPPLIATION OF STREET STR
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SIMILARITY: BELOGGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
SIMILARITY: CONTAINS 1 VWFA DOMAIN.
SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
DATABAGE: NAME-PROW: NOTE-CD guide CD11b entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd11b.htm".
                                                                                                                                                                                                                                                                                                                                                                              3D-STRUCTURE MODELING OF 17-616.
MEDILTB-98250734; Pubbadd-9560195;
Oxvig C., Springer T.A.:
"Experimental support for a beta-propeller domain in integrin alpha-
Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A., Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L., Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E., Mutchler V.T., Tomich C.S., Watenpauph K.D., Wiley V.H.; Cation binding to the integrin CD11b I domain and activation model
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AAA59903.1;
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S52154;
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S52227;
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S52157;
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PRINTS; PRO1185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; INC_alpha; 4
SMART; SM00327; VWA; 1.
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                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           ERRATUM
12;
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
101-MAR-2002 (Rel. 41, Last annotation update)
101-MAR-2002 (Rel. 41, Last annotation update)
102-MAR-2002 (Rel. 41, Last annotation update)
103-MAR-2002 (Rel. 41, Last annotation update)
103-MAR-2002 (Rel. 41, Last adhesion receptor p150,95) (CD11c) (Leu M5).
103-MAR-2003 (Manna)
103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 DLYFILDKSGSVL-HHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTED----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00242; INTEGRIN_ALPHA: 1.
PROSITE; PS500242; WNFA: 1.
INTEGRIN: Cell adhesion; Receptor; Glycoprotein; Transmembrane; Signal; 3D-structure; Repeat; Magnesium; Calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.4%; Score 145.5; DB 1; Length 1152; 26.2%; Pred. No. 0.00044; tive 45; Mismatches 81; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTEGRIN ALPHA-M.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FG-GAP 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1163 AA
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InterPro; IPR002035; vWFA.
InterPro; IPR012035; vWFA.
Profilan; Prof1893; FG-GAP; 5.
Pfam; Pr00092; vwa; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR001185; INTEGRINA.
PRINTS; PR001185; INTEGRINA.
SMART; SM00327; VWFADOMAIN.
SMART; SM00327; VWA.
                EMBL, S52221; AAB24821.1; JOINED. EMBL; S52222; AAB24821.1; JOINED. EMBL; M75222; AAB24821.1; JOINED. EMBL; M76724; AAB58410.1; EMBL; M8477; AA51960.1; PTR; A31108; RWH01B. PTR; A3108; RWH01B. PTR; A36091; A26091. PDB; 1BHO; 18-NOV-98. PDB; 1BHO; 18-NOV-98. PDB; 11DO; 01-AUG-96. PDB; 11DO; 01-AUG-96.
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                                                                                                                                                                                                                                                                                            PDB; 1JLM; 11-JAN-97.
Carbbank; CCSD:33581; -.
Carbbank; CCSD:33582; -.
Carbbank; CCSD:33584; -.
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1128
1152
84
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SIGNAL 1 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                  MIM; 120980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-87167965, PubMed-3549901;

MEDLINE-87167965, Watche M., Springer T.A.;

Miller L.J., Watche M., Springer T.A.;

RT Miller L.J., Watche M., Springer T.A.;

RT and alpha subunit N-terminal sequences of human Mac-1

RT and p150,95 leukocyte adhesion proteins.";

LJ. Immunol. 138:2381-2383(1987).

R. J. Immunol. 138:2381-2383(1987).

RECORNIZES THE SEQUENCE G-P-R IN FIBRINGEN. IT MEDIATES CELL-CELL

RECORNIZES THE SEQUENCE G-P-R IN FIBRINGEN. IT IS ESPECIALLY

INTERACTION DURING INFLAMMATORY RESPONSES. IT IS ESPECIALLY

SC INTERACTION DURING INFLAMMATORY RESPONSES. IT IS ESPECIALLY

ASSOCIATES WITH BETA-2.

1 SUBUNIT: HETERODIMEN OF AN ALPHA AND A BETA SUBUNIT. ALPHA-X

ASSOCIATES WITH BETA-2.

1 SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=88166645; PubMed=3327687; COTDI N.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.; Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.; COTDI A.L., Millor and complete primary structure of the alpha subunit of a leukocyte adhesion glycoprotein, p150,95."; EMBO J. 6:4023-4028(1987).
                                                                                                                                                                                                                                                                                                                        Corbi A.L., Garcia-Aguilar J., Springer T.A.; "Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corbi A.L., Garcia-Aguilar J., Springer T.A.;
J. Biol. Chem. 265:12750-12751(1990).
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Carbbank; CCSD:33581; -.
Carbbank; CCSD:33582; -.
Carbbank; CCSD:33584; -.
Carbbank; CCSD:33584; -.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vWFA.
InterPro; IPR0357; FG-GAP; 5.
Pfam; PF018357; integrin_A; 1.
Pfam; PF00357; uve; Integrin_A; 1.
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EMBL; W00093; CAA68283.1;
EMBL; M29165; -; NOTANNOTATED_CDS.
EMBL; M29487; AAA51620.1; ALT_SEQ.
EMBL; M29482; AAA51620.1; JOINED.
EMBL; M29484; AAA51620.1; JOINED.
EMBL; M29484; AAA51620.1; JOINED.
EMBL; M29486; AAA51620.1; JOINED.
EMBL; M29486; AAA51620.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                        p150,95 molecule.";
J. Biol. Chem. 265:2782-2788(1990)
                                                                                                                                                                                                                                                                                                  MEDLINE=90153906; PubMed=2303426;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 DIVFLIDGSGSISSRNFATMMNFVRAVISOFQRPSTQFSLMQFSNKFQTHFTFEEFRRTS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTAS-VIIALTDGELHED 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 NPLSLLASVHQLQ-----GFTYTATAIQNVVHRLFHASYGARRDATKILIVITDGKKEGD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 LFFYSEREANRSRDLGAIVYCVGV------KDFNETQLARIAD--SKDHVFPVNDG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
             PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
Signal; Magnesium; Calcium; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.3%; Score 143.5; DB 1; Length 1163; 24.8%; Pred. No. 0.00065;
Live 43; Mismatches 89; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6C4E19CC3F62A473 CRC64;
                                                                               EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAIC_CHICK STANDARD; PRT; 3124 AA. P1344; 004509; 01-JAN-1990 (Rel. 13, Created) 01-NN-1997 (Rel. 35, Last sequence update) 01-NNV-1997 (Rel. 41, Last annotation update) 01-MAR-2002 (Rel. 41, Last annotation update) COLlagen alpha 1(XII) chain precursor (Fibrochimerin).
                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 FQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
N-LINKED (GLCNAC.)
                                                                    INTEGRIN ALPHA-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> A (IN REF. -> D (IN REF.
                                                                                                                                                                 FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
POTENTIAL.
POTENTIAL.
GFFKR MOTIF.
                                                                                                                           FG-GAP 1.
FG-GAP 2.
VWFA.
PS00242; INTEGRIN_ALPHA; 1.
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Best Local Similarity 24.88
Marches 55; Conservative
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1022
1032
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1163 AA;
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1108
1129
34
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TRANSMEM
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DISULFID
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                                                                                                                                                                                                                                                                      CA_BIND
                                                      SIGNAL
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                                                                                                                                         REPEAT
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CA1C_CHICK
                                                                      CHAIN
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINAL TISSUE FORM OF COLLAGEN XII MAY CONTAIN HOMOTRIMERS OF EITHER THE LONGER OR THE SHORTER ISOFORM OR COMBINATION OF LONG AND SHORT ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTEOGLYCAN. THE LARGE ISOFORM HAS MORE RESTRICTED EXPRESSION IN EMBRYONIC TISSUE THAN
                                                                                                                                                                                                                                                               MEDLINE-92111862; PubMed=1918137; Yamada S.S., Shinomura T., Tanaka H., Yamagata M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka H., Nishida Y., Obara M., Kimata K.B., The complete primary structure of type XII collagen shows a chimeric molecule with reiterated fibronectin type III motifs, von Willebrand factor A motifs, a domain homologous to a noncollagenous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE SPLICING.
MEDLINE-95370352; Pubmed-7642694;
MEDLINE-95370352; Pubmed-7642694;
Koch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;
Koch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;
Earge and small splice variants of collagen XII: differential
expression and ligand binding.";
J. Cell Biol. 130:1005-1014(1995).
-1- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
CONTAINING FIBRILS, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE
SURFACE OF THE FIBRILS, AND THE COLL AND NC3 DOMAINS MAY BE
LOCALIZED IN THE PERIFIBRILLAR MATRIX.
-1- SUBJUNT: TRIMER OF IDEPTICAL CHAINS EACH CONTAINING 190 kDa OF
NONTRIPLE-HELICAL SEQUENCES.
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AT
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DOMAIN: THIS SEQUENCE DEFINES FIVE DISTINCT DOMAINS, TWO TRIPLE-HELICAL DOMAINS (COLL AND COL2) AND THREE NONTRIPLE-HELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (Ca-x-Y) ARE HYDROXYLAFED IN SOME OR ALLO OF THE CHAINS. PTM: GLYCOSYLATED. CHONDROITIN-SULFATED (BY SIMILARITY). SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILIX.
SIMILARITY: CONTAINS 4 VWFA DOMALIX.
SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-1283 FROM N.A. (SHORT FORM), AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2846-2873.

MEDLINE-90062079; PubMed=2584192;
Gordon M.K., Gerecke D.R., Dublet B., van der Rest M., Olsen B.R.;
"Type XII collagen. A large multidomain molecule with partial homology to type IX collagen.";
J. Biol. Chem. 264:19772-19778(1989).
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PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trueb J., Trueb B.; "The two splice variants of collagen XII share a common 5' end."; Biochim. Biophys. Acta 1171:97-98(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 2456-3124 FROM N.A., AND SEQUENCE OF 2772-2794 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 2960-3076 FROM N.A.
MEDLINE=87317590; PubMed=3476925;
Gordon M.K., Gerecke D.R., Olsen B.R.;
Type XII collagen: distinct extracellular matrix component discovered by cDNa cloning.";
Proc. Natl. Acad. Sci. U.S.A. 84:6040-6044(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93042014; PubMed-1420368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell Biol. 115:209-221(1991).
                                                                                                                                                                                                                                  STRAIN-WHITE LEGHORN;
                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Embryo;
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                                                                                                                                                                                         CC EMEL; DOUGLEY; BAA00701.1; --
DR EMBL; M17375; AAA48718.1; --
DR EMBL; M17375; AAA48718.1; --
DR EMBL; J05137; CAAA47744.1; --
DR PIR; A34485.
DR PIR; A34485.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003962; FINII_repeat.
DR InterPro; IPR003962; FNIII_repeat.
DR InterPro; IPR003962; FNIII_repeat.
DR InterPro; IPR003129; TSPN.
DR Pfam; PF02210; TSPN. 1.
DR Pfam; PF0092; vw axi 4.
DR PRINTS; PR00061; FNN; 1.
DR PRART; SM0060; FNN; 1.
DR SWART; SM00327; VWA; 4.
DR SWART; SM00327; VWA; 4.
DR PRINTS; PF00092; vw FNN; 1.
DR SWART; SM00327; VWA; 4.
DR PRINTS; PS50234; VWFA; 4.
DR PGOSTPE; VWFA; 4.
DR PGOSTPE; PS50234; VWFA; 4.
DR PGOSTPE; VWFA; 4.
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CELL ATTACHMENT SITE (POTENTIAL).
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TRIPLE-HELICAL REGION (COL1)
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FIBRONECTIN TYPE-III 15.
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-III 17.
FIBRONECTIN TYPE-III 18.
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NONHELLICAL REGION (NC1).
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha
subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MOI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Amilio acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willebrand factor.";
EMBO J. 7:1371-1378(1988).
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STRAIN-BALB/C; TISSUB-Spleen;
MEDLINE=86287312; PubMed=2942940;
MEDLINE=86287312; PubMed=2042940;
Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,
Larson R.S., Roberts T.M., Springer T.A.;
"A partial genomic DNA clone for the alpha subunit of the mouse
"A partial genomic DNA clone for the alpha subunit of the mouse complement receptor type 3 and cellular adhesion molecule Mac-1.";
                                                                                                                                                                                                                                                                                                                                                                                               497 NRVKDIIQAINTFPYRGGSTNTGRAMTYVREKVFVTSK-GSRPNVPRVMILITDGK-SSD
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
N-INKED (GLCNAC. ..) (POTENTIAL).
N-S (IN REF. 4).
D -> E (IN REF. 4).
D -> F (IN REF. 2).
V -> F (IN REF. 2).
OP -> AG (IN REF. 2).
                                                                                                                                                                                                                                                              8.3%; Score 143; DB 1; Length 3124; 26.1%; Pred. No. 0.0025;
                                                                                                                                                                                                                                                                                           97; Indels
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094285AFE7F346CF CRC64;
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MEDLINE=88312584; Pubmed=3044779;
                                                                                                                                                                                                                           340578 MW;
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Best Local Similarity 26.1%
Matches 65; Conservative
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                                   Springer T.A., Teplow D.B., Dreyer W.J.;
"Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
"Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
"Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
"Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
"Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
"I sequence homology of the LFA-1 and Mac-2 is Labelachar of Tale Thereofor Lower Complement OF The THIRD COMPLEMENT COMPONENT. IT PROBABLY RECGNIZES THE R-G-D PEPTIDE IN C3B. INTEGRIN ALPHA-M/BETA-2 IS ALSO A RECEPTOR FOR THE THIRD COMPLEMENT AND ICAMI. IT RECGNIZES PI AND P2 PEPTIDES

CHENRINGEN FACTOR X AND ICAMI. IT RECGNIZES PI AND P2 PEPTIDES

CF PER TIONINGEN, PACTOR X AND ICAMI. IT RECGNIZES PI AND P2 PEPTIDES

CF PER TOWNINGEN, PACTOR X AND ICAMI. IN IMMONE COMPLEX MEDIATED

GLOMERULONEPHRITIS. HOLE EXPRESSING A NULL MUTATION OF THE ALPHA-M
SCHOWITT GENE DEMONSTRATE INCREASE IN NEUTROPHILA CCUMULATION, IN

RESPONSE TO A IMPARRED DEGRANULATION AND PHAGOCYTOSIS, EVENTS THAT

CONTRACTOR AND PACTOR AND PACTOR AND PACTOR THE ALPHA-M
SCHOWITT GENE DEMONSTRATE INCREASE IN NEUTROPHILS. THESE MICE DEVELOP
                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             -!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
-!- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
-!- SIMILARITY: CONTAINS I VWFA DOMAIN.
-!- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
                                                                                                                                                                                                                                                                                                                        SÜBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
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PRINTS; PROUBLES; INTEGRINA.
PRINTS; PROUBLES; INTEGRINA.
SMART; SMOOD19; Int_alpha; 4.
SMART; SMOOD27; WAs; 1.
PROSITE; PS50234; VWFA: 1.
PROSITE; PS50234; VWFA: 1.
PROSITE; PS50234; VWFA: 1.
STGNAL; Call adhesion; Receptor; Glycoprotein; Transmembrane; Signal; Calcium; Repeat.
                                                                                                                                                                                                                                                                                                SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. ALPHA-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
 Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTEGRIN ALPHA-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
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FG-GAP 2.
VWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S00551; S00551.
HSSP; P11215; 1A8X.
MGD; MGI:96607; Itgam.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR02035; vWFA.
Pfam; PF01839; FG-GAP; S.
Pfam; PF00357; integrin_A: 1.
Pfam; PF00092; vwa: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X07640; CAA30479.1; -. EMBL; M14293; AAA39484.1; -.
                                                                                                                                                                                                                                                                                                              ASSOCIATES WITH BETA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1153
1105
1129
1153
84
                          SEQUENCE OF 17-28.
                                                                                                                                                                                                                                                                                                                                                     GRANULOCYTES.
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337
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CA_BIND
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Query Match 8.2%; Score 141; DB 1; Length 1153;
Best Local Similarity 24.2%; Pred. No. 0.001;
Matches 71; Conservative 50; Mismatches 96; Indels 76; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 ----REQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYE-NRQGYRTASVIIALT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNETQLARIAD-----SKDHVFP 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFIS---PQLRMSFIVFSTRGTTLMKLTED-- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
STRAIN=SWISS WEBSTER, AND C57BL/6J; TISSUE=Skin;
MEDLINE=96170761, PubMed=8601036;
Boohme K., Li Y., Oh P.S., Olsen B.R.;
"Primary structure of the long and short splice variants of mouse collagen XII and their tissue-specific expression during embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178DB988AECB0343
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BY SIMILARITY.
BY SIM
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15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(XII) chain precursor.
                                                                                                  SIMILARITY
POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA; 127480
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537
1136
1136
1123
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1033
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86
774
772
861
881
772
991
9907
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1051
1076
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1045
1051
1051
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16;

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CO2_MOUSE
P21180;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
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                                                                                                                                                                                                                                                                      BINDING
BINDING
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CO2_MOUSE
                                                                                                                                                                                                                                                         BINDING
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                   SURFACE OF THE FIREILE, AND THE COLEARN NOS DUCATURED FIREILE SURFACE OF THE PERIFIBRILLAR MATRIX (BY SIMILARITY).

LOCALIZED IN THE PERIFIBRILLAR MATRIX (BY SIMILARITY).

-1- SUBGUNIT: TRIMBR OF IDENTICAL CHAINS EACH CONTAINING 190 kDa OF NONTRIPLE-HELICAL SEQUENCES (BY SIMILARITY).

-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING: THE FINAL TISSUE PORM OF COLLAGEN XII MAY COMBINATION OF EITHER THE LONGER OR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTECGLYCAN.

-1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN TENDONS, PERICHONDRIUM, SKIN, CORNEA, SCLERA, BLOOD VESSELS, AND PERIOSTEUM.

-1- DEVELOPMENTAL STAGE: LONG FORM OF COLLAGEN XII, XIIA, IS THE PREDOMIANAT FORM AT EARLY STAGES (ED? AND 11); AT LAFER STAGES OF PREDOMIANAT FORM AT EARLY STAGES (ED? AND 11); AT LAFER STAGES OF FORM. AS THE SHORT FORM SECOMES THE MAJOR FORM. AS THE SHORT FORM BECOMES THE MAJOR PRODUCT, THE LONG SPLICE FORM. AS THE SHORT FORM BECOMES THE MAJOR PRODUCT, THE LONG SPLICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMARY; SMO0327; VWA: 4.
SMARY; SMO0327; VWA: 4.
EXCRACELLULAR matrix; Connective tissue; Repeat; Hydroxylation;
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
24 POTENTIAL.
                                                                                                                                                                                                                                                                                                     PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT EACH END (BY STAILARITY). PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
               Dev. Dyn. 204:4432-445(1995).

-i- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
CONTAINING FIBRILS, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE
SURFACE OF THE FIBRILS, AND THE COLL AND NC3 DOMAINS MAY BE
                                                                                                                                                                                                                                                                                                                                                                            -i- PTM: GLYCÓŚYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY.
-i- SIMILARITY: COWTAINS 4 WWFA DOMAINS.
-i- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLLAGEN ALPHA 1(XII) CHAIN FIBRONECTIN TYPE-III 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD: MGI:88448; CO112al.
InterPro; IPR003087; COllagen.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FN_III.
InterPro; IPR003129; TSPN.
InterPro; IPR003129; TSPN.
InterPro; IPR002129; TSPN.
InterPro; IPR002129; TSPN.
InterPro; IPR0041; FN FN.
Pfam; PF00141; fn 3; 18.
Pfam; PF00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VWFA 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U25652; AAA99719.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00060; FN3; 16
SMART; SM00210; TSPN; 1
                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY
            development.";
                                                                                                                                                                                                                                                                                                   BIRTH.
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211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDRE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VEDIIKAINTEPYRGGSINTGKAMTYVREKIFVPNK-GSRSNVPKVMILITDGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 HEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGI
                                                                                                                                                                                                                     WITH CLASSING (NCI).

TO CHONDROITH SULFATE (POTENTIAL).

TO CHONDROITH SULFATE (POTENTIAL).

TO CHONDROITH SULFATE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

HYDROXYLATION (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY).
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() (POTENTIAL).
() (POTENTIAL).
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DOLY - THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.0%; Score 139; DB 1; Length 3067; 30.3%; Pred. No. 0.0053; 1.1ve 37; Mismatches 75; Indels 20
                                                                                                                                       NONHELICAL REGION (NC3).
TRIPLE-HELICAL REGION (COL2)
WITH 1 IMPERFECTION.
                                                                                                                                                                             NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION (COL1)
WITH 2 IMPERFECTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3FB5DEFB8A2CDB95 CRC64
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                     11.
12.
13.
14.
15.
15.
17.
                                                            FIBRONECTIN TYPE-III 1-
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 1
                                   FIBRONECTIN TYPE-III
                                                 FIBRONECTIN TYPE-III
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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                                                                                                                                 VWFA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA; 334094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 IHSILKKSCIEI---LAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   613 SFVLTQSICLRIEQELAA 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60; Conservative
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                                                                                                                                                                                                                            3064
802
883
983
868
22486
22948
22946
22960
22960
22960
23001
3001
3001
3003
1474
1568
1652
1757
1848
1938
2029
2208
2297
2501
2751
2899
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Best Local Similarity
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2533
2684
2684
3067
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2966
2969
2972
2972
2984
3001
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3015
3024
3027
3030
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704
1769
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2456
2752
 1388
1480
1569
1659
1758
1849
1939
2030
2209
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12;

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372 KEIRHTIILLTDGK--SNMGDSPKKAVTRIRELLSIEQNRDDYLDIYAIGVGKLDVDWKE 429
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PROSITE; PS00134; TRYPSIN_HIS: 1.
PROSITE; PS00135; TRYPSIN_SER: 1.
PROSITE; PS50234; VWFA: 1.
Complement pathway: Plasma; Glycoprotein; Hydrolase; Serine protease; Signal; Repeat; Sushi; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE-------NRQGYRTAS- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| | : : : | : : | :: | :: ERSQ------DVTEVITSLDSASYKDHENATGANTYEVLIRVYSMMQTQMDRLGMETSAW 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 -----VIIALTDGELHEDLFFYSEREANRSRDLGAI------VYCVGV-----KD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :|| :|| || || GHLNLYLLLDASQSVTEKDFDIFKKSAELMVERIFSFEVNVTVAIITFASQPKTIMSILS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 GGFDLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLR--MSFIVFSTRGTTLMKLTE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ED (GLCNAC. . .) (POTENTIAL).
D (GLCNAC. . .) (POTENTIAL).
D (GLCNAC. . .) (POTENTIAL).
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SUSHI 2.
SUSHI 3.
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InterPro; IPR001456; Sushi_SCR_CCP.
InterPro; IPR001254; Trypsin.
InterPro; IPR001255; vWFA.
Pfam; PF00084; sushi; 2.
Pfam; PF00099; trypsin; 2.
Pfam; PF00099; trypsin; 2.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM00032; CCP; 2.
SWART; SM00032; CCP; 2.
M60578; AAA37381.1; JOINED.
KEMBL; M57891; AAA63294.1; -...
PIR; A38876; C2MS.
HSSP; P00757; 1SCT.
MGPOPS; SO''
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                                                                                                                                                                                                                                                                                                                                         IShikawa N., Nonaka M., Wetsel R.A., Colten H.R.;

"Murine complement C2 and factor B genomic and cDNA cloning reveals
different mechanisms for multiple transcripts of C2 and B.";
J. Biol. Chem. 265:19040-19046(1990)

-1- FUNCTION: COMPONENT C2 WHICH IS PART OF THE CLASSICAL PATHWAY OF
THE COMPLEMENT SYSTEM IS CLEAVED BY ACTIVATED FACTOR C1 INTO TWO
THE COMPLEMENT C2B AND C2A. C2A. A SERINE PROTEASE, THEN COMBINES WITH
COMPLEMENT FACTOR 4B TO GENERATE THE C3 OR C5 CONVERTASE.

-1- CATALYTIC ACTIVITY: CLEAVES C3 IN THE ALPHA-CHAIN TO YIELD C3A AND
C13B. CLEAVAGES TAKE PLACE AT THE C-TERMINAL OF AN ARGININE RESIDUE.
-1- MISCELLANBOUS: C2 IS A MAJOR HISTOCOMPATIBILITY COMPLEX CLASS-III
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-!- SIMILARITY: CONTAINS 3 SUSHI (SCR) DOMAINS.
-!- SIMILARITY: CONTAINS 1 WHAS DOMAINS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                           01.MAX-1991 (Rel. 18, Created)
U-MAX-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Complement C2 precursor (EC 3.4.21.43) (C3/C5 convertase).
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Gaps

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PROSITE; PS50234; VWFA: 4. Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing. SIGNAL 1 24
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TRIPLE-HELICAL REGION (COL1)
WITH 2 IMPERFECTIONS.

NONHELICAL REGION (NC1).

TO CHONDROITIN SULFATE (POTENTIAL).

TO CHONDROITIN SULFATE (POTENTIAL).

TO CHONDROITIN SULFATE (POTENTIAL).

TO CHONDROITIN SULFATE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

HYDROXYLATION (BY SIMILARITY).

HYDROXYLATION (BY SIMILAR
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TRIPLE-HELICAL REGION (COL2)
WITH 1 IMPERFECTION.
                                                                                                                                                                                                                                                                                                                                             COLLAGEN ALPHA 1(XII) CHAIN. FIBRONECTIN TYPE-III 1.
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FIBRONECTIN TYPE-III II
FIBRONECTIN TYPE-III II
FIBRONECTIN TYPE-III II
FIBRONECTIN TYPE-III II
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FIBRONECTIN TYPE-III 2.
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FIBRONECTIN TYPE-III 4
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 7.
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FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
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          Interpro; IPR003961; FN III.
Interpro; IPR003962; FNIII_repeat.
Interpro; IPR003129; TSPN.
Interpro; IPR02035; VWFA.
Collagen.
                                                                                                                                                                    PRINTS; PRO0014; PNTYPEIII.
PRINTS; PRO0453; VWFADDMAIN.
SMART; SMO0060; FN3: 17.
SMART; SMO010; TSPN: 1.
SMART; SMO0327; VWA; 4.
                                                                                              Pfam; PF01391; Collagen; 4.
Pfam; PF00041; fn3; 18.
Pfam; PF02210; TSPN; 1.
Pfam; PF00092; vwa; 4.
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      RX MEDLINE-97288521; PubMed-9143499;
RA Gerecke D.R., Olson P.E., Koch M., Knoll J.H.M., Taylor R.,
Gerecke D.R., Olson P.E., Koch M., Knoll J.H.M., Taylor R.,
Hudson D.L., Champliaud M.-F., Olson B.R., Burgeson R.E.;
RT "Complete primary structure of two splice variants of collagen XII,
RT and assignment of alpha 1(XII) collagen (COL12A1), alpha 1(IX)
COL13GEN COL13GEN L. And alpha 1(XIX) collagen (COL12A1) to human
RT Genomics 41:236-24(1997).
RI GENOMICS THE FIBRILS, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE
CONTAINING FIBRILS, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE
CONTAINING FIBRILS, AND THE COLL AND NC3 DOMAINS MAY BE
LOCALIZED IN THE PRRIFIBRILLAR MATRIX (BY SIMILARITY).
CC SUBUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 kDa OF
CC SUBUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 kDa OF
CC SHORT FORM; ARE PRODUCES.
CO ALTERNATIVE PRODUCTS: 2 ISOCOMAS: A LONG FORM (SHOWN HERE) AND A
SHORT FORM; ARE PRODUCES.
CC SHORT FORM; ARE PRODUCES.
CC SHORT FORM; ARE PRODUCTS: 2 ISOCOMAS SPICIAL
CC SHORT FORM; ARE PRODUCTS: 2 ISOCOMAS SPICIAL
CC SHORT AND LONG ISOCOMA OR ANY COMBINATION OF LONG AND SHORT
CC SHORT AND LONG ISOCOMA OR ANY COMBINATION CELLS.
CC SHORT AND LONG ISOCOMA OR ANY COMBINATION CELLS.
CC CARCINOMA CELL LINE.
CC PLYM: THE TRIPEPLELELE TRILE APPROVED OF THE TRIPEPTIDE REPEATING
CC STATIARRY PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE STAINS (BY
CC STATIARRY.
CC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                      243 GNGFRHARNVDRV--LCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMK--AALQVS 298
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
INTERRUPTED HELICES (FACIT) FAMILY.
SIMILARITY: CONTAINS 4 WWFA DOMAINS.
SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (LONG AND SHORT FORM). MEDLINE-97288521; Pubmed-9143499;
                                                                                                                                                                                                                                                CAIC_HUMAN STANDARD: PRT; 3063 AA. 099715; 099716; 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) collagen alpha 1(XII) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, U73778; AAC51244.1; -.
EMBL, U73779; AAD40483.1; -.
HSSP, P02751; ITTF.
                                                                                                                                                     531 VGDPTSQHGKEFLVEDVII 549
                                                                                                                 299 MND-----GLSFISSSVII 312
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HSSP; P02751; 1:
MIM; 120320; -.
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Jaquinod M., van der Rest M., Deleage G., Penin F.;
Jaquinod M., van der Rest M., Deleage G., Penin F.;
Jaquinod M., van der Rest M., Deleage G., Penin F.;
Jaquinod M., van der Rest M., Deleage G., Penin F.;
Biochemistry 38:6479-6488(1999).
I-FONCTION: AN ADHESIVE ROLE BY INTEGRATING COLLAGEN BUNDLES. IT IS
PROBABLY ASSOCIATED WITH THE SURFACE OF INTERSTITAL COLLAGEN
WHICH STICKS OUT FROM THE FIRBIL AND PROTRUDES THE LARGE N-
TERMINAL GLOBULAR DOMAIN INTO THE EXTRACELLULAR SPACE, WHERE IT
MIGHT INTERACT WITH OTHER MATRIX MOLECULES OR CELL SURFACE
                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                           98 DREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYRT--ASVIIALTDGEL 153
                                                                                                                                                                                          154 HEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGI 211
                                                                       Gaps
                                                                                             44 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFST---RGTTLMKLTE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCULT: HOMOTRIMER (PROBABLE).
SUBCELLULAR LOCATION: Extracellular matrix.
TISSUE SPECIFICTY: WIDE TISSUE DISTRIBUTION; HIGH PRESENCE IN DENSE CONNECTIVE TISSUE IN SKELETAL MUSCLE.
PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trueb B.;
                                               Score 131; DB 1; Length 3063;
                                                                       75; Indels
 MISSING (IN SHORT ISOFORM). W; 75FEA78FA8E48293 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waelchli C., Trueb J., Kessler B., Winterhalter K.H., "Complete primary structure of chicken collagen XIV."; Eur. J. Blochem. 212:483-490(1993).
                                                                                                                                                                                                                                                                                                                                                  01-JUL-1993 (Rel. 26, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
01-MRT-2002 (Rel. 41, Last annotation update)
COllagen alpha 1(XIV) chain precursor (Undulin).
                                                         Pred. No. 0.024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        undulin.";
                                                                                                                                                                                                                                                                                                                             PRT; 1888 AA
                                                                     38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 402-1549 FROM N.A. MEDLINE=92339443; PubMed=1339349; Trueb J., Trueb B.; a variant of "Type XIV collagen is a variant of Eur. J. Blochem. 207:549-557(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99280705; PubMed-10350466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Embryo;
MEDLINE=93185668; PubMed-8444186;
           333189 MW;
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STRUCTURE BY NMR OF 1852-1885.
                                              7.6%;
                                                                                                                                                                                                                                          212 IHSILKKSCIEI---LAA 226
                                                                                                                                                                                                                                                                609 SFELTOSICLRIEGELAA 626
                                                                       59; Conservative
                                                                                                                                                                                                                                                                                                                             STANDARD;
 1188
25 118E
3063 AA;
                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTORS.
                                                                                                                                                                                                                                                                                                                          CA1E_CHICK
P32018;
VARSPLIC
SEQUENCE
                                              Query Match
                                                             Best Local
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                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; F...
SMART; SM00060; FN3; 7.
SMART; SM00210; TSPN; 1.
SMART; SM003210; TSPN; 1.
SMART; SM003217; VWA; 2.
PROSITE; PS50334; VWRA; 2.
EXTRACELlular matrix; Connective tissue; Repeat; Hydroxylation;
Collagen; Glycoprotain; Signal; 3D-atructure.
The collagen; Glycoprotain; Signal; 3D-atructure.
Collagen; Glycoprotain; Signal; 3D-atructure.
The collagen; Glycoprotain; Signal; 3D-atructure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                UNTERMITATE TRANSPORTED TO THE TRANSPORTED TO THE TRANSPORTED TO THE TRANSPORTED TO THE FIBER STOUCHED TO THE TRANSPORTED T
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CELL ATTACHNENT SITE (POTENTIAL).
CELL ATTACHNENT SITE (POTENTIAL).
WW. 39915BB9F46DB973 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.5%; Score 130; DB 1; Length 1888;
                                          ARE HYDROXYLATED IN ALL CASES AND BIND CARBOHYDRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIBROMECTIN TYPE-III 1.
FIBROMECTIN TYPE-III 2.
FIBROMECTIN TYPE-III 3.
FIBROMECTIN TYPE-III 4.
FIBROMECTIN TYPE-III 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NONHELICAL REGION (NC4).
TRIPLE-HELICAL REGION 1.
TRIPLE-HELICAL REGION 2.
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PDB: 189P; 25-FEB-99.
InterPro: 187000087; Collagen.
InterPro: 187000087; Collagen.
InterPro: 187000087; FN_III.
InterPro: 1870003962; FN_III.
InterPro: 187002035; VWFA.
Pfam: PF001391; Collagen; 4.
Pfam: PF001391; Collagen; 4.
Pfam: PF00041; fn3; 8.
Pfam: PF00092; VWa: 2.
PRINTS; PR00014; FNTYPEIII.
PRINTS; PR000143; VWFADOMAIN.
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              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                          156 DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII 212
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NCBI_TaxID=6239;
                                                                                                             213 HSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPF
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01-FEB-1994 (Rel. 28, Last sequence update)
11-CCT-2001 (Rel. 40, Last annotation update)
14-CCT-2001 (Rel. 40, Last annotation update)
17-CCT-2001 (Rel. 40, Last annotation update)
17-CCT-2005 3 in chromosome III (Fragment).
17-CCT-2005 3.
Caenorhabditis elegans.
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SEQUENCE FROM N.A.
SEQUENCE ROW N.A.
STRAIN-BRISTOL N2;
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Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
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SIMILARITY: CONTAINS 1 VWFA DOMAIN.
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CYTOPLASMIC (POTENTIAL).
EGF-LIKE 1 (PARTIAL).
EGF-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                            PRT; 3051 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00010; ASX_HYDROXYL; 28.

PS00022; EGF_1; 1.

PS01186; EGF_2; 5.

PS01187; EGF_CA; 1.

PS50024; SEA; 2.

PS50034; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 230423; CAA83007.1; -.
PIR; S42373; S42373.
HSSP; P02468; 1TLE.
WOLMPEP; T20G5.3; CE00478.
InterPro; IPR001051; BGF-like.
InterPro; IPR001061; EGF-like.
InterPro; IPR001081; EGF-Ca.
InterPro; IPR001081; EGF-Ca.
InterPro; IPR001082; SEA.
InterPro; IPR001082; SEA.
Ffam; PF00008; EGF; 30.
Pfam; PF01390; SEA; 2.
Pfam; PF01390; SEA; 2.
Pfam; PF01390; SEA; 1.
SWART; SW00179; EGF-CA; 1.
SWART; SW00179; EGF-Like; 38.
SWART; SW00200; SEA; 2.
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                                                                                                                                                                                                                                                            1267 NVYPCYRL 1274
                                                                                                                                                                                                                  273 SVEDTYLL 280
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P34576;
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                                                   542
                                                                                    121
                                                                                                                    601
                                                                                                                                                      --EGFERASEQIYYENRQGYR----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 174
                 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-91060568; PubMed=2246248;
MEDLINE-91.060568; PubMed=2246248;
Medrins R.N., Obborne-Lawrence S.L., Sinclair A.K., Eddy R.L. Jr.,
Byers M.G., Shows T.B., Duby A.D.;
"Structure and chromosomal location of the human gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cartilage matrix protein.";
J. Biol. Chem. 265:19624-19631(1990).
-!- FUNCTION: CARTILAGE MATRIX PROTEIN IS A MAJOR COMPONENT OF THE EXTRACELLULAR MATRIX OF NONARTICULAR CARTILAGE. IT BINDS TO
                 ----DLYFILDKSGSVLHH--WNEIYYFVEQLA
                                     ELFEIGRSKTRVGLIQYSDQIRHEFDLDQYGDRDSLLKGISETQ-YLTGLTRTGAAIQHM
                                                                                                                                                                                        602 VQEGF------SERRGARPQQSDIARVAIILTDGRSQDNV----TGPADSARKLSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                     HKFI--SPQLRMSFIVFSTRGTTLMKLTE--DREQIRQGLEELQKVLPG----GDTYMH-
                                                                                                                                                                                                                          175 VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 229
                                                                                                                                                                                                                                            649 TFAIGVTDHVLASELESIAGSPNRWFYV-DKFKDLDTRLRSMIQK-----AACPS 697
                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cartilage matrix protein precursor (Matrilin-1).
MATNI OR CRTM OR CMP.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrai Mammalia; Eutheria; Primates; Catarrhini; Hominia, Coll. TaxID=9606;
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EMBL, M55689; AAB38702.1; JOINED.
EMBL, M55681; AAA63902.1; JOINED.
EMBL, M55683; AAA63904.1; ALT_SEQ.
PIR; A37979; A37979.
HSSP, P05099; 1AQ5.
MIN; 118437; ---
INTERPRO; IPR002035; VWFA.
INTERPRO; IPR002035; VWFA.
Ffam; PF00008; EGF; 1.
Pfam; PF00092; VWa; 2.
PRINTS; PR00453; VWFADOMAIN.
SWART; SW00181; EGF; 1.
SWART; SW00181; EGF; 1.
SWART; SW00181; EGF; 1.
SWART; SW00181; EGF, 1.
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                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                   CYGGF
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P21941;
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Pred. No. 0.042;
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27.1%; Pre-
tive 31;
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Best Local Similarity 27.1%
Matches 64; Conservative
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A DEVELOPMENTAL ROLE IN REGENERATION.
SUBUNIT: TRIMER OF IDENTICAL CHAINE BACH CONTAINING 190 KDB OF NOWTRIPLE-HELICAL SEQUENCES (BY SIMILARITY).
DEVELOPMENTAL STAGE: EXPRESSION STARTS AT 3 DAYS AFTER AMPUTATION IN CELLS OF THE WOUND EPITHELIUM. AT DAY 10, IN CELLS OF THE BASAL LAYER OF THE WOUND EPITHELIUM. A DAY 10, THE DISTAL MESENCHYME CELLS. AT MID-BUD AND LATE-BUD BLASTEMA STAGES, WOUND EPITHELIUM EXPRESSION HAS DECREASED, WHEREAS THE MESENCHYME REMAINS STRONGLY ACTIVE IN TRANSCRIPTION AND SHOWED A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95246925; PubMed=7729585; MEDLINE-95246925; PubMed=7729585; MEDLINE-95246925; PubMed=7729585; Mei Y., Yang B.V., Klatt K.P., Tassava R.A.; Monoclonal antibody MT2 identifies the urodele alpha 1 chain of type XII collagen, a developmentally regulated extracellular matrix protein in regenerating newt limbs."; Protein in regenerating newt limbs."; Dev. Biol. 168:503-513(1995).

Dev. Biol. 168:503-513(1995).

- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-1-FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-1-FUNCTION: TYPE XII COLLAGEN THE COLL DOMAIN GOULD BE ASSOCIATED WITH THE SURPACE OF THE FIBRILS, AND THE COLL AND NC3 DOMAINS MAY BE SURPACE OF THE FIBRILS, AND THE COLL AND NC3 DOMAINS MAY BE SURPACE OF THE FIBRILS, AND THE MATRIX (BY SIMILARITY). COULD PLAY
                                                                                                                                                                                                                                                                                                                                                                                315 GLVQYSSSVRQEFPLGRFHTKKDIKAAVRNM-----SYMEKGTMTGAALKYLIDNSF 366
                                                                                                                                                                                                                                                                                                                                                                                                           134 ENROGYRTAS--VIIALIDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARI 191
                              Signal; Glycoprotein; Cartilage; Repeat; Coiled coil.
                                                                                                                                                                                                                                                                                                                           264 VCSGGGGS-----SATDLVFLIDGSKSVRPENFELVKKFISQIVDTLDVSDKLAQV 314
                                                                                                                                                                                                                                                                                                                                                      82 FIV---FSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY----Y 133
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                  24 ICAGQGGRREDGGPACYGGFDLYFILDKSGSVL-HHWNEIYYFVEQLAHKF-ISPQLRMS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADS--KDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGES---FQVVVRG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEPVAEHYFYTAD-FKTINQIGKKLGKKICVE---EDP---CACESLVKFQAKVEG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                      TVSSGARPGAQKVGIVFTDGRSQD----YINDAAKKAKDLGFKMFAVGVGNAVEDELREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha I(XII) chain (Fragment).
Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                                                                                         . .) (POTENTIAL)
                                                                                                                                                                                                                                                                          45;
                                                                                                                                                                                                                                                Length 496;
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                                                          CARTILAGE MATRIX PROTEIN.
                                                                                                           COLLED COLL (POTENTIAL).
N-LINKED (GLCNAC. . .) (
POTENTIAL.
                                                                                                                                                                                                                                                                           95;
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(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                7.0%; Score 120.5; DB 25.3%; Pred. No. 0.017;
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BY SIMILAR
POTENTIAL.
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EGF-LIKE.
VWFA 2.
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        EGF_2; 1.
VWFA; 2.
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496
222
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467
76
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227
227
249
496 AA;
                                                                                                                                                                                                                                                                    Similarity
          PS01186; PS50234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8316;
                                        domain;
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Best Local Simi
Matches 60;
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Q91145;
                                                                                                                     DOMAIN
CARBOHYD
                                                                                                                                                                                                                 SEQUENCE
            PROSITE;
PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 LKKSCIEILAA----EPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKP 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 RQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGY----RTASVIIALTDGELHED 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQI 102
                                                               --- PTM: THE TRIPLE-HELLICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT EACH END (BY STMILARITY).
--- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
TENDENCY TOWARD DISTAL REGIONALIZATION. CONDENSING CARTILAGE SHOW SIGNAL. FINALLY, AT THE LATE DIGIT STAGE, EXPRESSION BECOMES LARGELY RESTRICTED TO THE PERICHONDRIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    693 KKSLMDAVANLPYKGGNTNTGSALKFILENNF---RPGVGMREKARKIALLLTDGKSQDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVN-DGFQALQGIIHSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIBROWECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 8.
TO CHONDROITH SULFATE (POTENTIAL).
TO CHONDROITH SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00060; FN3; 5.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 2.
Extracellular matrix; Connective tissue; Repeat; Cell adhesion;
                                                                                                                                                                     -1- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY.
-1- SIMILARITY: CONTAINS 2 VWFA DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.8%; Score 118; DB 1; Length 929; 21.2%; Pred. No. 0.061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW; AE5D7485254FD954 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 6.
VWFA 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VWFA 1.
FIBRONECTIN 7
FIBRONECTIN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSVEDTYLLCPAPILKEVGMKAALQVSMN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003961; FN_III.
InterPro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U19494; AAA80217.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.2%;
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154
245
245
338
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612
805
907
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324
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Pfam; PF00092; vwa; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
57; Conserv
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98
929
929
                                                                                                                                                                   SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
155
246
339
433
520
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Search completed: August 9, 2002, 10:47:07 Job time: 830 sec

us-09-970-076-8.rsp

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 9, 2002, 10:44:32; search time 507.33 Seconds

(without alignments)
151.246 Million cell updates/sec

1131 1 MSFIVFSTRGTTLMKLTEDR.....STSGFKEGNSHPCLPARPHT 218 US-08-970-076-10 Perfect score: Sequence:

Scoring table:

3502263 seqs, 351980561 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: rotal number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Database :

Pending\_Patents\_AA\_Main:\*

1: /cgn2\_6/ptodate/2/paa/PCTUS\_COMB.pep:\*

3: /cgn2\_6/ptodate/2/paa/USO6\_COMB.pep:\*

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17: /cgn2\_6/ptodate/2/paa/USO9\_COMB.pep:\*

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22: /cgn2\_6/ptodate/2/paa/USO9\_COMB.pep:\*

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24: /cgn2\_6/ptodate/2/paa/USO9\_COMB.pep:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 10, Appl Sequence 2121, Ap Sequence 50, Appl Sequence 132, App Sequence 132, App Sequence 33, App Sequence 30, Appl Description Acho US-09-970-076-10 US-09-488-725A-2121 PCT-US99-31025-50 3 US-09-471-179-50 PCT-US99-31025-132 3 US-09-471-179-132 PCT-US99-31025-30 Match Length DB 100.0 100.0 85.4 85.4 85.4 85.4 Query Result

•	Sequence 51, Appl	, 6 , 6	ó,	σì	12	equence β,	'n	Sequence 94, Appl	621, A	621,	187	232,	6	125,	620,	620	194,	301,	105,	e 105,	1574,	574,	27, 4	27	56	Sequence 26, Appl	H	Sequence 107, App	N	Ś		9		57	⋖ .
	09-471-179-	6 US-09-223-546	8 US-09-471-179-	6-965-665-60-SD 6	1 US-09-796-753-	US-09-970-07	3 US-09-970-076	PCT-US00-30045	PCT-US01-11988	2 US	3 US-09-918-715-18	3 US-09-918-715	3 US-09-970-076	PCT-US00-30045	PCT-US01-11988	2 US-09-833-24	3 US-09-918-715	3 US-09-918-715-30	31025	71-179-10	-US01-16450-15	-US01-16450	PCT-US00-05226	-09-516-745	PCT-US00-05226-2	-09-516-745-2	-uS00-05226-1	-09-516-74	-US00-05226-2	-US00-05226-	-US00-05226-	PCT-US00-05226	-60-Sn 6	-09-516-74	0-SN 6
306	306	333	333	333	333	333	368	403	403	403	564	564	564	403	403	403	262	262	172	172	272	272	284	284	455	455	487	487	488	488	488	488	488	488	488
	85.4				85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	ŗ.	'n	5.	-	84.9	ä	ä	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7
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ထတ	10	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

APPLICANT: Young, John A.T.
APPLICANT: Bradley, Renneth A.
APPLICANT: Bradley, Renneth A.
APPLICANT: Bradley, Renneth A.
APPLICANT: Collier, Robert J.
APPLICANT: Mogridge, Jeremy S.
TITLE OF INVENTION: Anthrax Toxin Receptor FILE REFERENCE: 96026.9745
CURRENT PELING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR APPLICATION NUMBER: 60/251,481
PRIOR FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1 Sequence 10, Application US/09970076 GENERAL INFORMATION: ; ORGANISM: Homo sapiens US-09-970-076-10 US-09-970-076-10 SEQ ID NO 10 LENGTH: 218 PRT

Gaps ö Ouery Match 100.0%; Score 1131; DB 23; Length 218; Best Local Similarity 100.0%; Pred. No. 4.5e-112; Matches 218; Conservative 0; Mismatches 0; Indels 0;

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Gaps

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RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50, Application US/09471179
Sequence 50, Application US/09471179
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REPERENCE: 7853-173
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1999-1:2-23
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSFIVFSTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGY
                                                                                                                                                                                                                                                                                                                                                                                          1 MSFIVESTRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENROGY
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                                                                                                                                                                                                                                                                                                                 Score 966; DB 1; Length 274;
Pred. No. 2.9e-94;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
APPLICANT: Millennium Pharmaceticals, Inc.; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS TITLE OF INVENTION: ENCODING THEM; FILE REFERENCE: TOOMER'S POINT THEM STATES OF THE REFERENCE: 1983-173-228; CURRENT APPLICATION NUMBER: PCT/US99/31025; CURRENT APPLICATION NUMBER: 09/223,546; EARLIER APPLICATION NUMBER: 09/223,546; SARLIER APPLICATION NUMBER: 09/223,546; SARLIER FILING DATE: 1998-12-30; NUMBER OF SEQ ID NOS: 135; SEQ ID NO 50; SEQ ID NO 50; LENGTH: 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 85.4%; Score 966; DB 18; Best Local Similarity 98.9%; Pred. No. 2.9e-94; Matches 188; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                         Query Match 85.4%;
Best Local Similarity 98.9%;
Matches 188; Conservative
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US-09-471-179-50
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PCT-US99-31025-50
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US-09-471-179-50
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LENGTH: 274
                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                         GENERAL LINGUESTION:

APPLICANT: Hyseq Inc.

TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides

FILE REFERENCE: 784FLPCT

FILE REFERENCE: 784FLPCT

CURRENT APPLICATION NUMBER: US/09/488,725

PRIOR PILICATION NUMBER: US/09/488,725

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-06-20

PRIOR FILING DATE: 2000-07-19

PRIOR FILING DATE: 2000-07-19

PRIOR FILING DATE: 2000-09-14

PRIOR PLICATION NUMBER: US09/693,036

PRIOR FILING DATE: 2000-10-19

PRIOR PLICATION NUMBER: US09/727,344

PRIOR PLICATION NUMBER: US09/727,344

SOFTWARE: PL-FL-Genes_D Versions 1.0

SED ID NO 2121

LENGTH 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1131; DB 18;
100.0%; Pred. No. 7.1e-112;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KINDSVTLSKSLQSPWVSSTSGFKEGNSHPCLPARPHT 218
                                                                                                                                                                                                             PCT-US99-31025-50
; Sequence 50, Application PC/TUS9931025
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       Sequence 2121, Application US/09488725A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ), ORGANISM: Homo sapiens
US-09-488-725A-2121
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TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: ENCODING THEM
FILE REPERENCE: 7853-173-228
CURRENT ELLING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: 09/223,546
EARLIER APPLICATION NUMBER: 09/223,546
SERLIER FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 135
SEQ ID NO 30
LENGTHR: 306
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GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceticals, Inc.
ATTLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS;
TITLE OF INVENTION: ENCODING THEM
FILE REFERENCE: 7653-173-228
CURRENT APPLICATION NUMBER: PCT/US99/31025
CURRENT APPLICATION NUMBER: 09/223,546
EARLIER PELING DATE: 1999-12-23
EARLIER PILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
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Pred. No. 3.4e-94;
2; Mismatches 0; Indels
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; GENERAL INFORMATION:
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98.98;
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pcr-us99-31025-30
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Best Local Similarity
Matches 188; Conserv
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PCT-US99-31025-30
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PCT-US99-31025-51
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GENERAL INFORMATION:
APPLICANT: Holtzman. Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 7853-173
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: ENCODING THEM
FILE REFERENCE: 7853-173-228
CURRENT APPLICATION NUMBER: PCT/US99/31025
CURRENT APPLICATION NUMBER: 09/223,546
EARLIER APPLICATION NUMBER: 09/223,546
SALIER RILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 132
LENGTH: 301
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Pred. No. 3.3e-94;
2; Mismatches 0
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98.98;
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Best Local Similarity 98.9
Matches 188; Conservative
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; ORGANISM: Homo sapiens
US-09-471-179-132
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PCT-US99-31025-132
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260 KINDSVTLNE 269
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Query Match
Best Local Similarity 98.9
Matches 188; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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US-09-471-179-51
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233 KINDSVTLNE 242
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PCT-US99-31025-9
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                                                                                 Gaps
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TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 783-1738
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1999-12-23
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 306
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Pred. No. 3.4e-94;
2; Mismatches 0;
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Pred. No. 3.4e-94;
2; Mismatches 0;
                                                                                    2; Mismatches
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GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
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Local Similarity 98.9%;
hes 188; Conservative
                                                          Query Match
Best Local Similarity 98.9%;
Matches 188; Conservative
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ORGANISM: Homo sapiens
TYPE: PRT
ORGANISM: Homo sapiens
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KINDSVTLNE
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US-09-471-179-51
                         PCT-US99-31025-51
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US-09-471-179-30
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61 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
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TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM FILE REFERENCE: 7853-173
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Pred. No. 3.8e-94;
2; Mismatches 0; Indels
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sequence 9 Application PC/TUS9931025
sequence INFORMATION:
APPLICANT: Mileanium Pharmaceticals, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: ENCODING THEM
FILE REFERENCE: 7853-173-228
CURRENT APPLICATION NUMBER: PCT/US99/31025
CURRENT FILING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: 09/223,546
EARLIER APPLICATION NUMBER: 09/223,546
SEALIER POPOLICATION NUMBER: 1998-12-30
NUMBER OF SEQ. ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 3.4e-94;
2; Mismatches 0;
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                                  CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SEQ ID NO 51
LENGTH: 306
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61 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
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GENERAL INFORMATION:
Sequence 9, Application US/09599596
GENERAL INFORMATION:
DOUGLEM HOLTZMAIN: BOLD HOLTZMAIN: 1998-12-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FRANCE: PRACE PRACE HOLTZMAIN: BOLD HOLTZMAIN: BOLD HOLTZMAIN: BOLD HOLTZMAIN: BOLD HOLTZMAIN: BRACE FRANCE: BRACE FRANCE FRANCE: BRACE FRANCE: BRACE FRANCE: BRACE FRANCE: BRACE FRANCE FRANCE: BRACE FRAN
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Sequence 12, Application US/09796753

Sequence 12, Application US/09796753

GENERAL INFORMATION:
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999

CURRENT APPLICATION NUMBER: US/99796,753

CURRENT APPLICATION NUMBER: 09/183,175

PRIOR APPLICATION NUMBER: 09/183,175

PRIOR FILING DATE: 1998-10-30

PRIOR FILING DATE: 1998-11-30

PRIOR FILING DATE: 1998-12-30

PRIOR PLING DATE: 1998-10-2-26

PRIOR PLING DATE: 1999-02-26
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Pred. No. 3.8e-94;
2; Mismatches 0;
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Best Local Similarity 98.9%;
Matches 188; Conservative
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US-09-599-596-9
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260 KINDSVTLNE 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVF 120
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                                                                                                                                                                                                                                                                                                 APPLICANT: Holtzman, Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 0940/406001
CURRENT APPLICATION NUMBER: US/09/223,546
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09471179
GENERAL INFORMATION:
APPLICANT: HOLIZMAN. Douglas
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR APPLICATION NUMBER: 09/223,546
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 85.4%; Score 966; DB 16; Best Local Similarity 98.9%; Pred. No. 3.8e-94; Matches 188; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                          Sequence 9, Application US/09223546 GENERAL INFORMATION:
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Matches 188; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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   181 KINDSVTLSK 190
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US-09-471-179-9
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TYPE: PRT
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PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-29
PRIOR PRICATION NUMBER: 09/345,687
PRIOR FILING DATE: 1999-06-20
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR PRICATION NUMBER: 09/474,071
PRIOR PRILING DATE: 1999-12-29
PRIOR PRILING DATE: 1999-12-29
PRIOR PRILING DATE: 1999-12-29
PRIOR PRILING DATE: 2000-02-29
PRIOR PRILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/550,799
PRIOR FILING DATE: 2000-03-01
PRIOR PRILING DATE: 2000-06-14
PRIOR PRILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/559,596
PRIOR FILING DATE: 2000-06-22
PRIOR PRILING DATE: 2000-06-22
PRIOR PRILING DATE: 2000-06-22
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PRIOR PRILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/65,666
PRIOR PRIOR PRILING DATE: 2000-06-22
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CORGANISM: Homo sapiens
US-09-796-753-12
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Search completed: August 9, 2002, 10:44:32 Job time: 870 sec

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/ Iab_host="Daylou"
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AL542724 AL542724 AL542724 GI:12875049
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1 (bases 1 to 1063)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Evil-length cDNA libraries and normalization
Unpublished (2001)

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EWRY cedex - France
BP 191 91006 EWRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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BI869089
AV749755
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BE478445
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BE842906
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AK013005 Mus muscu
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BC2403057
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BG323538 602422195
A1466645 mg81d04.y
A1084806 oz80d12.x
AU129171 AU129171
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                                                                                                                                                                                                                                                                                                                           Description
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   13736207 segs, 6748477542 residues
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BIC326444
BIC3264444
BIC3264446
BIC32641561
BIC41333
BIC31333
BIC31333
BIC323538
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    nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0
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gb_htc:*
gb_gss:*
em_gss_hum:*
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Maximum DB seq length: 200000000
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Score

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Fotal number of

Database

Searched:

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

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Query Match 52.4%;
Best Local Similarity 95.4%;
Matches 839; Conservative
              Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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              ORGANISM
                                   REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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     cch 55.2%;
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BI823853.1 GI:
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/note="Organ: pooled brain, lung, testis; Vector:
pcMv-SPORT6; Site_1: Not!; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 237; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRv site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1.3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
101. Note: this is a NHLMG Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
Vertebrata; Euteleostomi;
                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11448 row: n column: 07
High quality sequence stop: 804.
Location/Qualifiers
I. 878
//ob_xref="Homo sapiens"
//ob_xref="Hamo sapiens"
//lab.host="MIH_MGC_115"
//ob_xref="MIH_MGC_115"
//ob_xref="MIH_MGC_115"
//ob_xref="MIH_MGC_115"
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                                   1 (bases 1 to 878).
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                Hominidae;
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  Craniata; Ve
Catarrhini;
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Pred. No. 5.8e-93;
0; Mismatches 29;
     Chordata;
                                Primates;
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BG281561 820 bp mRNA linear EST 21-FEB-2001 602402412F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4544691 5',
the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." 217 c 292 g 193 t
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48.7%; Score 688; DB 10;
Best Local Similarity 96.8%; Pred. No. 9.6e-86;
Matches 724; Conservative 0; Mismatches 20;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 963)

NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortum (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1276 row: c column: 21

High quality sequence stop: 718.
                                                                                                                                                                                                                                                                                                                                                                                                                                    963 bp mRNA linear EST 27-FEB-2001 mRNA sequence.

BG326444.1 GI:13132881
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/db_xref="taxon.9606"
/clone="itaxon.9606"
/clone=lib="NHH_WGC_14"
/tissue_type="renal call adenocarcinoma"
/lab_nost="DH10B (plage-resistant)"
/note="Organ: kidney; Vector: poTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5/ adaptor: GGCAGGAG(G): Size-selected >5000p for average insert size 1.8kb. Library constructed by Ling Hong in
                        480
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                                                  tgagagg--aaacggcttccgacatgcccg--caacgtggacaggg
                                                                                                                                                                                                                                                                                                                                                     ttcaagatcaatgactcggtcacactcaatgagaagccc 916
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Eukaryota; Metazoa;
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Mus musculus
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Carninci,P.
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/ Organism="Homo sapiens"
/ Abzref="Laxon:9606"
/ Clone="IMAGE:4244691"
/ Clone=lib="NIH_MGC_20"
/ (Lisue=!rpe="melanotic melanoma"
/ Lisue="Lope="melanotic melanoma"
/ Lisue="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: Goorgi: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5: adaptor: GGCACCAG(G). Size-selected >500bp for average insert size 1: 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 820)

2 (bases 1 to 820)

3 (bases 1 to 820)

4 (bases 1 to 820)

5 (bases 1 to 820)

5 (bases 1 to 820)

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8 (bases 1 to 820)

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                      Euteleostomi;
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Pred. No. 2.2e-85;
); Mismatches 19; Indels
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TITLE
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linear HTC 19-JAN-2002 cDNA, RIKEN full-length to CDNA FLJ10601 FIS,
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Shibate, Titch, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Shibate, K., Itch, M., Aizawa, K., Natsunai, T., Tashiro, H., Itch, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
Genome, Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA,
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HTC: CARP trapper.
Mus musculus (strain:C57BL/6J) 10, 11 days embryo CDNA tolone_lib:RIKEN full-length enriched mouse CDNA library
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Functional annotation of a full-length mouse CDNA mature 409, 685-690 (2001)

Capacas i to 1614)
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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BE741333 725 bp mRNA linear EST 15-SEP-2000 601594179F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948114 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 725)
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National Institutes of Health, Mammalian Gene Collection (MGC)
                              371 acaaccttaatgaaactgacagaagacagagaacaaatccgtcaaggcctagaagaactc 430
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                                                                                                                               cagaaaagttctgccaggaagaagacacttacatgcatgaaaggatttgaaagggccagtgag
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration Research Group in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGGAGAGGGTCTTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot - 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter.
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hili, D., Hiramoto, K., Haracka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itch, M., Izawa, M., Kosukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, H., Saito, R., Sahai, C., Sakai, K., Sano, H., Sasaki, D., Schimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Takahashi, T., Tayami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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...forganism="Mus musculus"
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/dev_stage="10, 11 days embryo"
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QGYRTASVIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADS
KDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNV
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IITTTHCSDGSILAIALLVLFLLLALALLUWWFWPLCCTVIIKEVPPPVEESEEEDDD
GLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKMPEQEYE
FPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTRFRGWR
                                                                                                                                                                                                                                                                                                                                                              Submitted (10-JUL-2000) roshihide Hayashizaki, The Institute of Physical and Chemical Research (RTKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="data source:SPTR, source key:Q9NVP3, evidence:ISS homolog to CDNA FLJ10601 FIS, CLONE NT2RP2005000
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Pred. No. 6.4e-85;
); Mismatches 91; Indels 0;
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Matches 736; Conservative
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BG281831 964 bp mRNA linear EST 21-FEB-2001 602403057F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4545302 5',
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/note="Organ: skin; Vector: pOTBn; Site_1: XhoI: Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCAGGGG(). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using 2AP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
241 c. 283 g. 203 t.
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I bases 1 to 904)
NIH-MCC http://mgc.ncl.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nlh.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCML30 row: a column: 15 High quality sequence stop: 659.
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                                       22 AGGACCCGCGAGGAAGGGCCCGCGGATGGCGCGTCCCTGAGGGTCGTGGCGGAGTTCGCGG
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Pred. No. 3.6e-71;
0; Mismatches 5; Indels
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/clone_lib="NIH_MGC_20"
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Best Local Similarity 98.3%;
Matches 641; Conservative
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BG281831
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Best Local Similarity
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/dp_xref="taxon:9606"
/db_xref="taxon:9606"
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adaptor: GGCACGGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r(mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM810 row: n column: 19
Plate: LLCM810 row: n column: 19
High quality sequence stop: 711.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 725;
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Pred. No. 8.5e-79;
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98.8%;
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 542)

Diass Neto, E., Garcia (Orrea, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
            /clone_lib="HT0209"
/dev.stage="Adult"
/note="Corgan: head_neck; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the PUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MRO-HT0209-280300-106-b03 HT0209 Homo sapiens cDNA, mRNA sequence.
BE146075
BE146075.1 GI:8608799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 tctccccgggctgcgggccatggccacggcggaggggagagcctcggcatcggcttcca
                                                                                                                                                                                                                                                                                                                                                                                                tgtgctgcaccactggaatgaatctattactttgtggaacagttggctcacaaattcat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   gtggctctctttggccactctggtgctcatctgcgccgggcaaggggacgcagggagga
                                                                                                                                                                                                                                       Length 513;
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                                                                                                                                                                                                                                     Score 493; DB 9; L. Pred. No. 7.8e-59; 0; Mismatches 5;
                                                                                                                                                   low stringency conditions."
150 c 127 g 128 t
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Best Local Similarity 99.0%;
Matches 496; Conservative C
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1 (bases I to 513)

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1 bolases I to 513,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/cripts/gethtml2.pl?tl-&t2=MRO-HT0209-280 300-106-909&t3-2000-03-28x(4-1) Seq primer: puc 18 forward High quality sequence start: 21 High quality sequence start: 21 High quality sequence storp: 513.
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MRNA sequence.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                   298
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                                                                   acttcattttggacaaatcaggaagtgtgctgcaccactggaatgaaatctattac-ttt
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MRO-HT0209-280300-106-909 HT0209 Homo sapiens CDNA, BE146084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE146084.1 GI:8608808
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                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MRO-HT0209-280
300-106-b03&t3=2000-03-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 51
High quality sequence start: 51
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gcgggccatggccacggcggagcggagagccttcggcatcggcttccagtggctcttt 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457 ttacatgcatgaaggatttgaaagggccagtgagcagatttattatgaaaacagacaagg 516
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          sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 472.2; DB 9;
Pred. No. 5.5e-56;
0; Mismatches 3;
                                                                                                                                                                                                                               1. .542
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0209"
                                                                                                                                                                                                                                                                                                                                                                                                                    33.48;
99.28;
                                                                                                   rel: +55-11-2704922
                                                                                                               Fax: +55-11-2707001
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This is a simpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MRO-HT0209-010
500-ll0-f09&t3=2000-05-01&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 30
High quality sequence stop: 487.
Location/Qualifiers
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/organism="Homo sapiens"

/organism="Homo sapiens"

/dolone_lib="HrWolog"

/dev_stage="Adult"

/note="Organis head_neck; Vector: puc18; Site_1: SmaI;

/note="Organis head_n
bE146355
MRO HT0209-010500-110-f09 HT0209 Homo sapiens CDNA, mRNA sequence.
BE146355
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 487)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                    BE146355.1 GI:8609079
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Homo sapiens
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BM050390 569 bp mRNA linear EST 07-NOV-2001 603632635F1 NIH_MGC_43 Homo sapiens CDNA clone IMAGE:5423217 5',
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 569)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                             1 TCAGGAAGTGTGCTGCACCACTGGAATGAAATCTACTACTTCGTGGAGCAGCTGGCTCAT
                                                                                                                                                                                                                                              495 tttattatgaaaacagacaagggtacaggacagccagcgtcatcattgctttgactgatg
                                                                                                                                                                                                                                                                                                    615 ttggtgcaattgtttactgtgttggtgtgaaagatttcaatgagacacagctggccgga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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High quality sequence stop: 569.
Location/Qualifiers
1. 569
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BM050390.1 GI:16779657
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(Dases 1 to 638)

NIH-MGC http://mgc.nci.nih.gov/.

NiH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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/organism="Mus musculus"
/strain="CZECH II (feral)"
/db_xref="taxon:10000"
/clone="INAGE:3589875"
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/tlssue=Lyppe="spontaneous tumor, metastatic to mam /clope:"DH10B"
              tgggggtccagcctgctacggcggatttgacctgtacttcattttggacaaatcaggaag
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85.8%; Pred. No. 1.3e-52;
.ive 0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
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BE369415.1 GI:9314778
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                  /clone_lib="NHLMGC_43"
/clone_lib="NHLMGC_43"
/clone_lib="NHLMGC_43"
/tissue_rype="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)" is ite_1:
/note="Organ: eye: Vector: poTB); Site_1: Xhoi; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/Xhoi sites using the following 5'
adaptor: GGCACGGG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
140 c 181 g 109 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 21-JUN-200
mRNA sequence.
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  465 bp mRNA linear
MRO-HT0209-100100-103-f09 HT0209 Homo sapiens cDNA,
BE145958
BE145958.1 GI:8608682
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 432; DB 10;
Pred. No. 1.8e-50;
0; Mismatches 10;
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates;
1 (bases 1 to 465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 30.6%;
al Similarity 95.7%;
511; Conservative
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Best Local S
Matches 511
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cloo_lib="Hq0209"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puci8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
Enail: aslmpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MRO-HT0209-100 100-103-f05&t3=200-001-105&t4=1)
Seq Primer: puz 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <del>.</del>;
                                                                                                                                                 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                   Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 8.3e-49;
0; Mismatches 13
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                                                                                                                                                                                                                                                                                                                                                                             High quality sequence start: 12
High quality sequence stop: 464
Location/Qualifiers
                                                                                         U.S.A.
                                                                                                                               Contact: Simpson A.J.G.
                                                                                           Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 29.7%;
Best Local Similarity 96.9%;
Matches 439; Conservative 0
                                                                                         Proc. Natl. Acad.
20202663
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                                                                           sequence tags
                 ,M.J., Soares
Simpson,A.J.
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
Mashington University School of Medicine
Mat44 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               539 bp mRNA linear EST 15-MAR-2000 mg81d04.yl Soares mouse embryo NbMEl3.5 14.5 Mus musculus cDNA clone IMAGE:439399 5', mRNA sequence.
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Mylle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R. and Wilson, R., Cardenas, M., McCann, R., McCann, R., Mopublished (1999)
                                                                                                                                                                                                                                                               396 acagagaacaaatccgtcaaggcctagaagaactccagaa-agttctgccagga-ggaga 453
                                                                                                                                                                                                                                                                                                                                                                                 276 actggaatgaaatctattactttgtggaacagttggctcacaaattcatcagcccacagt 335
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                                                                                                                                                                            439 ACAGAGAACAAATCCGTCAAGGCCTAGAAGAACTCCAGAACAGTTCTGCCAGGATGGAGA
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:439399"
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KEYWORDS
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/clone_inp="NIH_MGC_14"
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ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GCGAGCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (Gniversity of
Callfornia, Berkeley) using ZaP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                BG323538 1014_MGC_14 Homo sapiens cDNA clone IMAGE:4560214 5',
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 693)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM4268 row: n column: 23
High quality sequence stop: 571.
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Pred. No. 9.5e-45;
0; Mismatches 63; Indels
45 GCAGATTTATGAAAACTAGACAAGGTACAG 13
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4560214"
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KEYWORDS
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AUTHORS
TITLE
JOURNAL
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/clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                      27.0%; Score 381.2; DB 9; Length 539; 86.9%; Pred. No. 1.8e-43; Indels 0; Mismatches 63; Indels 0
                                                                                     Query Match
Best Local Similarity 86.9
Matches 419; Conservative
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CDNA encodin

Cartilage-associat EST clone GG874. Human cDNA clone (

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Human metastasis a Human immune syste Human immune syste Tumour suppressor Human immune syste

Human cervical can immune syste

Human immune syste Chemically treated

Human

Human secreted exp Human immune syste

Human 1mmune/haema

Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database

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Human; secreted protein; proliferative disorder; cancer; tumour; foctal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; pregnancy-related disorder; gastrointestinal disorder; pregnancy-related disorder; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; chromosome 19; ss.
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ABL33531
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Human 1mmune syste

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Macaque TANGO 232 Tumour suppressor

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26456786

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Result

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And Androis and Angulas corresponding to 28 human secreted protein genes, and Angulas -AAEG1513 represent the proteins they encode. AREG1514 -AAEG1544 -AAEG1543 represent the protein fragments or variants. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. The genes the protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the amount of the new genes. Specific uses are described for each of the proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allerdes, neurological disorders (e.g., Alzheimer's diseases, each asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, skin disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to culture of primary tissues, to regenerate tissues, to identify their comparate ligands or binding partners, and in chemotaxis, and in can be used and comparate is a propertine.
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Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human
                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid molecules encoding 28 human secreted proteins for {\it shoot} proventing, treating or ameliorating medical conditions and
/product= "Mature human secreted protein"
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2000US-0215133.
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30-JUN-2000;
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Sequence 2447 BP; 673 A; 562 C; 587 G; 625 T; 0 other;

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Score 1193.6; DB
Pred. No. 3e-283;
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AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode. AAE01514-FAAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the camount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the cand include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune disorders (e.g., Intemmation, allorages, neurological disorders (e.g., Alzheimer's disease, asthma, ethma, et
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166..1377
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AAD05334;
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skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell colluture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioinmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the invention.
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                                                                                                                           Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumaton; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; pregnancy-related disorder; kidney disorder; endocrine disorder; pregnancy-related disorder; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; chromosome 19; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_except= (pos:688..690, aa:xaa)
/transl_except= (pos:1123..1125, aa:Xaa)
/transl_except= (pos:1156..1158, aa:Xaa)
/transl_except= (pos:1267..1269, aa:Xaa)
/note= "Xaa equals any of the twenty naturally ocurring
L-amino acids"
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                                                                                     Human secreted protein-encoding gene 4 cDNA clone HWLFR02, SEQ ID NO:45
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bl nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, and 239 polypeptides useful for the treatment of asthma, rheumatoid
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prognosis; prophylatic; therapeutic; human; ds
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213..1214
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Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, postnasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachearia and autoimmune disease, osteoarthritis, Lyme's disease, cachearia and autoimmune disease, osteoarthritis, Lyme's disease, acahearia and autoimmune disease, osteoarthritis, Lyme's disease, acahearia and stroimmune clupus erythematosus. The nucleic acids are also useful for producing transpenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in cornsic biology, for diagnostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO colypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a colipped associated with aberrant TANGO expression. A wide range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 aggacccgcgaggaagggaccgcgggatggcgcgtccttgagggtcgtggcgagttcgcgg 169
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Pred. No. 1.5e-248;
0; Mismatches 1;
arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                                                                              cellular disorders can be treated
                         Claim 1; Fig 4; 209pp; English
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Best Local Similarity 99.9%;
Matches 1053; Conservative
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                  CCGBCatgcCcGcaacgtggacagggtcctctgcagcttcaagatcaatgactcggtcac
actcaatgagaagcccttttctgtggaagacacttatttactgtgtccagcgcctatctt
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Yang Y,
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Xu C, Xue AJ,
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Wang Z, Wehrman T, Xu
Zhou P, Goodrich R,
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2000US-0552317.
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09-JUL-2000;
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03-AUG-2000;
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19-OCT-2000;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and concainsed neuropathies and central nervous system diseases, auch as alzaheimer's, Parkinson's disease, Mutingfon's disease, amyotrophic cutilisation of the activity changes such as: Immune system suppression, Activin,Anhibin activity, chancer disagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and convergence of the patent did not form part of the printed
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99.8%; Pred. No. 7.6e
ive 0; Mismatches
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full-length cDNAs defined in the specification. Where a primer set

comprises: (a) an oligo-dT primer and an oligonucleotide complementary

to the complementary strand of a polynucleotide which comprises one of

the 5602 nucleotide sequences defined in the specification, where the

oligonucleotide comprises at least 15 nucleotides; or (b) a combination

of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to a

polynucleotide which comprises a 3'-end sequence, where the

coligonucleotide which comprises a 1'-end sequence, where the

coligonucleotide which comprises at least 15 nucleotides and the combination of

the 5'-end sequence, 3'-end sequence 15 selectide from those defined in

the specification. The primers are useful for synthesising polynucleotides,

particularly full-length cDNAs. The primers are also useful for the

detection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers are also useful for the

detection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers are also useful for the

detection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers are also useful for the

ANH3631 to AAH18412 represent human cDNA sequences; AAH362446 to

AAH3633 to AAH38412 represent human cDNA sequences; and AAH3629.
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               primer; detection; diagnosis; antisense therapy; gene therapy;
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by the
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, Otsuki
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A, Nagai K
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T, Wakamatsu
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11-JAN-2200; 2000JP-0118776.
02-MAX-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-02418997.
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   Length 1436;
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  Score 890; DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uncleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus host diseases, theumatoid arthritis, postriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Cohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachexia and autoimmune disease, osteoarthritis, Lyme's disease, cachexia and autoimmune clasease e.g. myasthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial cransgenic animals and for TANGO polypeptides themselves. Partial for pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                               TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host disease; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; Crohn's disease; chronic myelogenous leukemia; cancer; liver disease; Hodgkin's disease; osteoarthritis; lyme's disease; cachexita; altroimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus erythematosus; transgenic animal; diagnosis; prophylatic; therapeutic; mouse; ds.
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                                                                                                                                                                                                                               Location/Qualifiers
3.1148
/*tag= a
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/product= TANGO 197
                                                                               Murine TANGO 197 coding sequence.
         standard; cDNA; 4417 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 27; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                           98US-0223546.
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                                                          entry)
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P-PSDB; AAB01428.
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BP

(first entry)

1079

369

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899

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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saito K,
Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 3023; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA clone (5'-primer) SEQ ID NO:3023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                             29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MXY-2000; 2000JP-018376.
09-JUN-2000; 2000JP-0241899.
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                                                                                                 Homo sapiens
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Gaps

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21; Length 4417;

Score 453.2; DB 21; Length Pred. No. 3.6e-101; 0; Mismatches 53; Indels

Query Match 32.1%; Best Local Similarity 90.1%; Matches 485; Conservative

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us-09-970-076-1.rng

WO200151628-A2

The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oilgo-dT primer and an oilgouncleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oilgonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oilgonucleotide comprises a 3'-end sequence complementary to a
polynucleotide comprises a 1'-end sequence complementary to a
coligonucleotide comprises a 1'-end sequence therefore
the 5'-end sequence/3'-end sequence is selected from those defined in
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
converse assily without any specialised methods. AAH03166 to AAH13628 and
AAH13633 to AAH1874 represent human cDNA sequences? AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification the present invention. 

Sequence 464 BP; 101 A; 122 C; 141 G; 90 T; 10 other;

ï 251 291 311 351 53 ggaaaggcccgcgggatggcgcgtccctgagggtcgtggcgagttcgcggagcgtgggaag 112 231 371 411 gcatcggcttccagtggctctctttggccactctggtgctcatctgcgccgggcaagggg 191 Gaps ggaagggcccgcgggatggcgcgtccctgagggtcgtggcgagttcgcggagcgtgggaag 71 acaaatcaggaagtgtgctgcaccactggaatgaaatctattactttgtggaacagttgg ctcacaaattcatcagcccacagttgagaatgtcctttattgttttctccacccgaggaa gacgcagggaggatgggggtccagcctgctacggcggatttgacctgtacttcattttgg 1; Length 464; 24; Indels Score 368; DB 22; Pred. No. 1.1e-80; 0; Mismatches 24; 26.0%; 93.9%; Matches 388; Conservative Query Match Best Local Similarity 312 412 232 372 132 192 252 12 a a δ g ò ద ò g ö ö g ò δ g

Human breast cancer expressed polynucleotide 11500. Human; breast cancer; cell marker; cytostatic; ss. AAL19043 standard; cDNA; 356 (first entry) Homo sapiens 07-DEC-2001 AAL19043; AAL19043 RESULT 

The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is affilicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic New peptide useful as a marker for the diagnosis of breast cancer (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC Wang Y, Steinmann K; Claim 1; Page 2056; 3695pp; English. 2000US-0192099. 2000US-0193480. 2000US-0205230. 2000US-0211315. 2001WO-US00798 2000US-0189167 2000US-0220534 2000US-0176077 WPI; 2001-451856/48. Xu X, 24-MAR-2000; 29-MAR-2000; 15-MAY-2000; 09-JUN-2000; 25-JUL-2000; 10-JAN-2001; 14-MAR-2000; 14-JAN-2000; 19-JUL-2001 Lillie J, 

Gaps ö Length 356; Indels DB 22; 4.7e-76; Score 349; DB; Pred. No. 4.760; Mismatches 24.7%; Sccilarity 100.0%; Pr Conservative 0; Query Match Best Local Similarity Matches 349; Conserv

Sequence 356 BP; 91 A; 78 C; 95 G; 92 T; 0 other;

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635 127 695 187 755 247 815 307 67 8 ggtacaggacagccagcgtcatcattgctttgactgatggagaactccatgaagatctct tgtttcccgtgaatgacggctttcaggctctgcaaggcatcatccactcaattttgaaga tgtttcccgtgaatgacggctttcaggctctgcaaggcatcatccactcaattttgaaga agteetgeategaaattetageagetgaaceateceaceatatgtgeaggagagteattte ttggtgtgaaagatttcaatgagacacagctggcccggattgcggacagtaaggatcatg 128 188 156 216 89 989 969 g g q 음 δ g ö ð ö à

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AAL08133 standard; cDNA; 355 AAL08133

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100.0%; Pred. No. 8.3e-76;
ive 0; Mismatches 0;
                                     Human breast cancer expressed polynucleotide 590.
                                                                          breast cancer; cell marker; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Steinmann K;
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2000US-0192099.
2000US-0193480.
2000US-0205230.
2000US-0211315.
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07-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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nes 348; Conserv
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15-MAY-2000;
09-JUN-2000;
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                                                                                                                   Homo sapiens
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24-MAR-2000;
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(AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynocleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynocleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                   relates to human breast cancer expressed
                                                                           polynucleotide 18335
                                                                                                   Human; breast cancer; cell marker; cytostatic; ss
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2000US-0211315.
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2000US-0189167
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24-MAR-2000; 2
29-MAR-2000; 2
15-MAY-2000; 2
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                                                                                                                                                                                                                                                                                                                  TANGO 266; TANGO 216;; TANGO 261; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer; hematopoletic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardlovascular disorder; ischemic heart disease; hydrocephalus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a human TANGO 216 polypeptide. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differentiation and/or modulate cellular adhesion. The proteins can be used to treat any von Willebrand catotr-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS.
              cctgcatcgaaattctagcagctgaaccatccaccatatgtgcaggagagtcatttcaag 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                                                                                                                                                                                                                                                                                                                                                                                                               brain herniation; tatrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder;
819 ttgtcgtgagaggaaacggcttccgacatgcccgcaacgtggacag 864
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                                                                                                                                                                                                                                                                                      cDNA encoding a human TANGO 216 polypeptide
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                                                                                                                                                                             ВР
                                                                                                                                                                           AAA75149 standard; cDNA; 3677
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chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, cerebral oedema, hydrocephalus, brain herniations, istrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic
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Pred. No. 8.2e-75;
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Query Match
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Matches
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                                                                                                                                   taaagctggagaaactcttgatgtttcagtgagctttaatggaggaaaatctgtcatttc 1220
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                                           gctgggcagtcggaatggcagtgttctctgcacttacactgtaaatgaaacatatacaac 1100
                                                                              Novel human and murine secreted proteins designated TANGO 216, 261, 266, 266 and 267 useful as modulating agents of cellular processes, e.g. for treating cancer -
                        acatgocogoaacgtggacagggtcctctgcagcttcaagatcaatgactcggtcacact
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                                                                                                                                                                                                                                                                                                                                                                                                                      266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;
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AAA75157-59 encode human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO cellular proliferation, modulate cellular adhesion, modulate cellular adhesion. The polypeptides can be used to modulate cellular adhesion. The discrete extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions, modulate cell adhesion in proliferation, modulate cellular interactions, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematropoteic associated diseases and disorders, atelectasis, complete renal disorders, intestinal disorders, spleen associated disease, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disorders, intestinal disorders, spleen associated disease, modulate the proliferation, differentiation, as ischemic heart disorders disorders, treat cardiovascular disorders associated diseases or disorder. They may also be used to treat disorders associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral menhagitis, althemer's Disease, inflammations, bacterial and viral menhagitis, althemer's Disease, inflammations, bydrocephalus and encephalitis, and treat hepatic disorders.

Conterthe present sequence does not appear in the specification; it was not created using information provided.
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0; Mismatches
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Disclosure; Page -; 175pp; English.
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Fraser CC;

Sharp JD,

99US-0122458

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Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
                                                                       (MILL-) MILLENNIUM PHARM INC.
                         01-MAR-2000; 2000WO-US05226.
                                                                                                                                                                     262, 266 and 267 useful a
e.g. for treating cancer
                                                                                               Sarnes TM, Holtzman DA,
                                                                                                                     WPI; 2000-579269/54.
P-PSDB; AAB18456.
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modulate cell adhesion in proliferative disorders, such as cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, and cerebral oedema, hydrocephalus, brain herniations, latrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral choroplasmosis, parkinson's disease, multiple sclerosis, brain cancers, hydrocephalus and encephalitis, and treat hepatic disorders.

note: the present sequence does not appear in the specification; it was
                                                             AAA75157-59 encode human TANGO 216 proteins. The specification also describes TANGO 266, TANGO 261, TANGO 262, and TANGO 267. The TANGO polypeptides can be used to modulate cellular proliferation, modulate cellular differantiation and/or modulate cellular adhesion. The proteins can be used to tream you Willebrand factor-associated disorder, regulate extracellular matrix structuring, cellular adhesion, and cell trafficking and/or migration, modulate cellular interactions,
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Pred. No. 2e-74;
; Mismatches 4
Disclosure; Page -; 175pp; English.
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Best Local Similarity 57.0%;
Matches 671; Conservative
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controlled the control of 
bronchiectasis;
                                                                       brain herniation; latrogenic disease; inflammation; meningitis;
Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA75157-59 encode human TANGO 216 proteins. The specification also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes,
oedema; emphysema; chronic bronchitis; bronchial asthma; bronch
intestinal disorder; spleen associated disease; renal disorder;
cardiovascular disorder; ischemic heart disease; hydrocephalus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3677;
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                                                                                                                                                                                                                                                                                                                  "TANGO 216"
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                                                                                                                                                                                                                                     Location/Qualifiers 307..1773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262, 266 and 267 useful a e.g. for treating cancer
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P-PSDB; AAB18457.
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Best Local S
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Gaps

Indels

498;

Conservative

671;

Matches

Similarity

2e-74;

209 accccagagtgcgtgccgggtgactcccgccacctttgcgaccctcctgaggttagggga 268 gigggaaggagcggacccigciccccgggcigcgggccaiggccacggcggagcggag 123

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Search completed: August 9, 2002, 00:30:14 Job time: 8026 sec

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August 9, 2002, 10:46:58; Search time 31.3 Seconds (without alignments) 364.929 Million cell updates/sec
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1536
1 GGGRREDGGPACYGGFDLY......GLSFISSSVIITTHGSDGS 295
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                    Run on:
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

105224 segs, 38719550 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9h6x2 homo sapien	mus m	homo	homo	homo	P20702 homo sapien	gallu	P05555 mus musculu	mns		homo sa		caenor	notop	рошо	рошо	homo sa	042401 gallus gall	homo sa	mus m	Q02788 mus musculu	P51942 mus musculu		gallu	Q9ukx5 homo sapien		32	23	3 plasm	Omod (	homo	l homo	neise
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ITAL_CHICK CA36_CHICK CA36_CHICK ITAE_HUMAN ITAE_MOUSE ITAL_HUMAN V173 BORBU COCH_HUMAN ITAL_RAT ITAL_RAT ITAC_BOVIN
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285 3137 639 1179 1167 1151 341 550 642 1180
97 97 96 95.5 94.5 92.5 91.5 91.90
4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

## ALIGNMENTS

RESULT  AATR HUMAN  DD DT 01-M  AATR HUMAN  OOG BURDOO  OOG BURDOO
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Receptor;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120
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                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
EDDD -> NNIK (II ISOFORM 2).
EDDD -> NNIK (II ISOFORM 2).
NEKPESVEDTYLLCPAPILKEVGMKAALQV -> SKSLQS
WYSSTSGFREGUSHPCTPARPHT (IN ISOFORM 3).
                                                                                                         Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
                                                                                                                                                                                                                                                  MISSING (IN ISOFORM 3).
DGSILAIALLILFLL -> LHKIASGPTTAACME (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                              241 LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDGS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                               100.0%; Score 1536; DB 1; Length 564; 100.0%; Pred. No. 6.1e-120;
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01-MAR-2002 (Rel. 41, Last annotation update)
Antrax toxin receptor precursor (Tumor endothelial marker 8).
ATR OR TEM8.
                                                                                                                                                                    ASP/GLU-RICH (HIGHLY ACIDIC).
PRO-RICH.
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                          ANTRAX TOXIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                    ISOFORM 4).
MISSING (IN ISOFORM 4).
B118A00AD5DF2233 CRC64;
                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562 AA
                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                             POTENTIAL
                                     EMBL, AF279145; AAK52094.1; -.
EMBL, AK029429; BABL5128.1; ALT_INIT.
EMBL, AK001463; BAA91707.1; ALT_FRAME.
EMBL, BC012074; AAH12074.1; -.
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(Rel. 41, Last sequence)
                                                                                                                                                                                                                                                                                      62789 MW;
                                                                                Interpro; IPR002035; vWFA.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                 Conservative
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321
342
564
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Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                      564 AA;
                                                                                                                                                                                                                                                                                                                         Similarity
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184
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Best Local Simi
Matches 295;
                                                                         MIM; 606410;
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Q9CZ52;
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TRANSMEM
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CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        RA Kawai J., Shibadaa K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shibadaa R., Yoshino H., Adachi J., Fukuda S., Rawai J., Shibadaa R., Yoshino H., Adachi J., Fukuda S., Ra Arakawa T., Hara A., Enkunishi Y., Konon H., Kadachi J., Fukuda S., Yamanaka I., Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ra Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ra Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ra Kuchi P., Lewis S., Matsuo Y., Nikaido I., Reolle G., Quackenbush J., Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T., Ra Schriml L.M., Boildo T., Fletcher C., Fujita M., Gariboldi M., Ra Blake J., Boffelli D., Bojinga N., Carninci P., de Bonaldo M.F., Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Ra Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Ra Lyons P., Marchionni L., Mashima J., Mazzerlii J., Momberts P., Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Ra Nyabaw-Boris A., Yoshida K., Haseqawa Y., Kawaji H., Kohtsuki S., Rayashima J., Marashima J., Rayashima J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCPPPAPSAPTPPIPSPPSTLEPPPQAPPPNRAPPPSRPPP RPSV -> RFRGWRLTICLGSKHVHPGRHDKGPETPLLKQA WMFSSFLERAFQ (IN ISOFORM 2) 6AC92049B4BB4F7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
GRCINETRYKNSQPAKYPLNNTYHPSSPPPAPIXTPPPPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anthracis (By similarity).
SUBCELULAR LOCATION: Type I membrane protein (Probable).
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; seem to be produced by alternative splicing.
DOMAIN: Binding to PA seems to be effected through the VWA domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Glycoprotein; Signal; Alternative splicing.
                                                                                                                                                            "Cell surface tumor endothelial markers are conserved in mice and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y.;
Hayashizaki Y.;
Hayashizaki Y.;
Hayashizaki Y.;
Hauretional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).

-i- FUNCTION: Cellular role is not yet known.

-i- SUBGUNIT: Binds to the protective antigen (PA) of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASP/GLU-RICH (HIGHLY ACIDIC).
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=21443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein Kinzler K.W., St Croix B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL. CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (By similarity).
SIMILARITY: BELONGS TO THE ATR FAMILY.
SIMILARITY: CONTAINS 1 WWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 88-562 FROM N.A. (ISOFORM 2).
STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF378762; AAL11999.1; -.
EMBL; AK013005; BAB28591.1; ALT_INIT.
                                                                                                                                                                                                                                                          Cancer Res. 61:6649-6655(2001)
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InterPro; 1PR002035; vWFA.
PROSITE; PS50234; VWFA. 1.
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3319
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182
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477
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                                                                                                                                                                                                 121 ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ 180
                                                                                                                                                                                                                   61 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120
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                                                                                                 84
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                                                                                  25 GHGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHRFISPQLRMSFIVFS
                                                                  1 GOGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
                                                                                                                                                                                                                                                                  181 ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILINE-2153956; PubMed-11683410;
A MEDILINE-2153956; PubMed-11683410;
Bell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S.,
Bell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S.,
Bell S.E., Mavila A., Salezar R., Bayless K.J., Kanagala S.,
Differential gene expression during capillary morphogenesis in 3
T collagen matrices: regulated expression of genes involved in base
T membrane matrix assembly, cell cycle progression, cellular
differentiation and G-protein signaling.";
J. Cell Sci. 114:2755-2773(2001).
C -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
C -1- SIMILARITY: CONTAINS I VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                 241 LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDGS 295
                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL)
0F9B2D6688EAB17A CRC64;
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 Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAPILLARY MORPHOGENESIS PR
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capillary morphogenesis protein-2 precursor (CMG-2).
Score 1519; DB 1;
Pred. No. 1.6e-118;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2002 (Rel. 41, Created)
01-WAR-2002 (Rel. 41, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                386 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY040326; AAK77222.1; -.
PROSITE; PS50234; VWFA; 1.
Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
 98.98;
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
211
386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                  Similarity
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                  Local Simi
hes 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                              CMG2_HUMAN
P58335;
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SEQUENCE
   Ouery Match
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DOMAIN
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Wong D.A., Davis E.M., LeBeau M., Springer T.A.;
"Clonding and chromosomal localization of a novel gene-encoding a human beta 2-integrin alpha subunit.";
Gene 171:291-294(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH VCAMI.
MEDLINE=99059842; PubMed=9841932;
GraySON M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W.,
HOffman P.A., Staunton D.E., Bochner B.S.;
"alphadbeta2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule 1
                                                                                                                                                                                                                                                                                                                                                                           120 IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGF 179
                                                                                                                                                                                                                                                                                                                                                                                                           of the leukocyte integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D.E., Gallatin W.M.;
leukointegrin, alpha d beta 2, binds preferentially to ICAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A.
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Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITAD_HUMAN STANDARD; PRT; 1162 AA. 015379; 015575; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015576; 015
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MEDLINE-Sp[11956; PubMed-8777714;
Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T.,
Staunton D.E., Gallatin W.M.;
                                                                                                                                                           26 GPGGLLRAQEQPSCRRAFDLYFVLDKSGSVANNWIEIYNFVQQLAERFVSPEMRLSFIVF
                                                                                                                                                                                                                                                                                      1 GQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Length 386;
                                                                Indels
   DB 1;
                                                          43;
                                .4e-37
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MEDLINE=20187620; PubMed=10722744;
Noti J.D., Johnson A.K., Dillon J.D.;
"Structural and functional characterization of spee CD11d. Essential role of Spl and Sp3.";
J. Biol. Chem. 275:8959-8969(2000).
34.8%; Score 534.5;
llarity 57.1%; Pred. No. 4.46
Conservative 35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunity 3:683-690(1995).
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                                   Similarity
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                                   Local Simples 108;
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   Query Match
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                                                                                                         SUBCELLULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: EXPRESSED MODERATELY ON MYELOMONOCYTIC CELL LINES AND SUBSETS OF PERIPHERAL BLOOD LEUKOCYTES AND STRONGIY ON TISSUE-SPECIALIZED CELLS, INCLUDING MACROPHAGES FOAM CELLS WITHIN ATHEROSCLEROTIC PLAQUES, AND ON SPLENIC RED PULP MACROPHAGES.

-!- DOMAIN: THE INTEGRIN I DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS TO THE INTEGRIN ALPHA CHAIN FAMILY.

-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.

-!- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
"The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a binding interface between I domain and VCAM-1.";
J. Immunol. 163:1984-1990(1999).
-!- FUNCTION: INTEGRIN ALPHA-D/ETA-2 IS A RECEPTOR FOR ICAM3 AND VCAM1. MAY PLAY A ROLE IN THE ATHEROSCLEROTIC PROCESS SUCH AS CLEARING LIPOPROPEINS FROM PLAQUES AND IN PHAGOCYTOSIS OF BLOODBORNE PATHOGENS, PARTICULATE MATTER, AND SENESCENT ERYTHROCYTES FROM THE BLOOD.
                                                                                                   SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; WWFA; 1.
Integrin; Cell adheion; Receptor; Glycoprotein; Transmembrane; Signal; Repeat; Calcium;
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FG-GAP 5.
FG-GAP 6.
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FG-GAP 7.
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InterPro; IPR002035; vWFA.
Pfam; PF001839; FG-GAP; 5.
Pfam; PF00357; integrin_A; 1.
Pfam; PF00092; vWa; 1.
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EMBL; U40274; AAB60634.1; --
EMBL; U40275; AAB60635.1; --
EMBL; U40277; AAB60637.1; --
EMBL; U40277; AAB60637.1; --
EMBL; U40278; AAB60638.1; --
EMBL; U40278; AAB60638.1; --
EMBL; AF187881; AAF62875.1; --
HSSP; P11215; 1A8X.
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EMBL; AF18788;
HSSP; P11215;
MIM; 602453;
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MEDLINE-88190151; PubMed-2833753;
Arnaout M.A., Remold-O'Donnell E., Pierce M.W., Harris P., Tenen D.G.;
"Molecular cloning of the alpha subunit of human and guinea pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINES 8831503; PubMed-2457584; Miller L.J., Springer T.A.; Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.; The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD1D) alpha subunit. Cloning, primary structure, and relation to the integrins, von Willebrand factor and factor B."; J. Biol. Chem. 263:12403-12411(1988).
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01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CDILb) (Leukocyte adhesion receptor M (Neutrophil adherence receptor).
ITGAM OR CR3A OR CDILB.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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24.3%; Pred. No. 4.4e-05;
ive 50; Mismatches 119; Indels
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                                                     DISULFID
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MEDLINE-88257215; PubMed-2454931; Arnaout M.A., Gupta S.K., Plerce M.W., Tenen D.G.; Annout M.A., Gupta S.K., Plerce M.W., Tenen D.G.; Annino acid sequence of the alpha subunit of human leukocyte adhesion Gromplement receptor type 3)."; J. Cell Biol. 106:2153-2158(1988).
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MEDLINE-95171458; PubMed-7867070;
Lee J.O., Rieu P., Arnaout M.A., Liddington R.;
"Crystal structure of the A domain from the alpha subunit of integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T. RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
MEDLINE-96363671; PubMed-8747460;
Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                 MEDLINE-93123748; PubMed-8419480; Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.; Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-integrin gene family demonstrate remarkable conservation genomic organization and suggest early diversification during
                                                                                                                                                                                                                                                                                                         "cDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits."; Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
MEDLINE-98362595; PubMed=9687375;
Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
Fairbanks W.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,
Horton N.C., Kelley I.L., Mildner A.M., Moon J.B., Mott. J.E.,
Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;
"Cation binding to the integrin CD11b I domain and activation model
leukocyte adhesion glycoprotein Mol: chromosomal localization and homology to the alpha subunits of integrins. ^n; Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-87076671; PubMed=3539202;
Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.;
N'terminal sequence of human leukocyte glycoprotein Mol:
conservation across species and homology to platelet IIb/IIIa.";
                                                                                                                                                                                                                                                                                Hickstein D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L.,
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-9 FROM N.A.
MEDLINE=92073318; PubMed=1683702;
Shelley C.S., Arnaout M.A.;
The promoter of the CD11b gene directs myeloid-specific and developmentally regulated expression.";
Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92144986; PubMed-1346576;
Pabll H.L., Rosmarin A.G., Tenen D.G.;
"Characterization of the myeloid-specific CD11b promoter.";
Blood 79:865-870(1992).
                                                                                                                                                                                                                                                      SEQUENCE OF 9-1153 FROM N.A. MEDLINE-89098893; PubMed-2563162;

    Immunol. 150:480-490(1993).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CR3 (CD11b/CD18).";
Cell 80:631-638(1995).
                                                 SEQUENCE FROM N.A.
                                                                                                                                        SEQUENCE FROM N.A.
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MEDLINE-98226734; PubMed-9560195;

MEDLINE-98226734; PubMed-9560195;

Oxvig C., Springer T.A.;

RT "Experimental support for a beta-propeller domain in integrin alpha-
RT subunits and a calcium binding site on its lower surface.";

Proc. Natl. Acad. Sci. US.A. 95:4870-4875 (1998)

C. "Experimental support for a beta-propeller domain in integrin alpha-
RT subunits and a calcium binding site on its lower surface.";

PROC. Natl. Acad. Sci. US.A. 95:4870-4875 (1998)

C. "ENGTION: INTEGRIN ALPHA-N/ESTA-2 IS IMPLICATED IN VARIOUS
AS WELL. AS IN MEDIATING THE UPTAKE OF COMPLEMENT-COAPED PARTICLES.

THE THIRD COMPLEMENT COMPONENT. IT PROBABLY RECOGNIZES THE R-G-D
PETILISE IN CASE INTEGRIN ALPHA-N/RETA-2 IS ALSO A RECEPTOR FOR
FIBRINOGEN, FACTOR X AND ICAMI. IT RECOGNIZES PI AND P2 PEPTIDES
OF FIBRINOGEN GAMMA CHAIN.

C. SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-M
ASSOCIATES WITH BETA-2.

C. SUBGELLUIAR LOCATION: Type I membrane protein.

C. TESSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
-!- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
-!- SIMILARITY: CONTAINS I VWFA DOMAIN.
-!- SIMILARITY: CONTAINS I FG-GAP REPEATS.
-!- DATABASE: NAME-PROW; NOTE-CD guide CD11b entry;
WWW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd11b.htm".
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EMBL; M84477; AAAS1960.1; -
PIR; A31108; RWHU1B.
PIR; A56091; A26091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB24821.1; -
AAB24821.1; J
AAB24821.1; J
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AAB24821.1; J
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EMBL, J04145, A.
EMBL, S52127, A.
EMBL, S52154, A.
EMBL, S52154, A.
EMBL, S52154, A.
EMBL, S52154, A.
EMBL, S52157, A.
EMBL, S52161, A.
EMBL, S52161, A.
EMBL, S52167, A.
EMBL, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S52170;
S52173;
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S52181;
S52184;
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Carbbank; CCSD:33581; -. Carbbank; CCSD:33582; -. Carbbank; CCSD:33584; -.
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HSSP; P11215; 1A8X.
                                                                                                                                                                                                                                GRANULOCYTES.
                            p150,95 molecule.
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20
1108
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                                                       ERRATUM.
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12;
                                                                                                                                                                                                                                                                                                                                 200 FTFKEFQNNPNPRSLVKPITQLL--GRTHTATGIRKVVRELFNITNGARKNAFKILVVIT 257
                                                                                                                                                                                                                                                                                                                                                                                                          -----REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 123
                                                                                                                                                                                                                                                                                                                                                                                              124 DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKDFNETQLAR----IADS--KDHVFP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-8816645; Pubmed-3327687;
Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.;
"CDNA cloning and complete primary structure of the alpha subunit of a leukocyte adhesion glycoprotein, p150,95.";
EMBO J. 6:4023-4028(1987).
                                                                                                                                                                                                                                                                                                                     72
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c) (Leu M5).
ITGAX OR CD11C.
                                                                                                                                                                                                                                                                                                                     18 DLYFILDKSGSVL-HHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTED----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                 pfam; PF00357; integrin_A; 1.
Pfam; PF00092; vwa; 1.
PRINTS; PR01185; INTEGRANA.
PRINTS; PR00453; VWRADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWRA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                               Length 1152;
                                                                                                                                                                                                                                                                                                                                                                                                                                               175 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 223
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                               9.5%; Score 145.5; DB 1;
26.2%; Pred. No. 0.00032;
ive 45; Mismatches 81;
                                                                                                                                                                                                    Signal; 3D-structure; Repeat; Magnesium; Calcium; SIGNAL 1 16
                                                                                                                                                                                                                        INTEGRIN ALPHA-M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1163 AA.
                                                                                                                                                                                                                                                              FG-GAP 1.
                                                                                    InterPro; IPR000413; Integrin_alpha InterPro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                                         Local Similarity 26.2 nes 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                               CarbBank; CCSD:33581; -. CarbBank; CCSD:33582; -. CarbBank; CCSD:33584; -.
                                                                                                       Pfam; PF01839; FG-GAP; 5
                                                                                                                                                                                                                16
1152
1104
1128
1152
                   25-NOV-98.
01-AUG-96.
11-JAN-97.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                             MIM; 120980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITAX_HUMAN
                   1IDN;
1IDO;
                                        1JIM;
                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                  Query Match
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ITAX_HUMAN
                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                      DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECOGNIZES THE SEQUENCE G-P-R IN FIRRINGEN. IT MEDIATES CELL-CELL INTERACTION DURING INFLAMMATORY RESPONSES. IT IS ESPECIALLY IMPORTANT IN MONOCYTE ADHESION AND CHEMOTAXIS.
SUBJUNT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-X ASSOCIATES WITH BETA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
SIMILARITY: CONTAINS 1 VMFA DOMAIN.
SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
DATABASE: NAME-PROW; NOTE-CD guide CD11c entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11c.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and p150,95 leukocyte adhesion proteins.";
J. Immunol. 138:2381-2383(1987).
-!- FUNCTION: INTEGRIN ALPHA-X/BETA-2 IS A RECEPTOR FOR FIBRINOGEN.
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 20-43.
MEDLINE-87167596; PubMed=3549901;
Miller L.J., Wiebe M., Springer T.A.;
"Purification and alpha subunit N-terminal sequences of human Mac-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
MEDLINE=90153906; PubMed=2303426;
Corbi A.L., Garcia-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTEGRIN ALPHA-X.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                               rbi A.L., Garcia-Aguilar J., Springer T.A.;
Biol. Chem. 265:12750-12751(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M81695; AAA59180.1; -.
EMBL; Y00093; CAA68283.1; -.
EMBL; M29165; -; NOT_ANNOTATED_CDS.
EMBL; M29487; AAA51620.1; ALT_SEO.
EMBL; M29483; AAA51620.1; JOINED.
EMBL; M294843; AAA51620.1; JOINED.
EMBL; M294845; AAA51620.1; JOINED.
EMBL; M29485; AAA51620.1; JOINED.
EMBL; M294865; AAA51620.1; JOINED.
EMBL; M294865; AAA51620.1; JOINED.
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InterPro; IPR002035; vWFA.
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                                                                                                                                             Biol. Chem. 265:2782-2788(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01839; FG-GAP; 5.
Pfam; PF00357; integrin_A; 1.
Pfam; PF00092; vwa; 1.
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PRINTS; PR00453; WPFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
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Nishida Y., Obara
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                                                    site
  10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                131 LFFYSEREANRSRDLGAIVYCVGV------KDFNETQLARIAD--SKDHVFPVNDG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLDYKD-VIPMADAAGIIRYAIGVGLAFQNRNSWKELND----IASKPSQEHIFKVED- 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                           DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE-- 74
                                                                                                                                                                                                                                            (POTENTIAL).
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                                                                                                                                                                                                                                                                                   (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                  Length 1163;
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                             -> A (IN REF. 2).
-> D (IN REF. 2).
6C4E19CC3F62A473 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(XII) chain precursor (Fibrochimerin).
                                     FG-GAP 4.
FG-GAP 4.
FG-GAP 6.
FG-GAP 6.
FG-GAP 7.
POTENTIAL.
POTENTIAL.
POTENTIAL.
GFFRR MODIF.
BY SIMILARITY.
CGCNAC..)
N-LINKED (GLCNAC..)
N-LINKED (GLCNAC...)
(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                       89;
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24.8%; Pred. No. 0.00048;
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                                                                                                                                                                                                                                                                                                                                                                      43; Mismatches
CYTOPLASMIC
        FG-GAP 1.
FG-GAP 2.
VWFA.
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SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN;
MEDLINE-92011862; Pubmed-1918137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C_CHLLN
CA1C_CHICK
P13944; 004509;
01-JAN-1990 (Rel. 13, Created)
f 01-NOV-1997 (Rel. 31, Last seque
                                                                                                                                                                                                                                                                                                                   127885
                                                                                                                                                                                                                                                                                                                                                                       55; Conservative
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1022
1032
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490 49
756 75
1163 AA;
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NCBI_TaxID=9031;
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SEQUENCE
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REPEAT
DOMAIN
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MEDINE-95370352; PubMed-7642694;
MEDLINE-95370352; PubMed-7642694;
MCOCH M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;
Mcoch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;
Mcoch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;
Mcoch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;
Mcoch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M.;
Mcontaining Fightle, Miller M., Miller Colladen MITH The CONTAINING FIBRILS, THE COLL DOMAIN COULD BE ASSOCIATED WITH THE SIRRACE OF THE FIBRILAR MATRIX.

LOCALIZED IN THE PERRITIARILAR MATRIX.

LOCALIZED IN THE PERRITIAR MATRIX.

LOCALIZED IN THE PERRITIARILAR MATRIX.

LOCALIZED IN THE PERRITIARILAR MATRIX.

LOCALIZED IN THE PERRITIARILAR MATRIX.

LOCALIZED IN THE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINAL TISSUE OR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT OR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT ISOFORM CHAIRS. ONLY THE LONG VARIANT IS A PROTEOGLYCAN. THE LARGE ISOFORM HAS MORE RESTRICTED EXPRESSION IN EMBRYONIC TISSUE THAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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"The complete primary structure of type XII collagen shows a chimeric molecule with reiterated fibronectin type III motifis, von Willebrand factor A motifs, a domain homologous to a noncollagenous region of type ix collagen, and short collagenous domains with an Arg-Gly-Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LISSUE SPECIFICITY: TYPE XII COLLAGEN IS PRESENT IN TENDONS, . LIGAMENTS, PERICHONDRIUM, AND PERIOSTEUM, ALL DENSE CONNECTIVE TISSUES CONTAINING TYPE I COLLAGEN. DOMAIN: THIS SEQUENCE DEFINES FIVE DISTINCT DOMAINS, TWO TRIPLE-HELICAL DOMAINS (COLL AND COL2) AND THREE NONTRIPLE-HELICAL DOMAINS (NC1, NC2, AND NC3).

PTW: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT EACH END.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-1283 FROM N.A. (SHORT FORM), AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                             2846-2873.
MEDLINE=90062079; PubMed=2584192;
Gordon M.K., Gerecke D.R., Dublet B., van der Rest M., Olsen B.R.;
Grodon M.K., Gerecke D.R., Dublet B., van der Rest M., Olsen B.R.;
"Type XII collagen. A large multidomain molecule with partial homology to type IX collagen.";
J. Biol. Chem. 264:19772-19778(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end.";
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                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 2456-3124 FROM N.A., AND SEQUENCE OF 2772-2794 AND
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MEDLINE-87317590; Pubmed-3476925.
GOXDON M.K., GERCEKE D.R., Olsen B.R.;
"Type XII collagen: distinct extracellular matrix component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           discovered by cDNA cloning.";
Proc. Natl. Acad. Sci. U.S.A. 84:6040-6044(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Embryo;
MEDLINE=93042014; PubMed=1420368;
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Gaps

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01-NOV-1988 (Rel. 09, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MOI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                              131 LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIHS 188
                                                                                                                                                                                                                                                                                                          75 QIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHED 130
                                                                                                                                                                                                                                                                                 18 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDRE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BALB/C; TISSUE-Spleen; MEDLINE-86287312; PubMed-2942940; MEDLINE-86287312; PubMed-2942940; Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E., Larson R.S., Roberts T.M., Springer T.A.; T.A. and genomic DNA clone for the alpha subunit of the mouse complement receptor type 3 and cellular adhesion molecule Mac-1."; proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 ILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNV---DRVLCSFKINDSVTLNEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-85188276; PubMed-3887182; Springer T.A., Teplow D.B., Dreyer W.J.; Squence homology of the LFA-1 and Mac-1 leukocyte adhesion glycoproteins and unexpected relation to leukocyte interferon."; Nature 314:540-542(1985).
                                                                                                                                                                                                                                            36;
                                                                                                                                                                                             ; Score 143; DB 1; Length 3124;
; Pred. No. 0.0019;
51; Mismatches 97; Indels 31
              T -> S (IN REF. 4).
D -> E (IN REF. 4).
P -> A (IN REF. 2).
L -> F (IN REF. 2).
V -> F (IN REF. 2).
QP -> AG (IN REF. 3).
QP -> AG (IN REF. 3).
ISOFORM).
  SHORT
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  MISSING (IN
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MEDLINE=88312584; Pubmed=3044779;
                                                                                                                                            340578
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                                                                                                                                                                                                                                              65; Conservative
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|---EKSYLI 663
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PRINTS; PR0004; FNTYPEIII.
PRINTS; PR00453; VWTADOMAIN.
SMART; SM00060; FN3; 17.
SMART; SM00301; TSPN; 1.
SMART; SM00327; vWA: 4.
PROSITE; PS50234; VWRA, 4.
EXTracellular matrix; Connective tissue; Repeat; Hydroxylation;
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
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NUTH 2 IMPERFECTIONS (COLI)
ASPGU-RICH (ACIDIC)
ARG/LYS-RICH (BASIC).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
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(POTENTIAL)
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TRIPLE-HELICAL REGION (COL1)
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FIBRONECTIN TYPE-III 12.
FIBRONECTIN TYPE-III 13.
FIBRONECTIN TYPE-III 14.
FIBRONECTIN TYPE-III 15.
FIBRONECTIN TYPE-III 16.
FIBRONECTIN TYPE-III 16.
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FIBRONECTIN TYPE-111 3.
FIBRONECTIN TYPE-111 4.
FIBRONECTIN TYPE-111 5.
FIBRONECTIN TYPE-111 6.
FIBRONECTIN TYPE-111 7.
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N-LINKED GLCNAC...)
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FIBRONECTIN TYPE-III
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Interpro; IPR003961; FN_III.
Interpro; IPR003962; FnIII_repeat.
Interpro; IPR003129; TSPN.
Interpro; IPR002035; vWFA.
Pfam; PP001391; Collagen; 4.
Pfam; PP00041; fn3; 17.
Pfam; PP00041; fn3; 17.
Pfam; PP00092; vwa; 4.
      ; D00824; BAA00701.1; -.
x61024; CAA43388.1; -.
i, M17375; AAA48718.1; -.
j, J05137; AAA48655.1; -.
x67327; CAA47744.1; -.
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PIR; A28037; A28037.
PIR; A34485; A34485.
HSSP; P17301; 1AOX.
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Best Local Similarity 24.2%
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
FUNCTION: INTEGRIN ALPHA-M/BETA-2 IS IMPLICATED IN VARIOUS ADDESIVE INTERACTIONS OF MONOCYTES, MACROPHAGES AND GRANULOCYTES AS WELL AS IN MEDIATING THE UPTAKE OF COMPLEMENT-COATED PREFICLES.
IT IS IDENTICAL WITH CR-3, THE RECEPTOR FOR THE IG3B FRAGMENT OF PERTILE IN G3B. INTEGRIN ALPHA-M/BETA-2 IS ALSO A RECEPTOR FOR FOR FIBRINGEN, FACTOR X AND IAMA. MAPRA-2 PLAY A CRITICAL ROLE IN MAST CELL DEVELOPMENT AND IN IMMUNE COMPLEX-MEDIATED GLOMERULOREPHRITIS. MICE EXPRESSING A NULL MUTATION OF THE ALPHA-M SUBMINI GENE DEMONSTRATE INCREASE IN NEUTROPHIL ACCUMULATION, IN RESPONSE TO A IMPAIRED DEGRANULATION AND PHAGOCYTOSIS, EVENTS THAT
                                                                                                                                                                                                                      -!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
-!- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
-!- SIMILARITY: CONTAINS I VWFA DOMAIN.
-!- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
                                                                                                                                          APPARENTLY ACCELERATE APOPTOSIS IN NEUTROPHILS. THESE MICE DEVELOP
                                                                                                                                                                         ASSOCIATES WITH BETA-2.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN MONOCYTES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. ALPHA-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
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FG-GAP 4.
FG-GAP 5.
FG-GAP 7.
POTENTIAL.
POTENTIAL.
POTENTIAL.
BY SIMILARITY
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FG-GAP 2.
VWFA.
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InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO1185; INTEGRINA.
PRINTS; PR00453; VMFADOMAIN.
SMART; SM00191; Int_alpha; 4.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01839; FG-GAP; 5.
Pfam; PF00357; integrin_A; 1.
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1105
1129
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84
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HSSP; P11215; 1A8X.
                                                                                                                                                                                                               GRANULOCYTES.
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150 DIVFLIDGSGSI----NNIDF---QKMKEFVSTVMEQPFKKSKTLFS-----LMQYSDEFR 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 ----REQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYE-NRQGYRTASVIIALT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 IHFTFNDFKRNPSPRSHVSPIKQLNGRTKTASGIRKVVRELFHKTNGARENAAKILVVIT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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SUBUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 kDa OF NONTRIPLE-HELICAL SEQUENCES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFIS---PQLRMSFIVFSTRGTTLMKLTED-- 72
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STAIN-WANISS WEBSTER, AND C57BL/61; TISSUE-Skin;
MEDLINE-96170761; Pubmed-8601036;
Boehme K., Li Y., Oh P.S., Olsen B.R.;
Brinanty Structure of the long and short splice variants of mouse collagen XII and their tissue-specific expression during embryonic development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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-!- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 -SASITSN------GPLLGSVGSFDWAGGAFLYTSKDKVTFINTT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.2%; Score 141; DB 1; Length 1153; 24.2%; Pred. No. 0.00077; 1ve 50; Mismatches 96; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178DB988AECB0343 CRC64;
                      N-LINKED GLCNAC.
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15-JUL-1998 (Rel. 36, Last sequence update)
01-MR-2002 (Rel. 41, Last annotation update)
COllagen alpha 1(XII) chain precursor.
SIMILARITY
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16;

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ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINAL TISSUE FORM OF COLLAGEN XII MAY CONTAIN HOMOTRIMERS OF EITHER THE LONGER OR THE SHORTER ISOFORM OR ANY COMBINATION OF LONG AND SHORT ISOFORM CHAINS. ONLY THE LONG VARIANT IS A PROTEOGLYCAN. TISSUE SPECIFICITY: HIGHEST EXPRESSION IN TENDONS, PERICHONDRIUM, SKIN, CORNEA, SCIERA, BLOOD VESSELS, AND PERIOSTEUM.

DEVELOPMENTAL STAGE: LONG FORM OF COLLAGEN XII, XIIA, IS THE PREDOMINANT FORM AT EARLY STAGES (DF) AND 11); AT LAATER STAGES OF DEVELOPMENT (EDIS AND 17) THE SHORT FORM, XIIB, BECOMES THE MAJOR PRODUCT, THE LONG SPLICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0014; "WINTPELII.
PRINTS; PR00014; PR00051.
PRINTS; PR000519; TN3; 16.
SWART; SW00050; FN3; 16.
SWART; SW003210; TSPN; 1.
PROSTE; PS50234; VWPA; 4.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
                                                                                                                                                                                       VARIANT CONTINUES TO BE EXPRESSED IN SEVERAL TISSUES, EVEN AFTER
                                                                                                                                                                                                                      PTM: THE TRIPLE-HELICAL TAIL IS STABILIZED BY DISULFIDE BONDS AT EACH BOND (BY STAILARITY).
PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEAUNG UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
                                                                                                                                                                                                                                                                                                    PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
INTERRUPTED HELICES (FACIT) FAMILY.
SIMILARITY: CONTAINS 4 VWFA DOMAINS.
SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLLAGEN ALPHA 1(XII) CHAIN. FIBRONECTIN TYPE-III 1.
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InterPro; IPR000087; Collagen.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FN_III.
InterPro; IPR003129; TSPN.
InterPro; IPR002035; VWFA.
Pfam; PF001391; Collagen; 4.
Pfam; PF001391; Collagen; 4.
Pfam; PF00210; TSPN; 1.
Pfam; PF00092; VWa; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 QIRQGLEELQKVL-----PGGDTYMHEGFERASEQIYYENRQGYRT--ASVIIALTDGEL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDRE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 444 DIVFLVDGSYSIGTANFVKVRAFLEVLAKSFEISPNRVQISLVQYSRDPHTEFTLKEFNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                     TO CHONDROITIN SULFATE (POTENTIAL)
TO CHONDROITIN SULFATE (POTENTIAL)
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CELL ATTACHMENT SITE (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                            9.0%; Score 139; DB 1; Length 3067; 30.3%; Pred. No. 0.0039;
                                                                                                                                                                   HYDROXYLATION (BY SIMILARITY) HYDROXYLATION (BY SIMILARITY)
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U-MAY-1991 (Rel. 18, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Complement C2 precursor (EC 3.4.21.43) (C3/C5 convertase).
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SIMILARITY)
                                                          NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION (COL1)
WITH 2 IMPERFECTIONS.
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                            NONHELICAL REGION (NC3).
TRIPLE-HELICAL REGION (COL2)
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W; 3FB5DEFB8A2CDB95 CRC64;
                                                                                             NONHELICAL REGION (NC1).
                                                  WITH 1 IMPERFECTION.
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23.2%; Pred. No. 0.003;
Ive 56; Mismatches 115; Indels
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CHARGE RELAY SYST
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COMPLEMENT C2B F
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SUSHI 2.
SUSHI 3.
                                                                                                                 PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00032; CCP; 2.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM000327; WWA; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
InterPro; IPR000436; Sushi_SCR_CCP.
InterPro; IPR001254; Trypsin.
InterPro; IPR002035; wWFA.
Pfam; PF00084; sushi; 2.
Pfam; PF00089; trypsin; 2.
Pfam; PF00092; wwa; 1.
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    DORNAMA TETTT TETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                          ISHIAWA N., Nonaka M., Wetsel R.A., Colten H.R.;
"Murine complement C2 and factor B genomic and cDNA cloning reveals
different mechanisms for multiple transcripts of C2 and B.";
J. Biol. Chem. 265:19040-19046[1990].
-I- FUNCTION: COMPONENT C2 WHICH IS PART OF THE CLASSICAL PATHWAY OF
THE COMPLEMENT SEYSTEM IS CLEAVED BY ACTIVATED FACTOR C1 INTO TWO
FRAGMENTS: C2B AND C2A. A SERINE PROTEASE, THEN COMBINES WITH
COMPLEMENT FACTOR 48 TO GENERATE THE C3 OR C5 CONVERTASE.
-I- CATALYTIC ACTIVITY: CLEAVES C3 IN THE ALPHA-CHAIN TO YIELD C3A AND
C38. CLEAVES C5 IN THE ALPHA-CHAIN TO YIELD C5A AND C5B. BOTH
CLEAVAGES TAKE PLACE AT THE C-TERMINAL OF AN ARGININE RESIDUE.
-I- MISCELLANEOUS: C2 IS A MAJOR HISTOCOMPATIBILITY COMPLEX CLASS-III
                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: WITH COMPLEMENT FACTOR B.
-!- SIMILARITY: CONTAINS 3 SUSHI (SCR) DOMAINS.
-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
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MGD; MGI:88226; C2.
InterPro; IPR001314; Chymotrypsin.
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EMBL; M60563; AAA37380.1; JOINED
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M60577; AAA37381.1;
M60578; AAA37381.1;
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                                         SEQUENCE FROM N.A.
    NCBI_TaxID=10090;
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SIMILARITY). SIMILARITY). SIMILARITY).

(BY (BY (BY

FRAGMENT.

16;

Gaps

74;

(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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(POTENTIAL)
(POTENTIAL)
TISOFORM)

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Pfam; PF00092; vwa; 4.
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                         REPLIED FROW N.A., AND PARTIAL SEQUENCE (LONG AND SHORT FORM).

REPURENCE FROW N.A., AND PARTIAL SEQUENCE (LONG AND SHORT FORM).

REPURENCE FROW N.A., AND PARTIAL SEQUENCE (LONG AND SHORT FORM).

REPURENCE D.R., Olson P.F., Koch M., Knoll J.H.M., Taylor R.,

Hudson D.L., Champliaud M.F., Olson B.R., Burgeson R.E.,

RT "complete primary structure of two splice variants of collagen (COL9A1) alpha 1(XI)

RT "complete primary structure of two splice variants of collagen (COL9A1), and alpha 1(XII) collagen (COL12A1), alpha 1(XI)

RT "chromosome 6912-913."

CONTAINING FIBRILS, AND THE COL2 AND NG3 DOMAINS MAY BE CONTAINING FIBRILS, AND THE COL2 AND NG3 DOMAINS MAY BE CONTAINING FIBRILS, AND THE COL2 AND NG3 DOMAINS MAY BE SURPACE OF THE FIBRILS, AND THE COL2 AND NG3 DOMAINS MAY BE SURPACE OF THE FIBRILS, AND THE COL2 AND NG3 DOMAINS MAY BE SURPACE OF THE FIBRILS, AND THE COL2 AND NG3 DOMAINS MAY BE SURPACE OF THE FIBRILS. I SOFONES: A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE FINLA TISSUE SHORT FORM; ARE PRODUCED BY ALTERNATIVE OF LONG AND SHORT OF THE SHORTER ISOFONE OF ANY COMBINATIVE OF LONG AND SHORT OF THE SHORTER ISOFONE AND LONG FORM, SHEETAL SHORTER ISOFONE OF STRUCKES.

SHORT AND LONG ISOFONES APPEAR IN AMNION, CHORINON, SKELETAL SHORTE STOND IN LUNG, PLACENTA, KIDNEY, AND A SQUAMOUS CELL COLTAGEN IS FOUND IN LUNG, PLACENTA, KIDNEY, AND A SQUAMOUS CELL CORCINOMA CELL LINE.

CC CARCINOMA CONTAIN SOURCEDED OF THE CHARDEN CELL COLTAGEN CONTAIN C
                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PTM: GLYCÓGYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (PACIT) FAMILY.
-!- SIMILARITY: CONTAINS 4 VWFA DOMAINS.
-!- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                        PRT; 3063 AA
                                                                          CAIC_HUMAN STANDARD; PRT; 30 099715; 099716; 15-701-1998 (Rel. 36, Created) 15-701-1998 (Rel. 36, Last sequence up 01-MAR-2002 (Rel. 41, Last annotation collagen alpha 1(XII) chain precursor. COL12A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR000087; Collagen.
Interpro; IPR003961; FN_III.
Interpro; IPR003962; FNIII_repeat.
Interpro; IPR003129; TSPN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U73778; AAC51244.1; -. EMBL; U73779; AAD40483.1; -. HSSP; P02751; ITTF. MIM; 120320; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF01391; Collagen; 4. PF00041; fn3; 18. PF02210; TSPN; 1.
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InterPro;
                                                          HUMAN
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Gaps
                                                                                                                Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
SIGNAL 1 24 POTENTIAL.
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TRIPLE-HELICAL REGION (COL1)
WITH 2 LMPERFECTIONS.
NONHELICAL REGION (NC1).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
HYDROXYLATION (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
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HYDROXYLATION (BY SIMILARITY)
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SIMILARITY)
SIMILARITY)
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TRIPLE-HELICAL REGION (COL2)
WITH 1 IMPERFECTION.
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MISSING (IN SHORT ISOFORM).
MW: 75FEA78FA8E48293 CRC64;
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FIBRONECTIN TYPE-III 1.
VWFA 1.
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FIBRONECTIN TYPE-III 15
FIBRONECTIN TYPE-III 16
FIBRONECTIN TYPE-III 16
FIBRONECTIN TYPE-III 18
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FIBRONECTIN TYPE-III 5
FIBRONECTIN TYPE-III 6
FIBRONECTIN TYPE-III 7
FIBRONECTIN TYPE-III 8
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FIBRONECTIN TYPE-III
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PRINTS; PR00014; ENTYPEIII.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00060; EN3; 17.
SMART; SM00310; TSPN; 1.
SMART; SM00327; VWA; 4.
PROSITE; PS50234; VWFA; 4.
EXTRACELLULAR MATHIX; CONNECTI
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Best Local Similarity
Matches 59; Conserv
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13;

Conservative

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- :- SUBGNITT: HOMOTRIMER (PROBABLE).
- :- SUBGLILULAR LOCATION: EXTRAGELLULAR MATERIX.
- :- SUBGLILULAR LOCATION: EXTRAGELLULAR MATERIAR BOUNTER.
- :- TISSUE SPECIFICITY: WIDE TISSUE DISTRIBUTION; HIGH PRESENCE IN DENSE CONNECTIVE TISSUE IN SKRELFAL MUSCLE.
- :- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING OF THE TRIPEPTIDE REPEATING OF THE TRIPEPTIDE REPEATING OF THE TRIPEPTIDE REPEATING CONTAIN CYSTEINE RESIDUES INVOLVED IN INTER-AND INTRAMOLECULAR DISGULED BONDING.
- :- PTM: MAY CONTAIN CYSTEINE RESIDUES INVOLVED IN INTER-AND INTRAMOLECULAR DISGULED BONDING.
- :- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH CONTAINS 2 WARA DOMAINS.
- :- SIMILARITY: CONTAINS 2 WARA DOMAINS.
- :- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                            72 DREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYRT--ASVIIALTDGEL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TERMINAL GLOBULAR DOMAIN INTO THE EXTRACELLULAR SPACE, WHERE IT MIGHT INTERACT WITH OTHER MATRIX MOLECULES OR CELL SURFACE
                                                                              DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFST---RGTTLMKLTE
                                                                                                                        128 HEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Embryo;
MEDLINE-93185668: PubMed-8444186;
MEDLINE-93185668: Trueb J., Kessler B., Winterhalter K.H., Trueb B.;
"Complete primary structure of chicken collagen XIV.";
Eur. J. Blochem. 212:483-490(1993).
                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
01-OCT-1995 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(XIV) chain precursor (Undulin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-9339443; PubMed=1339349;
Trueb J., Trueb B.;
Truep XIV collagen is a variant of undulin.";
Eur. J. Blochem. 207:549-557(1992).
                                                                                                                                                                                                                                                                                              1888 AA.
                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                  609 SFELTOSICLRIEGELAA 626
                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                   186 IHSILKKSCIEI---LAA
                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                             CALE_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DV----NKVSREMQLDGFSFFAIGVADADYSELVNIGSKPSERHVFFVDD-FDAFTKIE 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1213 DELITFVCETASATCPLVFKDGDKLA-----GFKMMEMFGLVEKEFSAIDGVSMEPGTF 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 DREQIROGLEELQKVLPGGDTYMHEGFERASEQIYYENROGYRTA--SVIIALTDGELHE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 HSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPF
                                                                                                                                                                                                                                                                                                                                   PRINTS; PROOU4; FIVE ELIL.
PRINTS; PROO453; VWFADOMAIN.
SMART; SMO0060; FN3; 7.
SMART; SM0010; TSPN; 1.
SMART; SM00327; VWA; 2.
PROSITE; PS50234; VWFA; 2.
EXTRACELLULAR MATAIX; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NONHELICAL REGION (NC4).

TRIPLE-HELICAL REGION 1.

POLY-THR.

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .)
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W; 39915BB9F46DB973 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 130; DB 1; Length 1888;
Pred. No. 0.012;
44; Mismatches 116; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                          Collagen; Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLLAGEN ALPHA 1(XIV) CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                   EMBL; X70793; CAA50064.1; --
EMBL; X70792; CAA50063.1; --
FMRL; X66138; CAA4628.1; --
FMRL; S22916; S22916
PDB; 1B9P; 25-FEB-99.
InterPro; IPR000961; FN_III.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FNII_repeat.
InterPro; IPR003962; FNII_repeat.
InterPro; IPR003962; FNII_repeat.
InterPro; IPR003962; FNII_FPR0310; FRMPA.
FFam; PF001391; Collagen; 4.
FFam; PF001391; Collagen; 4.
FFam; PF0210; TSPN; 1.
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721
138
1398
1489
                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell adhesion;
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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PIR; 542373; CAA83007.1; -.

RYCMPEPP, 12026.3; CE00478

INTERFO: IPRO001561; BGF-like.

INTERFO: IPRO001825; SEA.

INTERFO: IPRO00081; SEA.

INTERFO: IPRO00091; SEA.

INTERFO: IPROFEER 
                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein T20G5.3 in chromosome III (Fragment).
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STRAIN=BRISTOL N2;
BETKS M., STITL A.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: CONTAINS 45 EGF-LIKE DOMAINS.
-! SIMILARITY: CONTAINS 2 SEA DOMAINS.
-! SIMILARITY: CONTAINS 1 VWFA DOMAIN.
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Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TENDENCY TOWARD DISTAL REGIONALIZATION. CONDENSING CARTILAGE SHOWS NO SIGNAL. FINALLY, AT THE LATE DIGIT STAGE, EXPRESSION BECOMES LARGELY RESTRICTED TO THE PERICHONDRIUM.
                                                                                                                                                                                                                                                      A DEVELOPMENTAL ROLE IN REGENERATION.
SUBUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 kDa OF NONTRIPLE-HELICAL SEQUENCES (BY SIMILARITY).
DEVELOPMENTAL STAGE: SEXPRESSION STARTS AT 3 DAYS AFTER AMPUTATION IN CELLS OF THE BASAL LAYER OF THE WOUND EPITHELIUM. AT DAY 10, EXPRESSION IS FOUND IN BOTH THE BASAL WOUND EPITHELIUM. AT DAY 10, THE DISTAL MESENCHYME CELLS. AT MID-BUD AND LATE-BUD BLASTEMA STAGES, WOUND EPITHELIUM EXPRESSION HAS DECRREASED, WHEREAS THE MESENCHYME REMAINS STRONGLY ACTIVE IN TRANSCRIPTION AND SHOWED A
            --EGFERASEQIYYENRQGYR----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 148
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PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS (BY
                                 602 VQEGF-----SERRGARPQQSDIARVAIILTDGRSQDNV----TGPADSARKLSIN
                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-1998 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Collagen alpha [KXII] chain (Fragment).
Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                     149 VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 203
                                                                  SIMILARITY: SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY.
-!- SIMILARITY: CONTAINS 2 VWFA DOMAINS.
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HSSP; P02731; IRNA.
InterPro; IPR003961; FN_III.
InterPro; IPR003035; VWFA.
Pfam; PF00041; fn3; 7.
Pfam; PF00092; VWa; 1.
SMART; SM00060; FN3; 5.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWA; 2.
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Jenkins R.N., Osborne-Lawrence S.L., Sinclair A.K., Eddy R.L. Jr.,
Byers M.G., Shows T.B., Duby A.D.;
"Structure and chromosomal location of the human gene encoding
cartilage matrix protein ";
J. Biol. Chem. 265:19624-19631(1990).
J. BIOL. CARTILAGE MATRIX PROTEIN IS A MAJOR COMPONENT OF THE
EXTRACELLULAR MATRIX OF NONARTICULAR CARTILAGE. IT BINDS TO
                                                                                                                             FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 8.
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
TO CHONDROITIN SULFATE (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Extracellular matrix; Connective tissue; Repeat; Cell adhesion; Collagen; Glycoprotein. Now_TER 1 1 ^{\rm 1}
                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                            7.7%; Score 118; DB 1; Length 929; 21.2%; Pred. No. 0.047; ative 51; Mismatches 135; Indels
                                                                                                                                                                                                              MW; AE5D7485254FD954 CRC64;
                                                 FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Carrilage matrix protein precursor (Matrilin-1).
MATN1 OR CRTM OR CMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN. SIMILARITY: CONTAINS 2 VWFA DOMAINS.
                                        VWFA 1.
FIBRONECTIN TFIBRONECTIN T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 FSVEDTYLLCPAPILKEVGMKAALQVSMN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               862 ---QEVYVRGTQTTTVLVGLKPETEYYVN 887
                                                                                                                     VWFA 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                              101647
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMOTRIMER.
                                                                                                                              907
>929
231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                     98
929
929 AA;
                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLLAGEN.
                                                                                                                                                                                                                                                                   57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAMA_HUMAN
P21941;
                                                                                                                                                                                                  NON_TER
SEQUENCE
                                                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                                                      CARBOHYD
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BINDING
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                                                                                 DOMAIN
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                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                     11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PROD453; VWFADOMAIN.
SMART; SM00181; EGF; 1.
SMART; SM00327; VWA; 2.
PROSITE; PS001082; EGF_1; FALSE_NEG.
PROSITE; PS50234; VWFA; 2.
EGF_1ike domain; Signal; Glycoprotein; Cartilage; Repeat; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 QEFPLGRFHTKKDIKAAVRNM-----SYMEKGTMTGAALKYLIDNSFTVSSGARPGA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --VIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADS--KDHVF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 CSGGGSSATDLVFLIDGSKSVRPENFELVKKFISQIVDTLDVSDKLAQVGLVQYSSSVR 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 GTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY----YENRQGYRTAS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 CYGG-----FDLYFILDKSGSVL-HHWNEIYYFVEQLAHKF-ISPQLRMSFIV---FSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COILED COIL (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGES---FQVVVRG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2D880A8114C7940F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARTILAGE MATRIX PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.4%; Score 113.5; Di
26.0%; Pred. No. 0.05;
ive 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY
SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VWFA 1.
EGF-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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                                                                                                                                                                                                JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
ALL_SEQ.
                                                                                                                                                                     EMBL, M55682; AAB38702.1; -...
EMBL, M55675; AAB38702.1; JOINED
EMBL, M55676; AAB38702.1; JOINED
EMBL, M55679; AAB38702.1; JOINED
EMBL, M55680; AAB38702.1; JOINED
EMBL, M55680; AAB38702.1; JOINED
EMBL, M55681; AAB38702.1; JOINED
EMBL, M55683; AAAS39702.1; JOINED
EMBL, M55683; AAAS39702.1; JOINED
EMBL, M55683; AAAS3970.1; ALT_SE
FIR; A37979; A37979.
HSSP, P05099; 1AQ5.
MIN, 115437; -..
InterPro; IPR000561; EGF-1ike.
InterPro; IPR002035; vWFA.
PFAM; PF00009; EGF; 1.
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BY
BY
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Best Local Similarity 26.09
Watches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222
263
453
495
76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249
265
496 AA;
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23
223
264
467
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